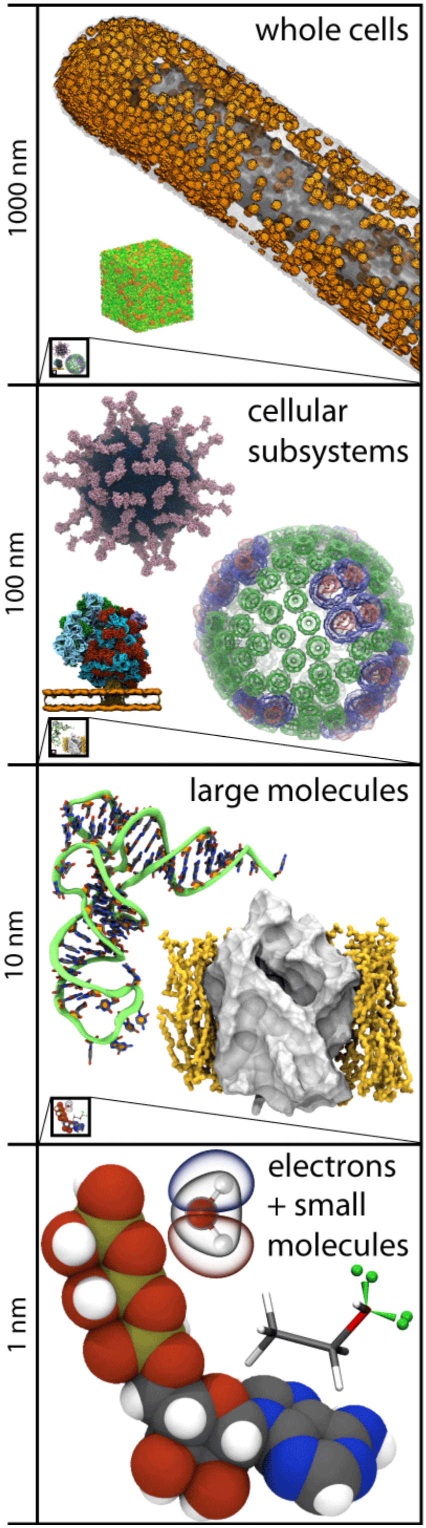
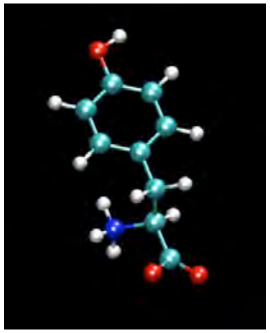
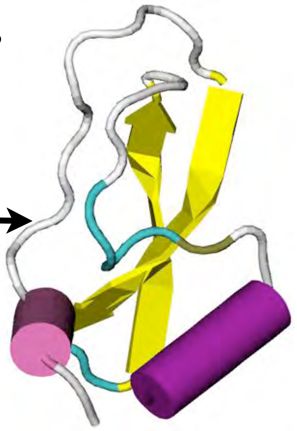
VMD: Visual Molecular Dynamics

Computational Microscope / Tool to Think



amino acid tyrosine

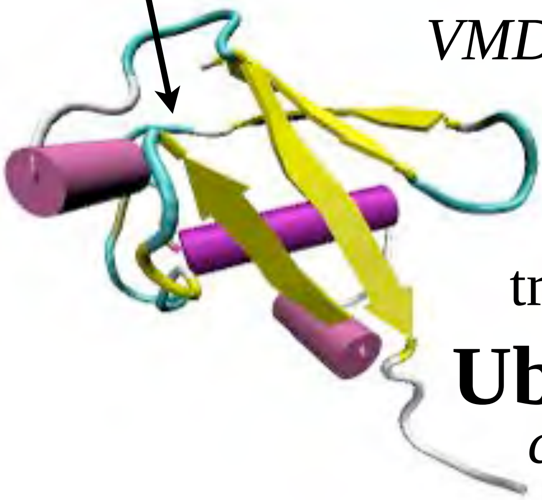




enzymatic control

BPTI

VMD tutorial



traficking

Ubiquitin

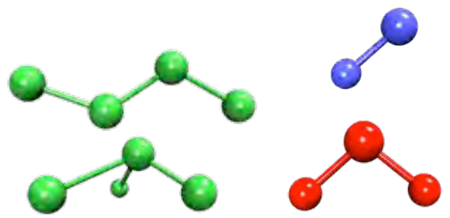
case study

http://www.ks.uiuc.edu/Training/CaseStudies/

http://www.ks.uiuc.edu/Training/Tutorials/

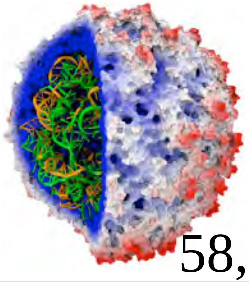
Our Microscope is Made of...

