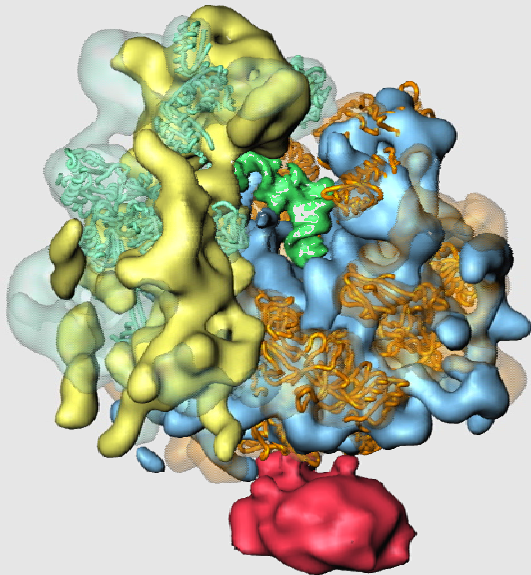
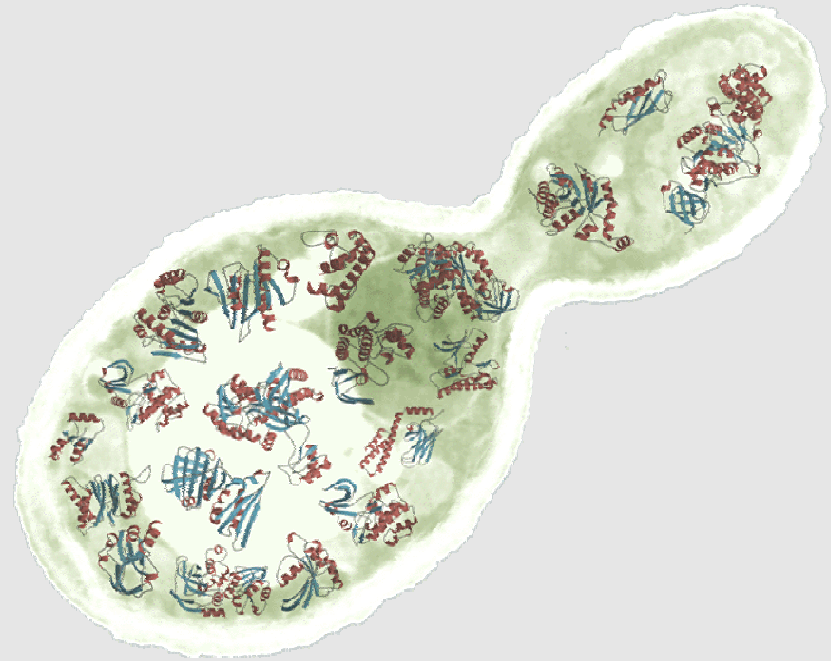
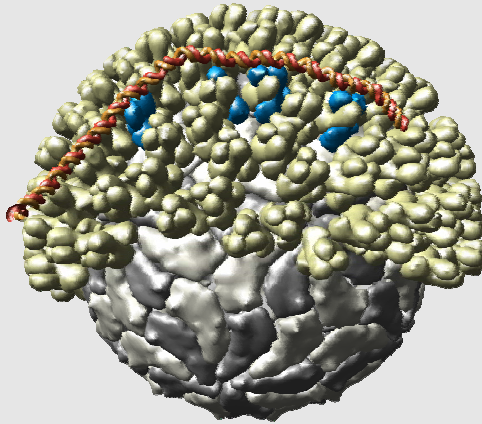


# UCSF Chimera Workshop



**Scooter Morris**

Resource for Biocomputing, Visualization, and Informatics  
University of California at San Francisco

UCSF

# Welcome

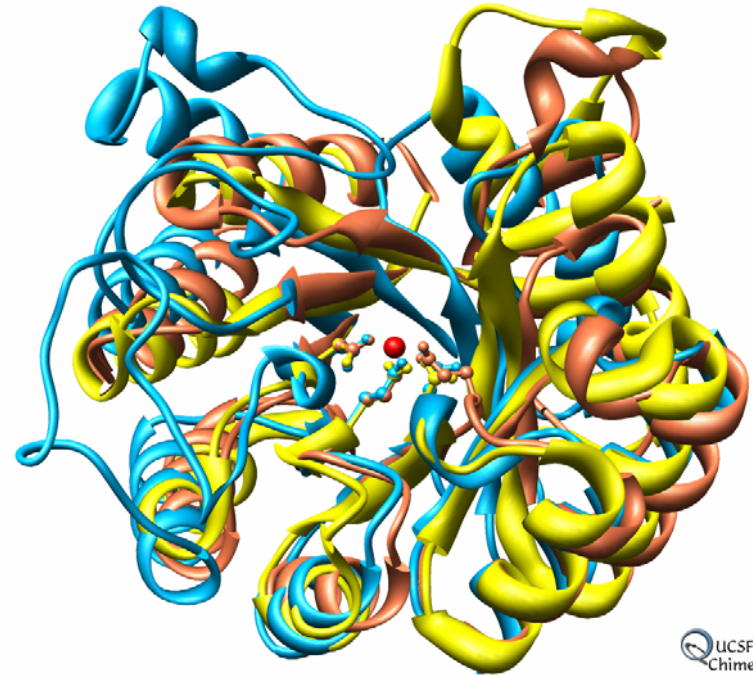
## Outline

Who we are

Why we're here

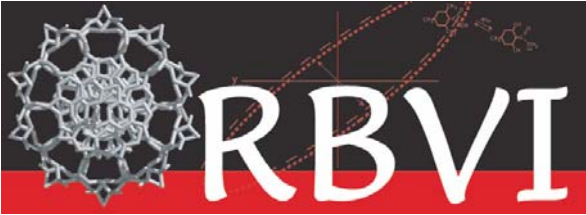
Today's agenda

High-level Chimera overview



UCSF  
Chimera

Alignment of three proteins in the enolase superfamily.



# Resource for Biocomputing, Visualization, and Informatics

We are an NIH Biomedical Technology Resource Center, funded by the National Center for Research Resources. We create innovative computational and visualization-based data analysis methods and algorithms, turn these into easy-to-use software tools which we distribute to the scientific community, and apply these tools for solving a wide range of genomic and molecular recognition problems within the complex sequence  $\rightarrow$  structure  $\rightarrow$  function triad.