Chemistry

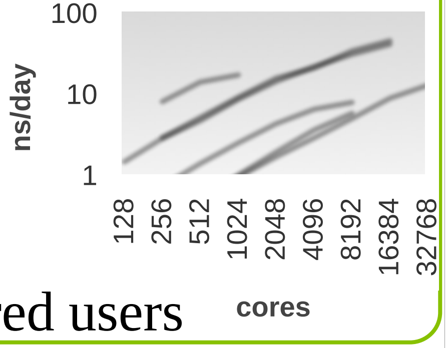


$$U(\vec{R}) = \underbrace{\sum_{bonds} k_i^{bond}(r_i - r_0)^2}_{U_{bond}} + \underbrace{\sum_{angles} k_i^{angle}(\theta_i - \theta_0)^2}_{U_{angle}} + \underbrace{\sum_{dihedrals} k_i^{dihe}[1 + \cos(n_i\phi_i + \delta_i)]}_{U_{dihedral}} + \underbrace{\sum_i \sum_{j \neq i} 4\epsilon_{ij}\left[\left(\frac{\sigma_{ij}}{r_{ij}}\right)^{12} - \left(\frac{\sigma_{ij}}{r_{ij}}\right)^{6}\right] + \sum_i \sum_{j \neq i} \frac{q_i q_j}{\epsilon r_{ij}}}_{U_{nonbond}}$$

NAMD Software



Virus



58,000 registered users

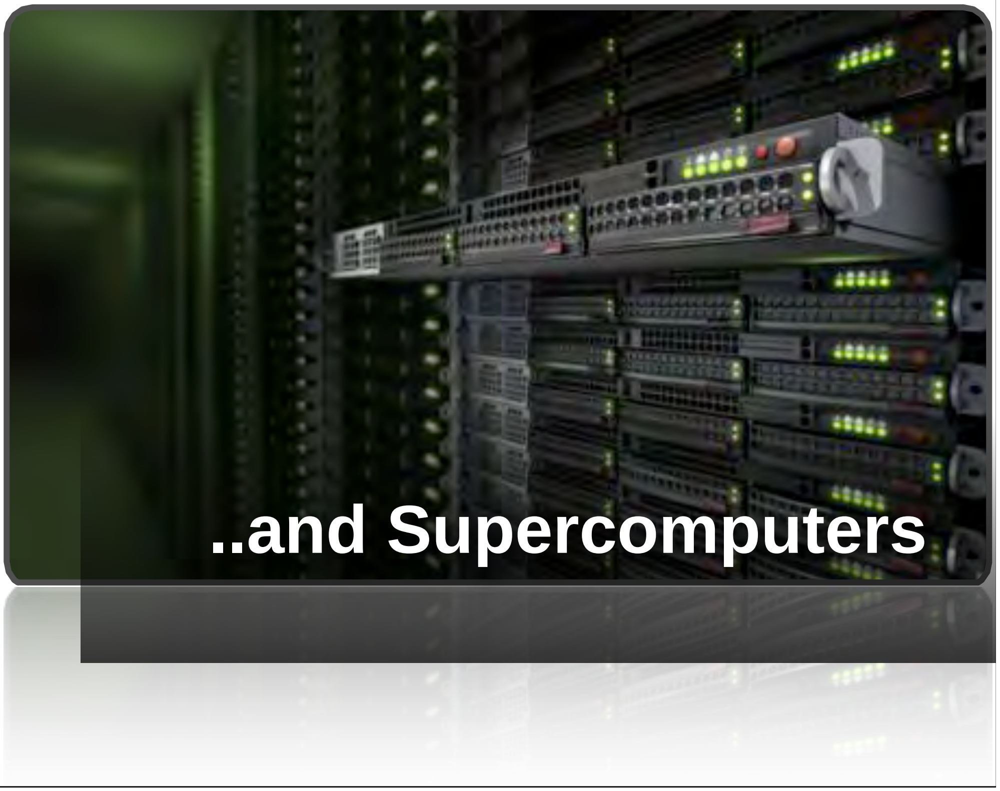
Physics

$$m_i \frac{d^2\vec{r}_i}{dt^2} = \vec{F}_i = -\vec{\nabla}U(\vec{R})$$

Math

$$\vec{r}_i(t + \Delta t) = 2\vec{r}_i(t) - \vec{r}_i(t - \Delta t) + \frac{\Delta t^2}{m_i}\vec{F}_i(t)$$