**National Center for  
Research Resources**

# Sample application areas

Insight into molecular structure and function:

- Protein engineering

- Drug design

- Biomaterials design

- Annotation of protein function from sequence and structure

Gene annotation, characterization, and interpretation:

- Pharmacogenetics - understanding and prediction of variation in drug response due to genetic factors

- Mouse gene knock-outs for modeling of human disease

# UCSF Chimera - an Extensible Molecular Modeling System

Chimera is an extensible interactive 3-D modeling system designed to allow developers to quickly incorporate novel visualization algorithms and analysis tools

Chimera runs on laptops/desktops and takes maximum advantage of low-cost, state-of-the-art graphics chips

\$500 today buys you 3-D interactive graphics capabilities that cost \$20,000 five years ago

Chimera has extensive documentation for users and developers to enable effective scientific studies to be accomplished rapidly and with a "low entry barrier"



# Today's Presenters

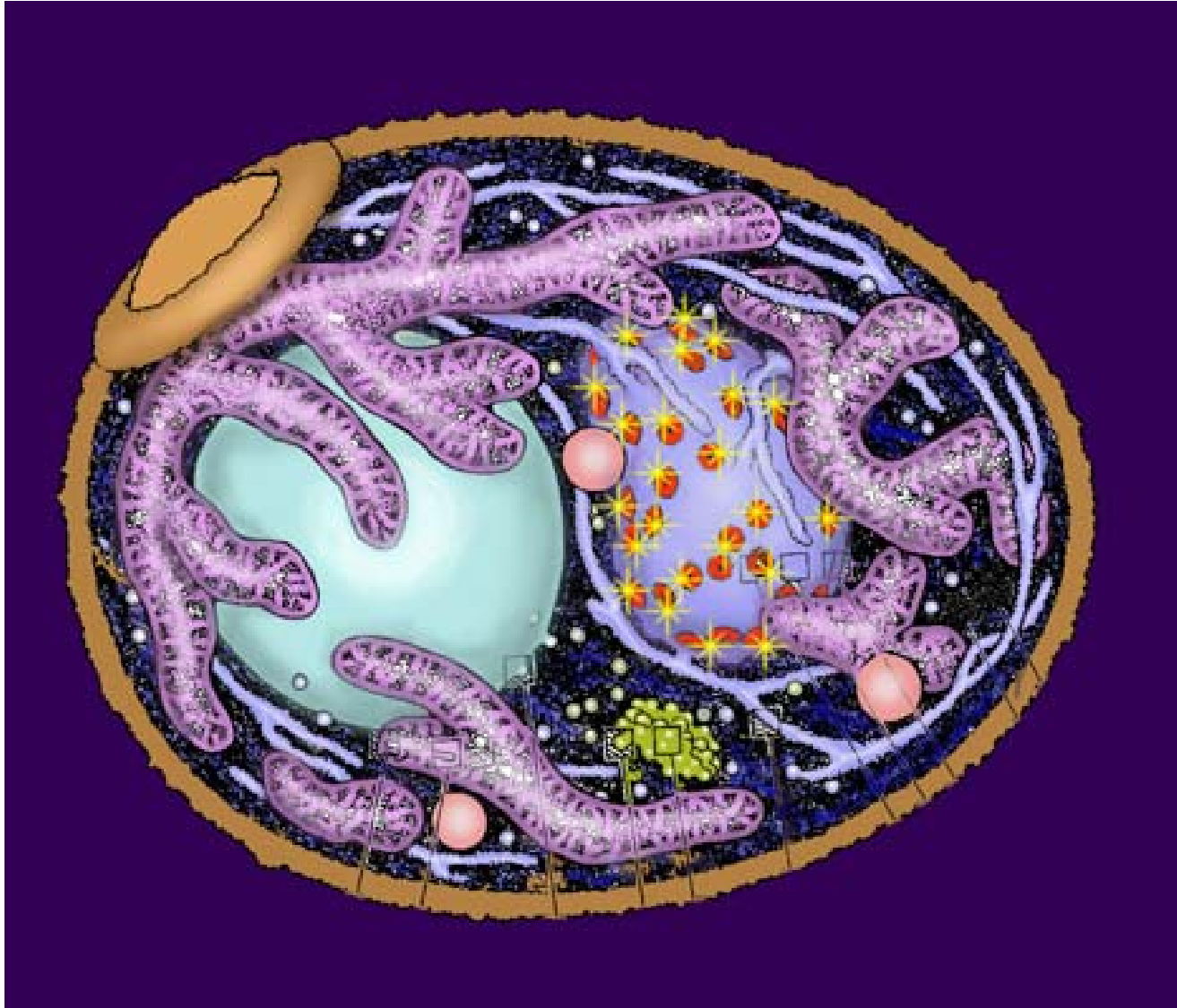
Scooter Morris	Executive Director, RBVI Chimera neophyte
Eric Pettersen	Chimera Developer Core system, Multalign viewer
Dan Greenblatt	Chimera Developer Collaboratory, Demo, Movie Recorder
Dr. Elaine Meng	Scientific Advisor Demos, Documentation, Tutorials
Tom Goddard	Chimera Developer Multiscale, Volume Visualization

# We We're Here

NCRR resource requirements:

- Research and Development
- Collaborative Research
- Service and Support
- Training
- Dissemination

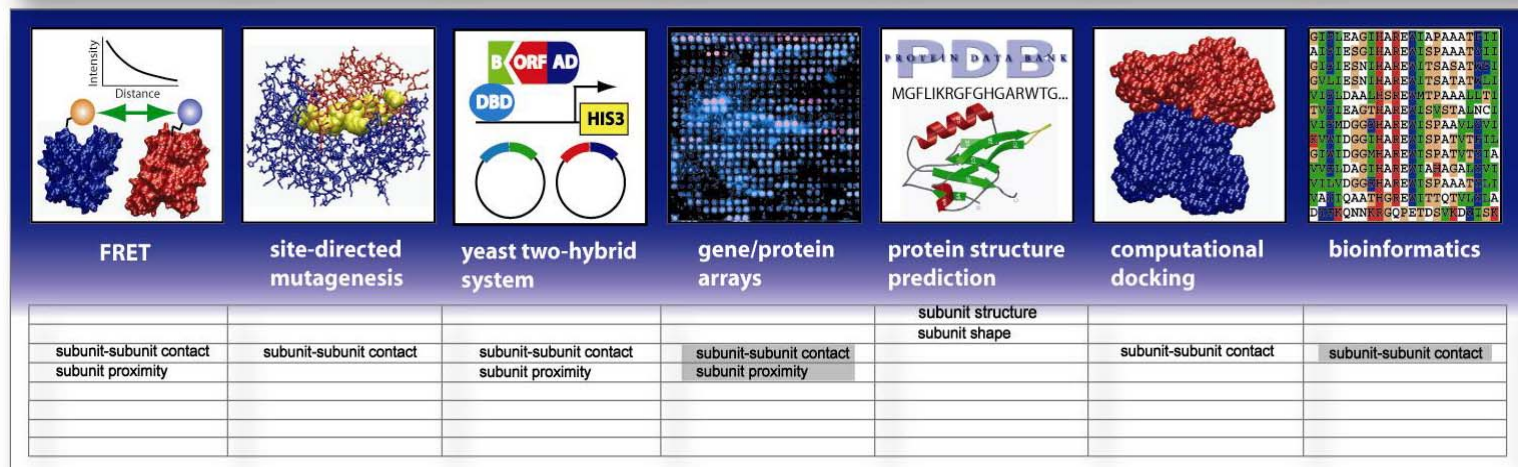
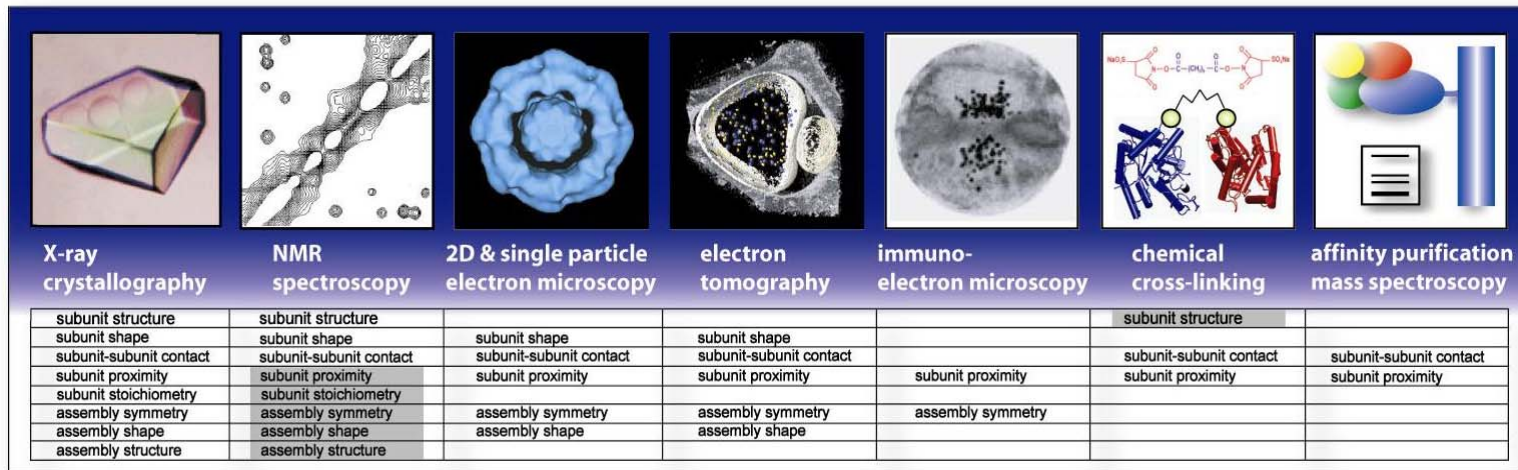
# Cell





# Determining the Structures of Proteins and Assemblies

Structural information from...  
 source: measurement and models  
 resolution: low or high resolution



Sali, Earnest, Glaeser, Baumeister. From words to literature in structural proteomics. Nature 422, 216-225, 2003.

# Documentation and Distribution

## Documentation

- Extensive User's Guide
- Basic Programmer's Guide

## Training

- Several on-line tutorials
- Periodic workshops

## Platforms

- Windows 98/2000/XP
- Mac OS X
- Linux, SGI, HP Alpha

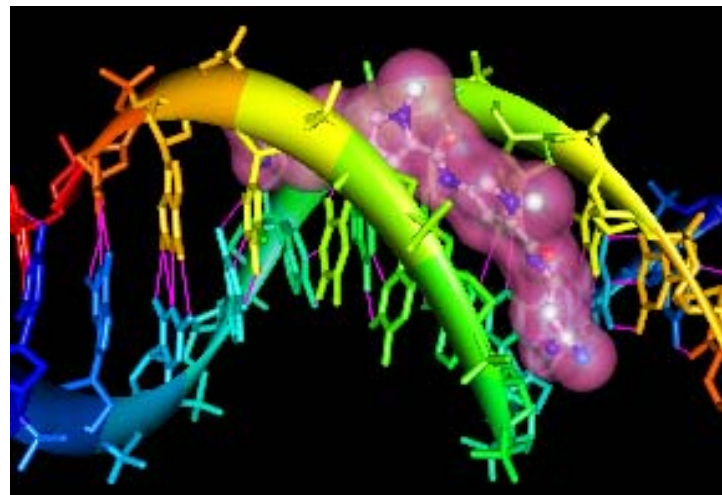
## Availability

- Download from our Research Resource Center web site after simple "click to accept" license agreement  
URL: <http://www.cgl.ucsf.edu/chimera>
- Releases ~1.5/year
- Snapshots ~3-4/year
- Check web site often!

# Chimera's Built-in Features

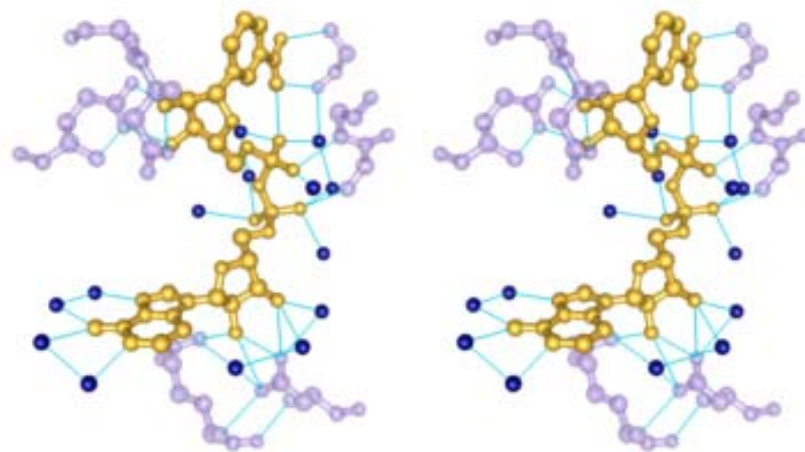
## Molecular Graphics:

- ✓ interactively manipulate stick, ball-and-stick, CPK, ribbon representations, and molecular surfaces
- ✓ highly intuitive model translation, scaling, and rotation
- ✓ interactive color editing
- ✓ ability to save high resolution images for presentation and publication
- stereo viewing