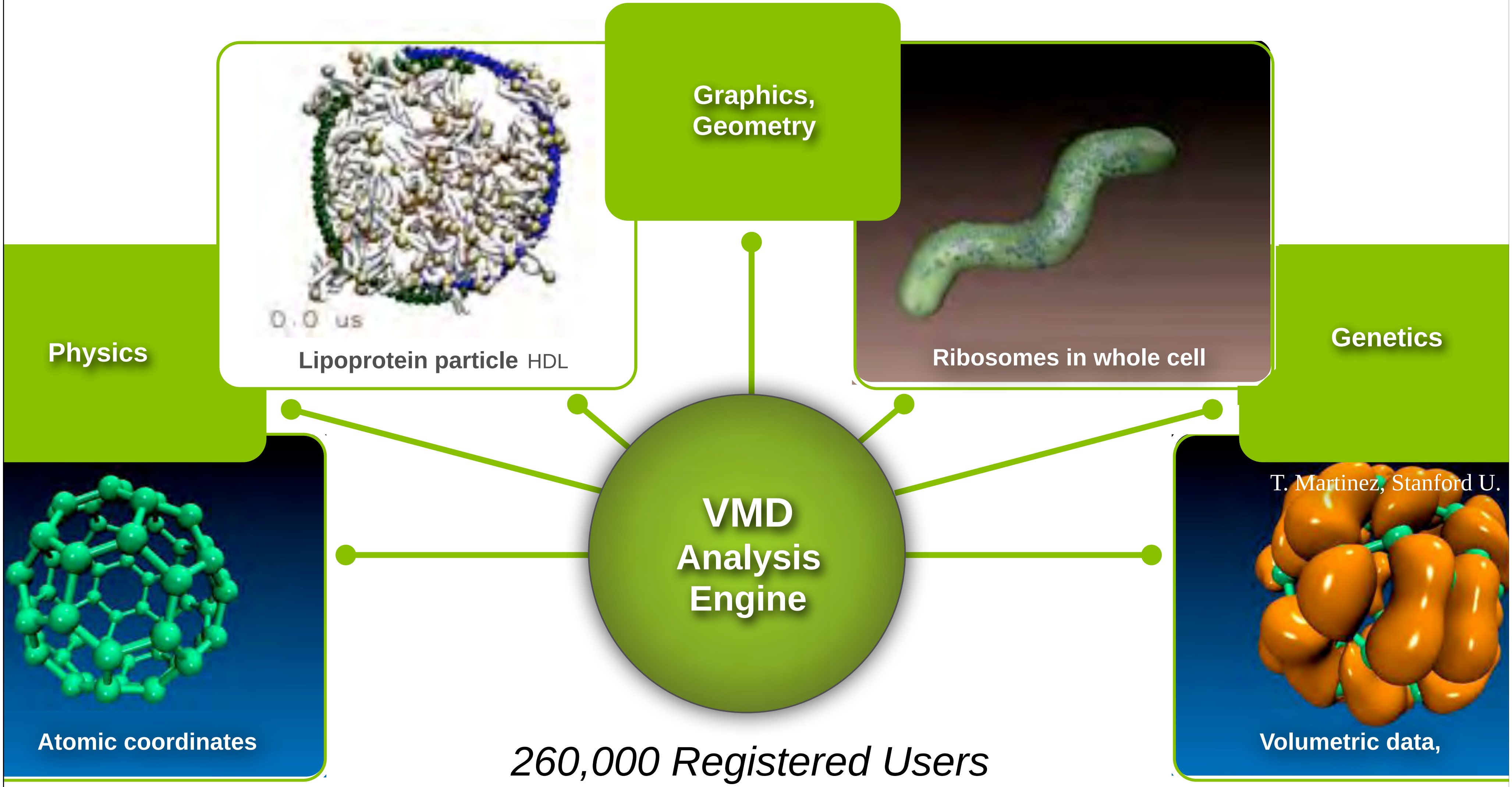
(repeat ***one billion times*** = microsecond)



..and Supercomputers

Our Microscope is Made of...

and of...



Physics

Lipoprotein particle HDL

Graphics, Geometry

Ribosomes in whole cell

Genetics

T. Martinez, Stanford U.

VMD Analysis Engine

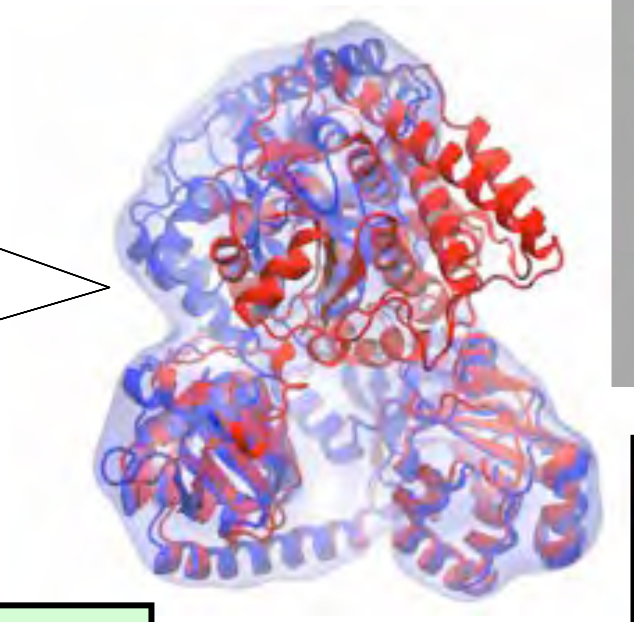
Atomic coordinates

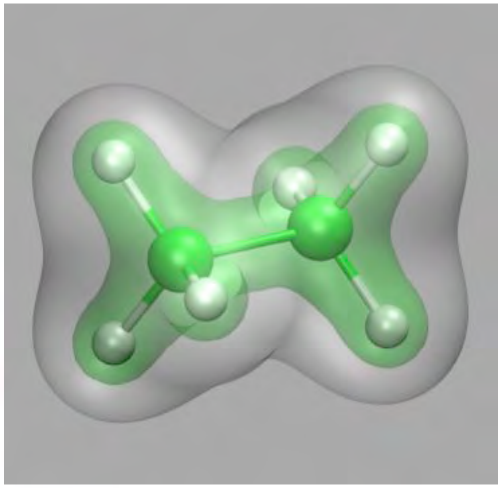
Volumetric data,

260,000 Registered Users

VMD – A Tool to Think

Volumetric Data:
Density maps,
Electron orbitals,
Electrostatic potential,
Time-averaged occupancy, …