## Chemical Knowledge:

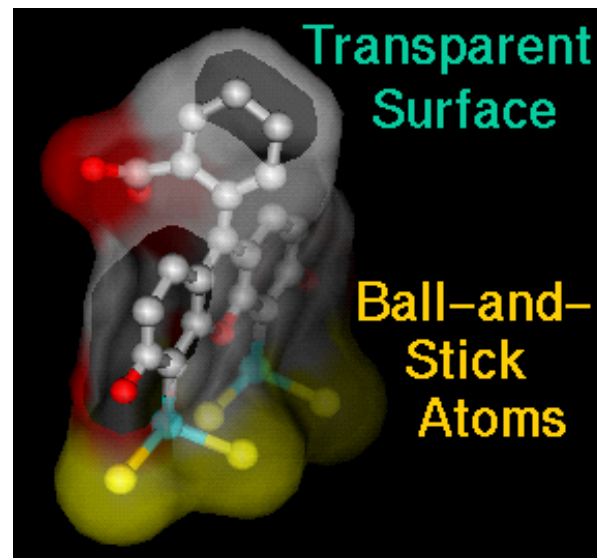
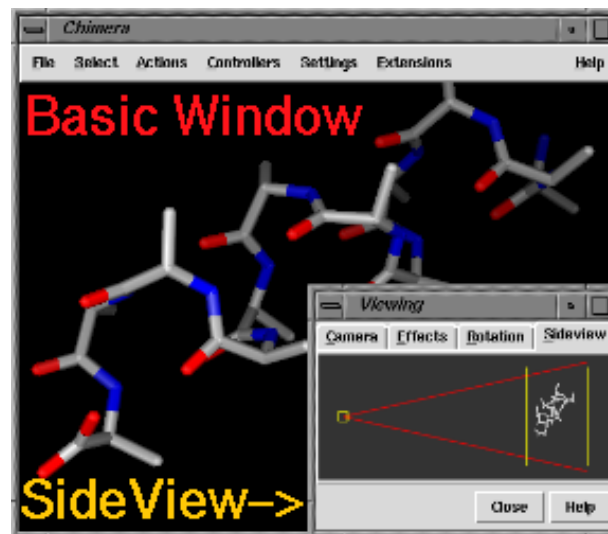
- ✓ determination of atom types in arbitrary molecules
- ✓ ability to add hydrogen atoms
- ✓ high-quality hydrogen bond identification
- ✓ selection of atoms/bonds by element, atom type, functional group, and amino acid category
- ✓ interactive bond rotation, distance, and angle measurements



# Chimera's Programmability/Extensibility

Chimera is designed to allow developers to quickly incorporate novel algorithms and analysis tools

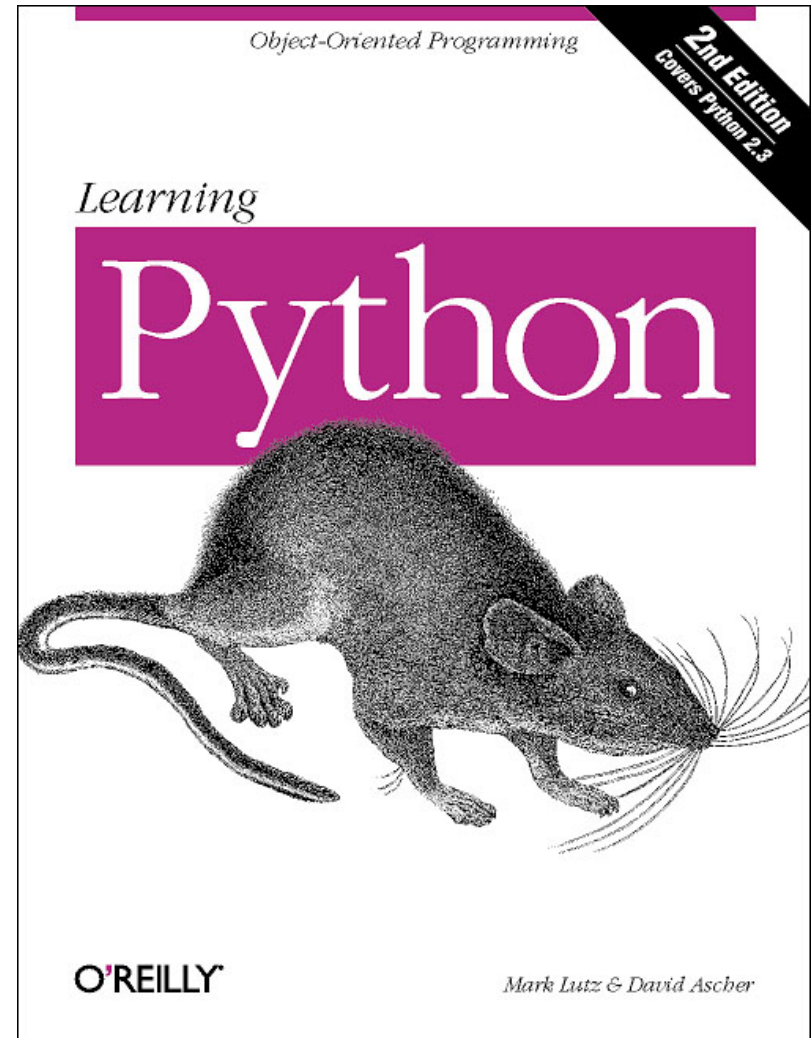
- ✓ Extensions can control standard Chimera user interface features (e.g. camera, help, menus, toolbar), as well as create their own custom graphical user interfaces
- Extensions are written in the Python programming language
  - Python is easy to learn, even for novice programmers
  - Python is object-oriented and provides features needed for development of complex codes
  - ~30 extensions written to date



# Learn more about Python

Python Web site:  
[www.python.org](http://www.python.org)

Good book:  
"Learning Python"  
by Mark Lutz & David Ascher  
Available from  
[www.oreilly.com/catalog/lpython2](http://www.oreilly.com/catalog/lpython2)





# Sample Chimera Extension

## ✓ Movie Recorder

Capture image frames from Chimera and assemble these into a movie file

Formats supported:

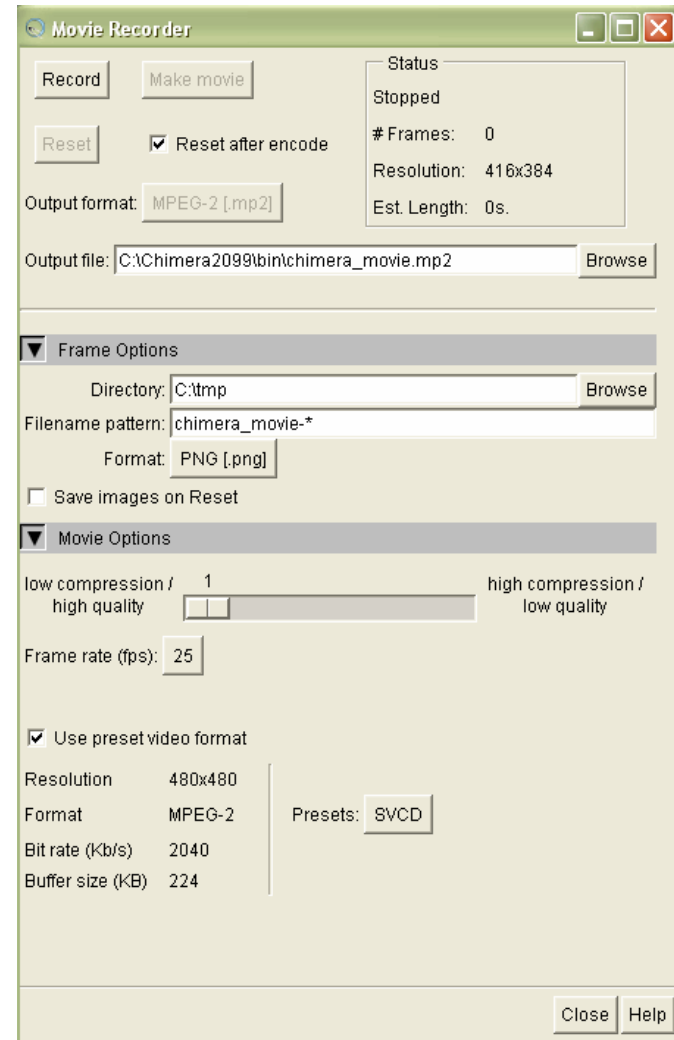
MPEG-1

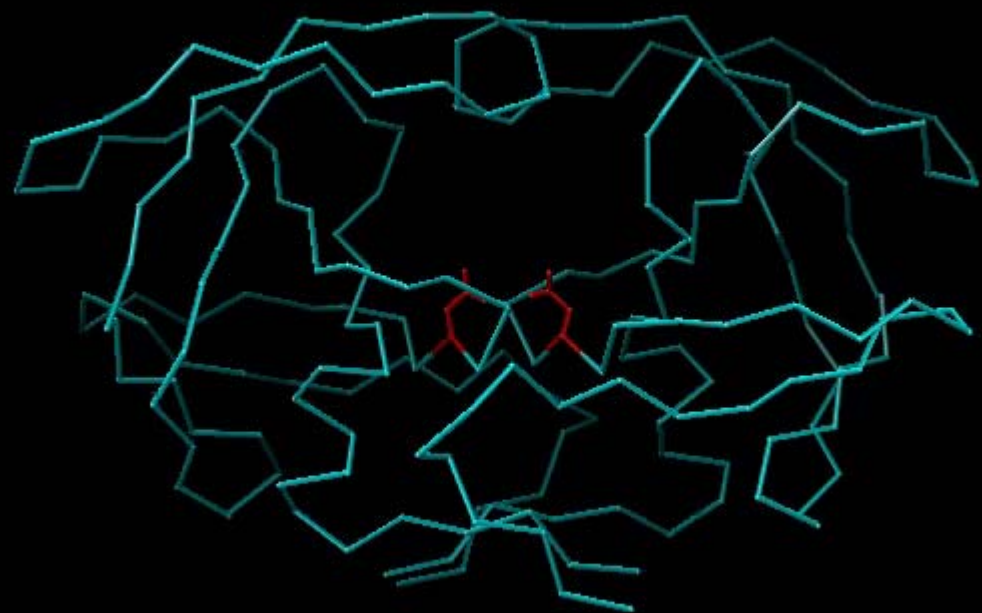
MPEG-2

MPEG-4

Quicktime

(New feature in release 1.2105)

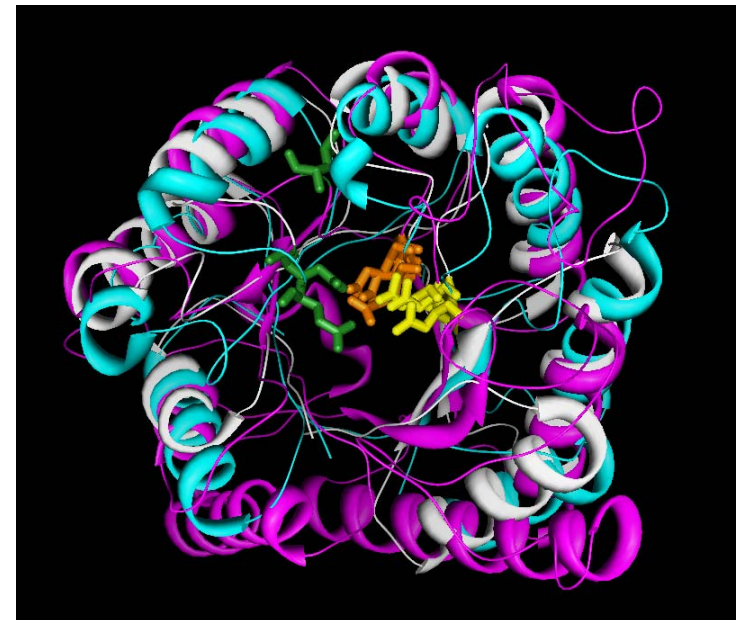
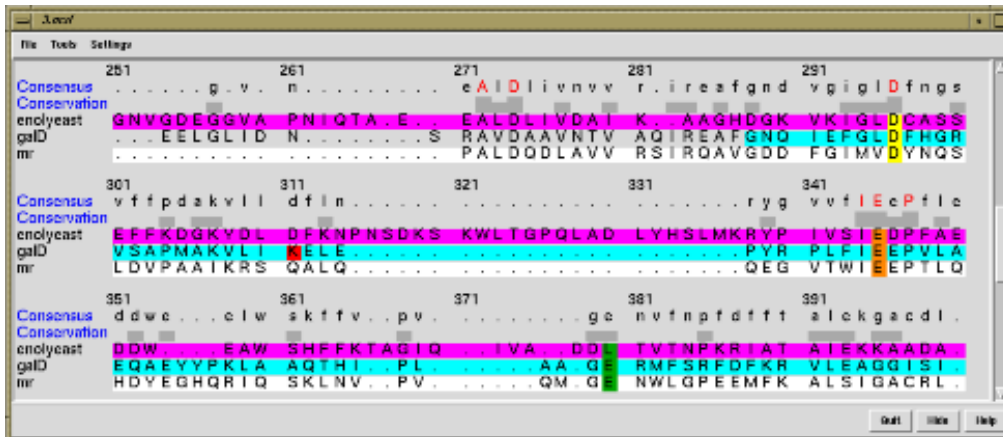




# Sample Chimera Extension

## ✓ Multalign Viewer

- Simultaneously displays multiple protein sequence alignments and corresponding structure superpositions, calculates and displays consensus sequence and conservation histogram, and highlights corresponding regions in both sequence space