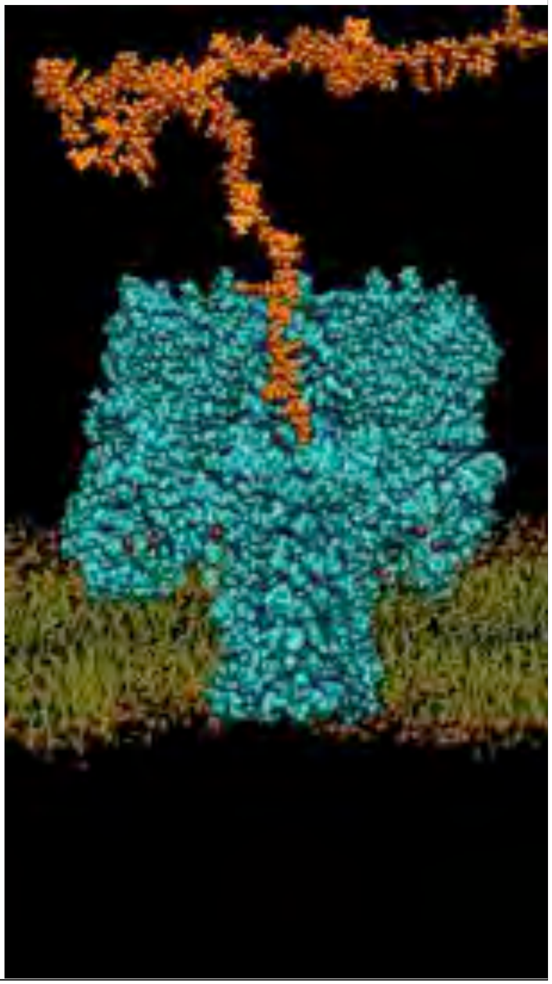




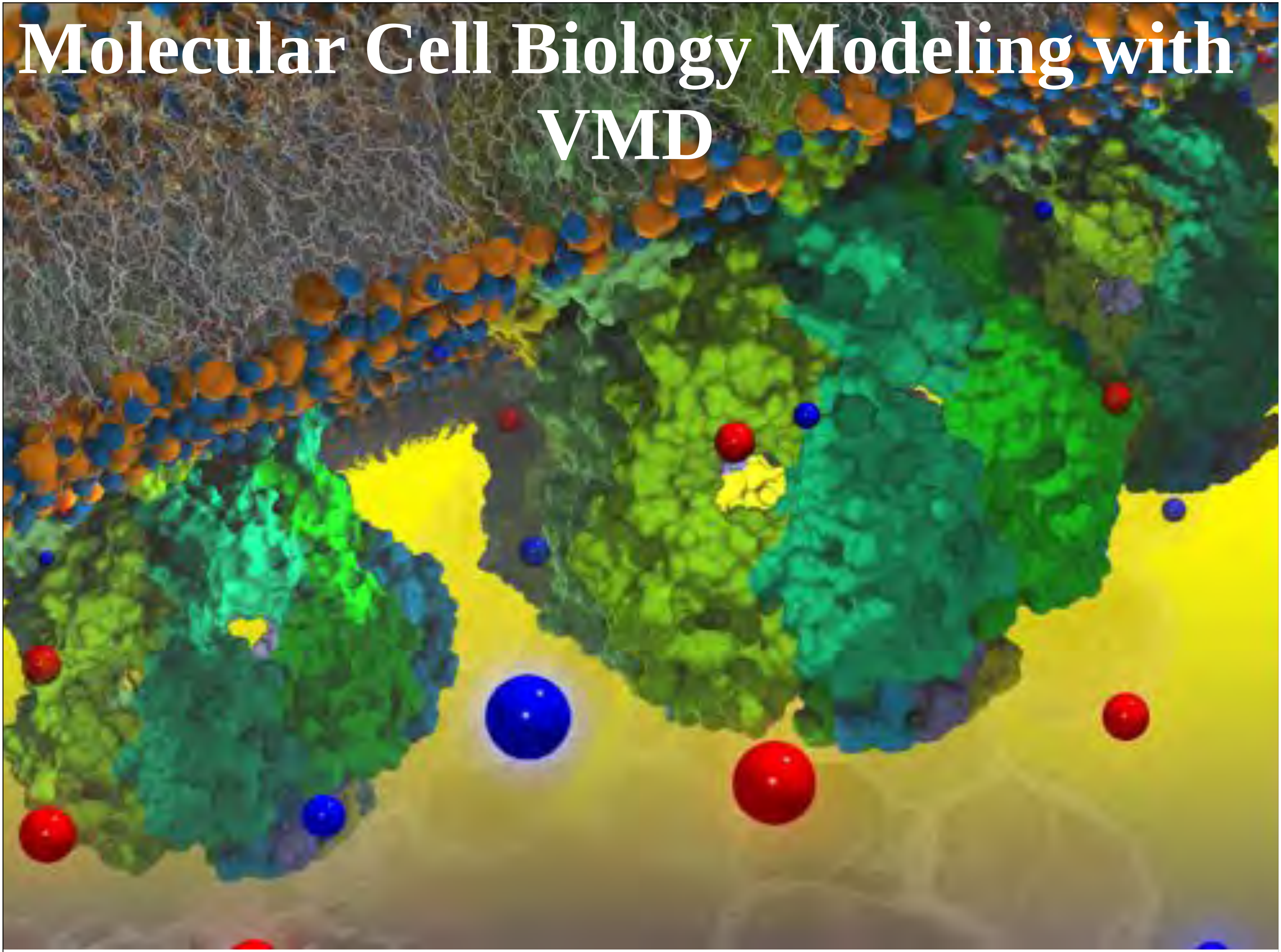
Sequence Data:
Multiple Alignments,
Phylogenetic Trees