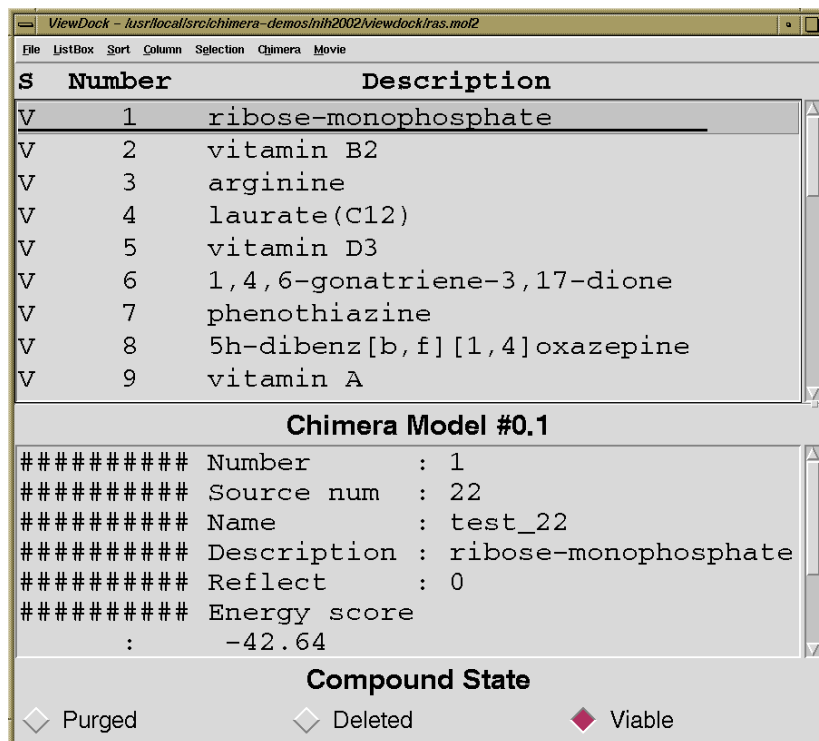




# Sample Chimera Extension

## ✓ ViewDock

- Rapid screening of promising drug candidates found with the UCSF DOCK program



ViewDock - /usr/local/src/chimera-demos/ih2002/viewdock/tras.mo2

File ListBox Sort Column Selection Chimera Movie

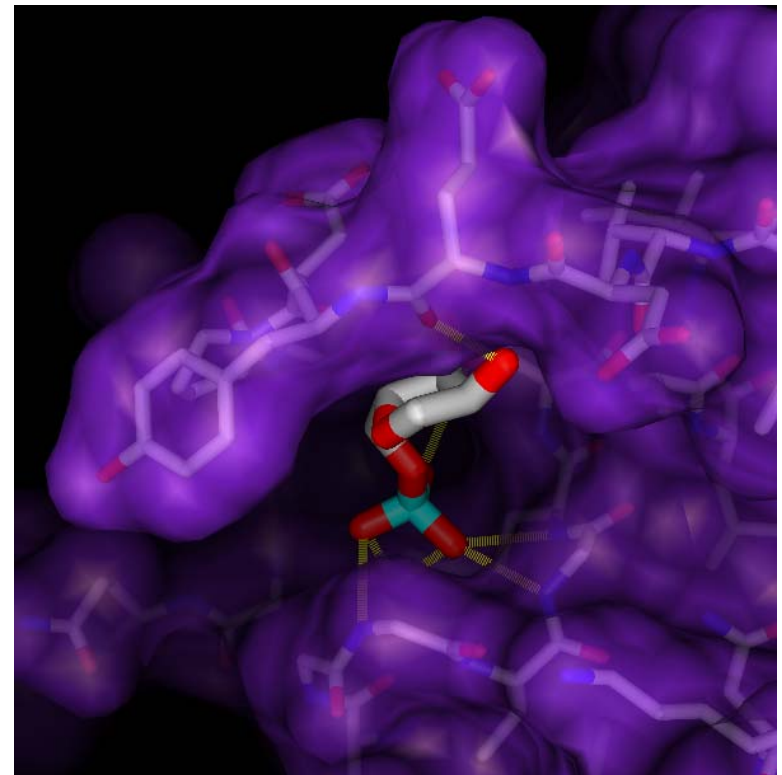
S	Number	Description
V	1	ribose-monophosphate
V	2	vitamin B2
V	3	arginine
V	4	laurate(C12)
V	5	vitamin D3
V	6	1,4,6-gonatriene-3,17-dione
V	7	phenothiazine
V	8	5h-dibenz[b,f][1,4]oxazepine
V	9	vitamin A

**Chimera Model #0.1**

```
##### Number      : 1
##### Source num  : 22
##### Name       : test_22
##### Description : ribose-monophosphate
##### Reflect    : 0
##### Energy score
:                -42.64
```

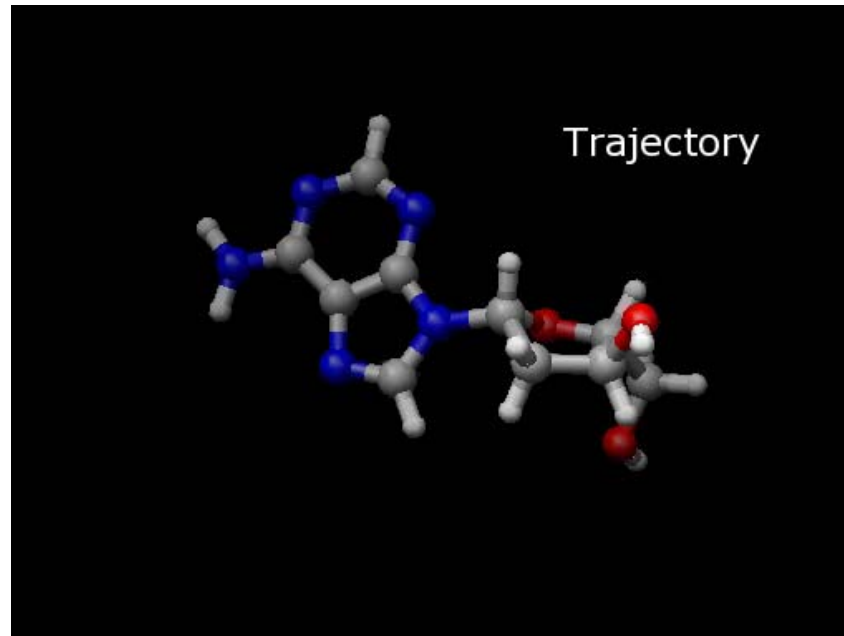
**Compound State**

Purged       Deleted       Viable



# Sample Chimera Extension

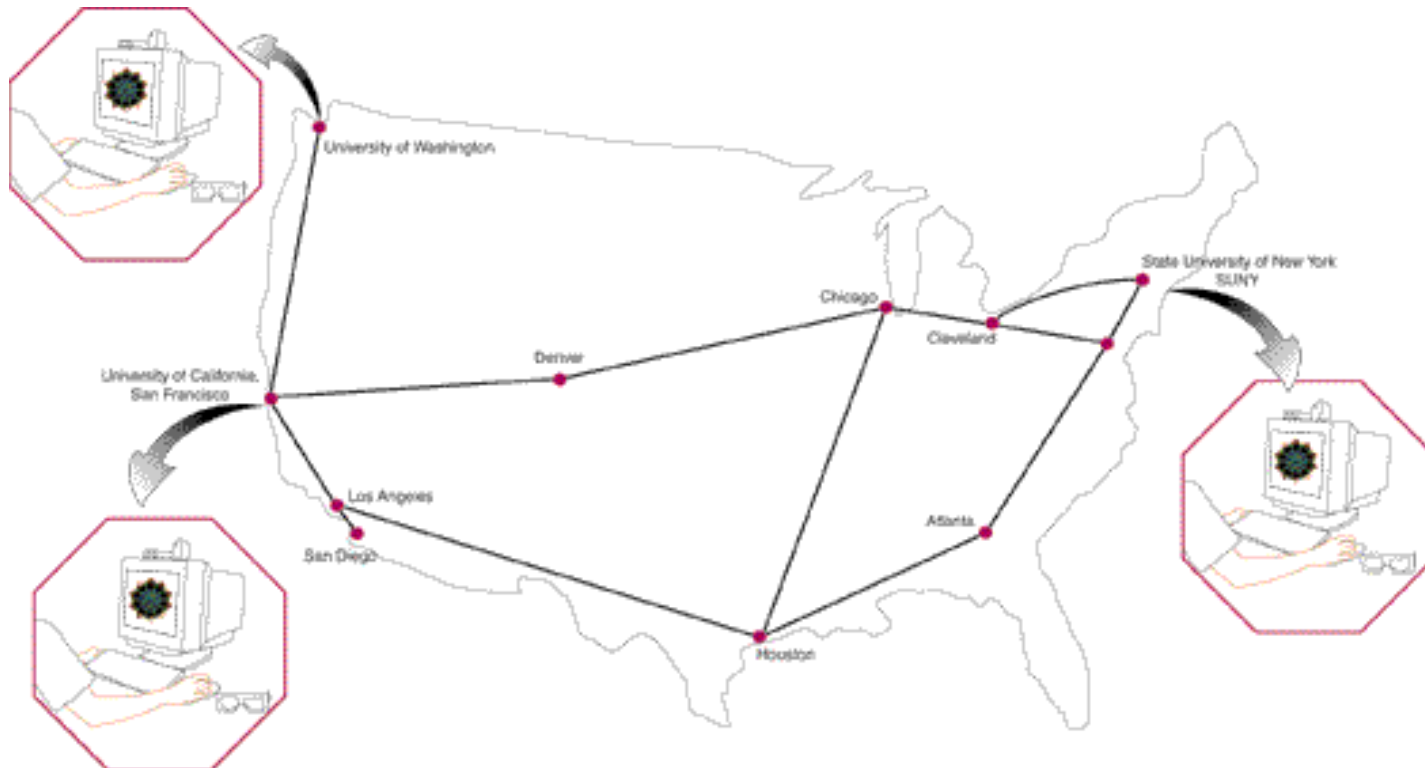
- ✓ Molecular Dynamics Trajectories
  - All built-in Chimera analysis and display capabilities also work with trajectories. Support is provided for a number of common programs: AMBER, CHARMM, GROMOS, MMTK, NAMD, PDB, and X-PLOR.



# Sample Chimera Extension

## Collaboratory

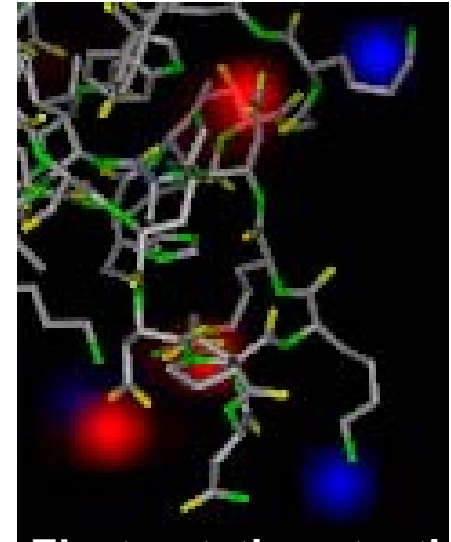
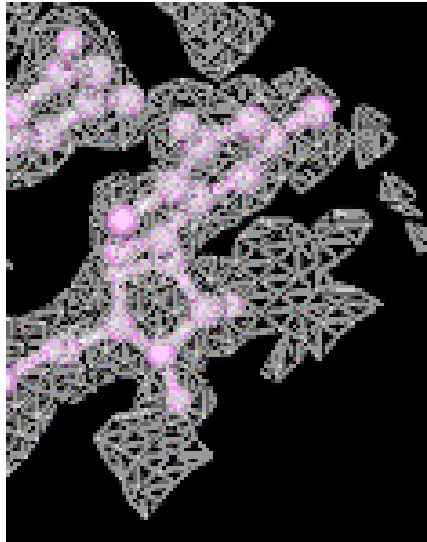
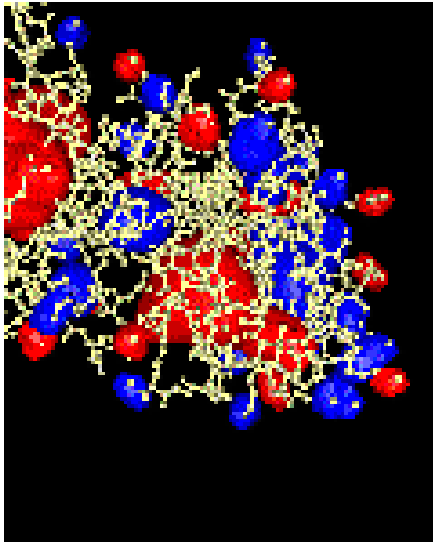
- Supports collaborative studies of molecular structure among scientists at multiple distant geographical locations