VMD

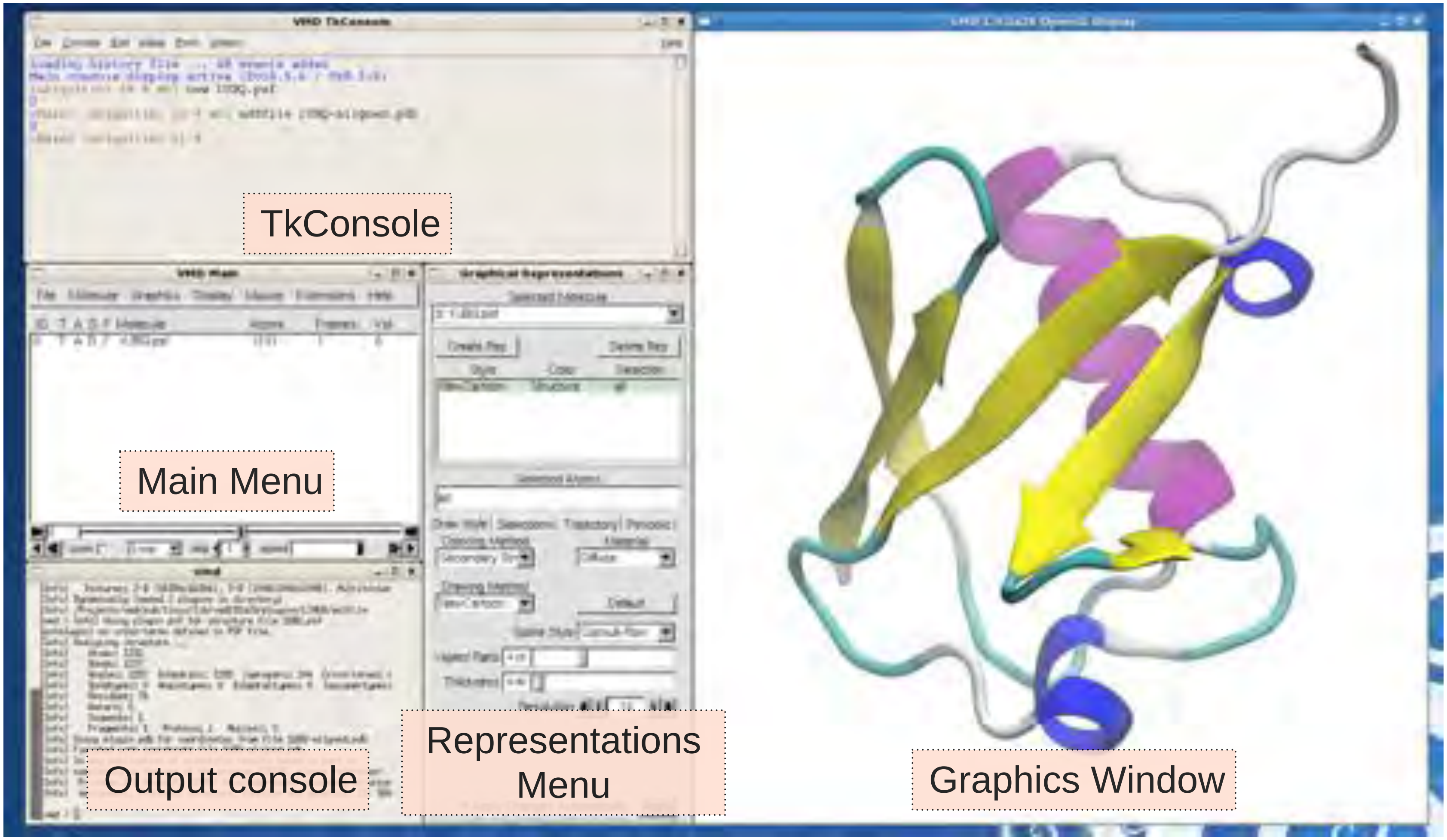
Atomic Data:
Coordinates,
Trajectories,
Energies,
Forces, …