# Sample Chimera Extension

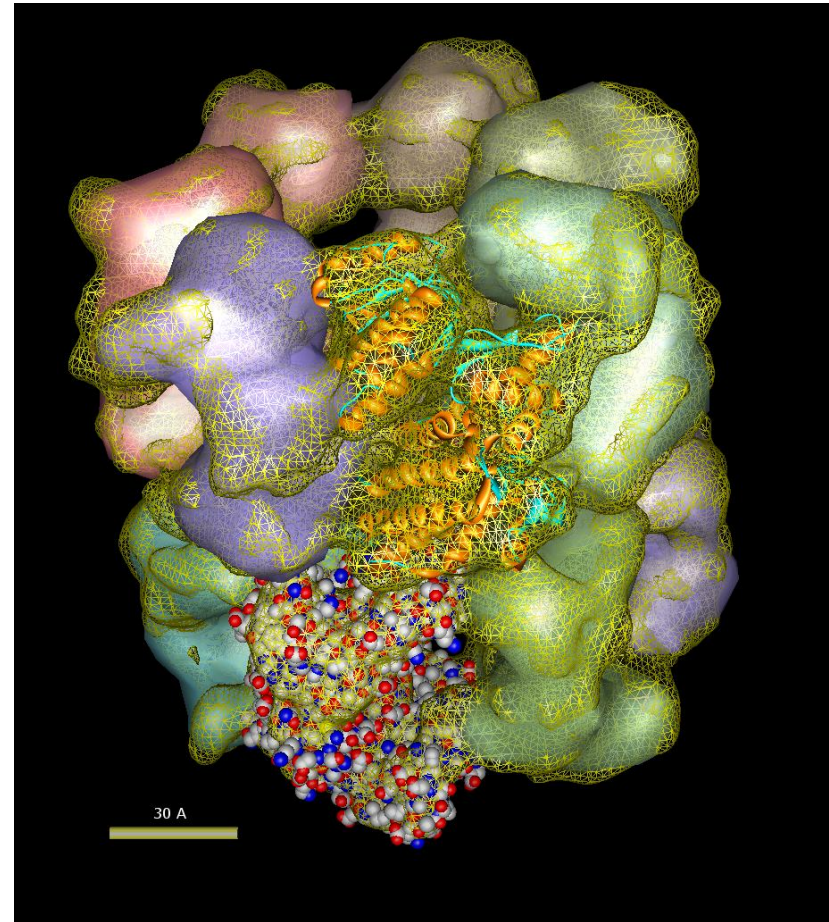
## ✓ Volume Viewer

- An extension for visualizing three-dimensional numerical data sets



# Sample Chimera Extension

- ✓ Multiscale Modeling
  - useful for exploring models of large molecular complexes
  - combines volume visualization and atomic resolution capabilities
  - example systems include viruses and chromosomes
  - GroEL model: 14 copies of the monomeric GroEL crystal structure docked to a 10.3 Å electron microscope map



# What's Left?

Lots!

- Core features:
  - Keyboard accelerators (Advanced topic)
  - Extending Chimera (Advanced topic)
  - Creating Chimera Demos (Advanced topic)
  - Stereo viewing
  - Advanced graphics features
- Extensions:
  - See Tools documentation

# Chimera Demonstration #1

Introduction to molecular representation and basic use

Files used: 2gbp.pdb

Features illustrated:

- Opening files

- Selecting and displaying atoms, bonds, and surfaces

- Manipulating models: rotate, translate, scale, clip

- Display styles: wireframe, sticks, balls&sticks, CPK

- Command line

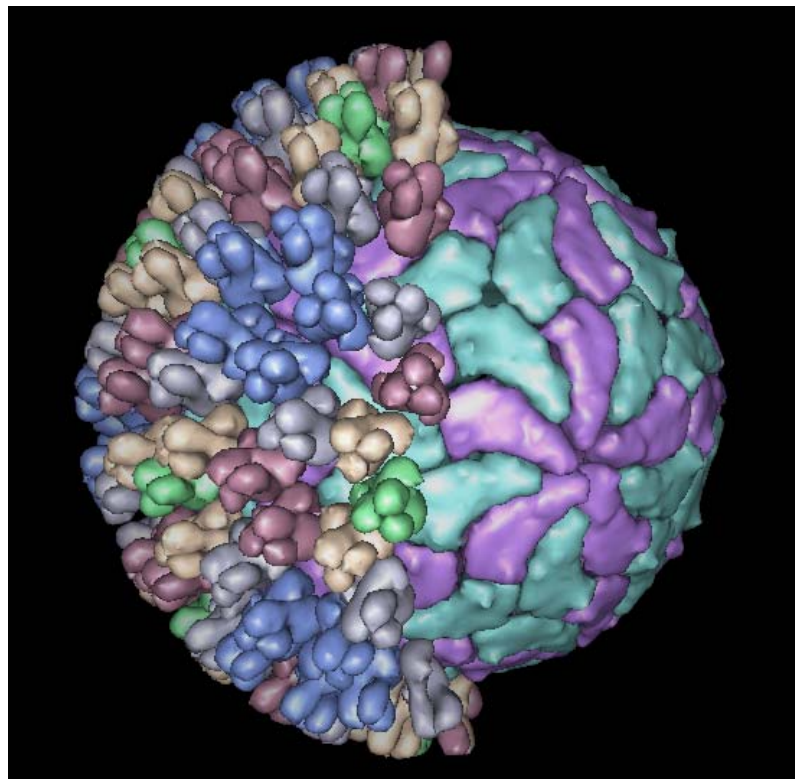
Additional information: UCSF Chimera - A Visualization System for Exploratory Research and Analysis, *J. Comp. Chem.*, 25(13):1605-1612, 2004.



# Chimera Demonstration #2

## Bluetongue Virus Core

- PDB structure 2btv by David Stuart's lab (Nature 395: 470-478, 1998)
- Full particle 700 Å diameter, 3.5 Å resolution, 1000 crystals and  $3 \times 10^6$  atoms (no hydrogens)
- Multiscale extension makes 60 copies of unit cell
  - Outer layer: 260 trimers of VP7 protein in 5 symmetry classes
  - Inner layer: 60 dimers of VP3
- Extension focuses on hierarchical structure relationships and their selection and display



Additional information: Software Extensions to UCSF Chimera for Interactive Visualization of Large Molecular Assemblies, Structure, 13(3):473-482, 2005.



# Overview

## Today's Workshop

### General format:

Short presentation/demonstration

Hands-on tutorial

### Topics may be domain-specific

Attend the topics of interest

## Tomorrow

### Scheduled one-on-one time

Your molecules/systems/problems/challenges

# Today's Agenda

<b>Time</b>	<b>Topic</b>	<b>Presenter</b>
9:00-10:45	Introduction & Chimera overview	Scooter & Eric
10:45-11:00	Break	
11:00-12:00	Publication/presentation images and animations	Dan
12:00-1:30	Lunch	
1:30-2:30	Exploring sequence-structure relationships	Elaine
2:30-3:15	Screening docked ligands	Elaine
3:15-3:30	Break	
3:30-5:00	Virus capsid and density map visualization	Tom
5:00-5:15	Wrap-up	
5:15-6:00	Advanced topics	Team

# Acknowledgements



## Staff:

Dr. Tom Ferrin, Dr. Conrad Huang, Tom Goddard, Greg Couch, Eric Pettersen, Dan Greenblatt, Al Conde, Dr. Elaine Meng, Dr. John "Scooter" Morris

## Collaborators (partial list):

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Wah Chiu and Steven Ludtke, Baylor  
John Sedat and David Agard, UCSF  
David Konerding and Steven Brenner, UCB

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## Further information:

[www.cgl.ucsf.edu/chimera](http://www.cgl.ucsf.edu/chimera)