Molecular Cell Biology Modeling with VMD



Molecular Graphics with VMD



typical VMD session

An Example: Ubiquitin and the Proteosome

Ubiquitin: a small protein of 76 amino acids

Present in all eukaryotes, and highly conserved

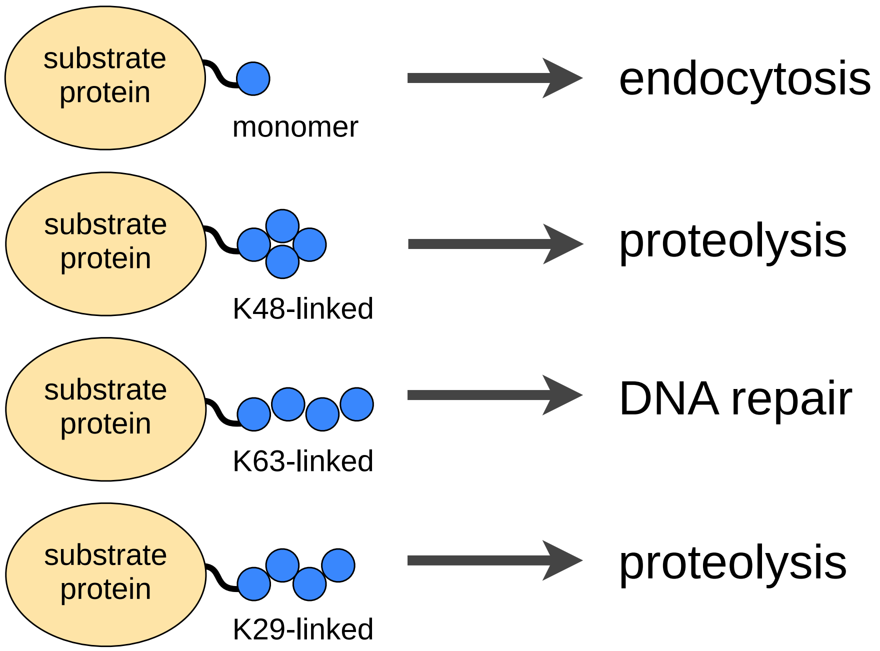
Regulates key cellular processes such as cell division, gene expression, cell trafficking, and protein degradation

Deficiency in ubiquitin expression can lead to neurodegenerative disorders

Tags misfolded proteins to be degraded in the proteosome (“kiss of death” protein)

Ubiquitin Chains

Ubiquitins monomers attach to others to make a poly-ubiquitin chain



substrate protein
monomer → endocytosis

substrate protein
K48-linked → proteolysis

substrate protein
K63-linked → DNA repair

substrate protein
K29-linked → proteolysis

7 conserved lysine residues can form differently shaped chains depending on which lysine is used to connect the monomers

A Glycine at C-terminal attaches to a lysine on the protein by an isopeptide bond

A chain of at least four ubiquitins is needed to be recognized by the proteosome for protein degradation

VMD Session 1:

ubiquitin

Case Study Ubiquitin http://www.ks.uiuc.edu/Training/CaseStudies/

Case Study: Ubiquitin

Eduardo Cruz-Chu and JC Gumbart

1 Introduction

Without a doubt, the most organized and coordinated machine known is the biological cell. Inside its micrometer-scale diameter, a wide variety of macromolecules (DNA, proteins, sugars, lipids, etc.) work together in a cooperative way, balancing energy and matter to keep the cell alive. Within the cell, proteins are the overachievers. They allow the movement of water and ions through the cell membrane, help ATP to store energy, assist DNA during replication, recognize foreign infections, and more. However, all of these functions don't work independently of each other. To maintain harmony and efficiency between various functions, most processes have to be turned on or off according to different cellular stages and changes within the environment.

To this end, together with the mechanisms to assemble functional proteins and to turn on their functions, there should be counterparts to suppress and disassemble proteins when they are no longer needed. The cellular machine depends on assembly and disassembly to regulate the effective concentration of proteins and their corresponding activities [1]. Furthermore, defective

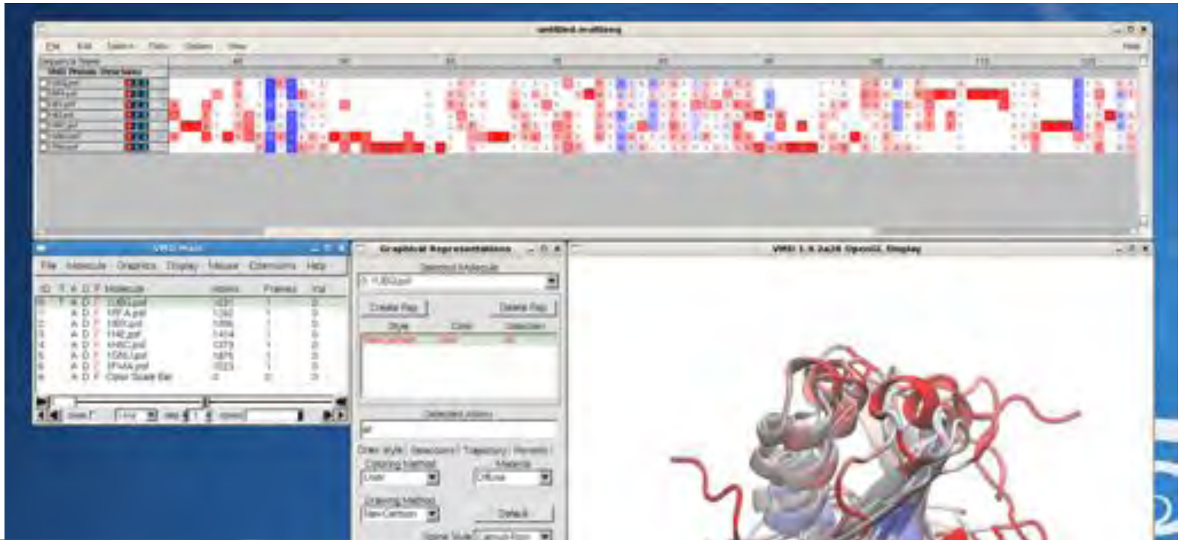
Bioinformatics

Link sequence to structure

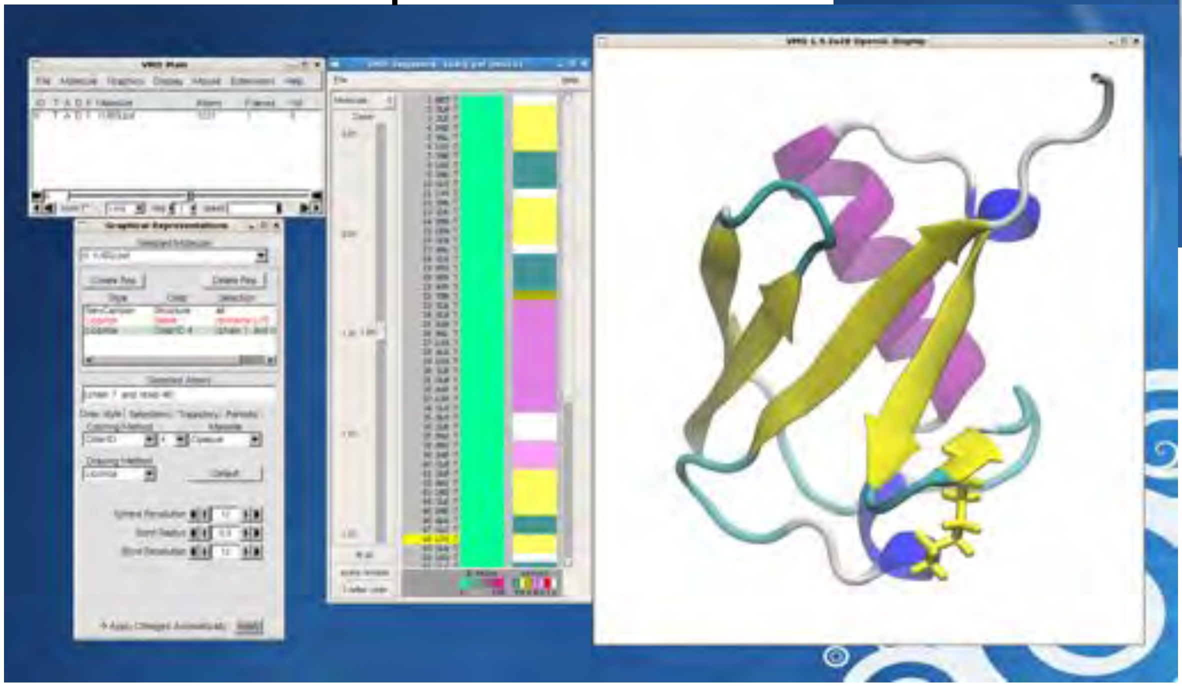
Multiple sequence/
structure alignments

Phylogenetic trees

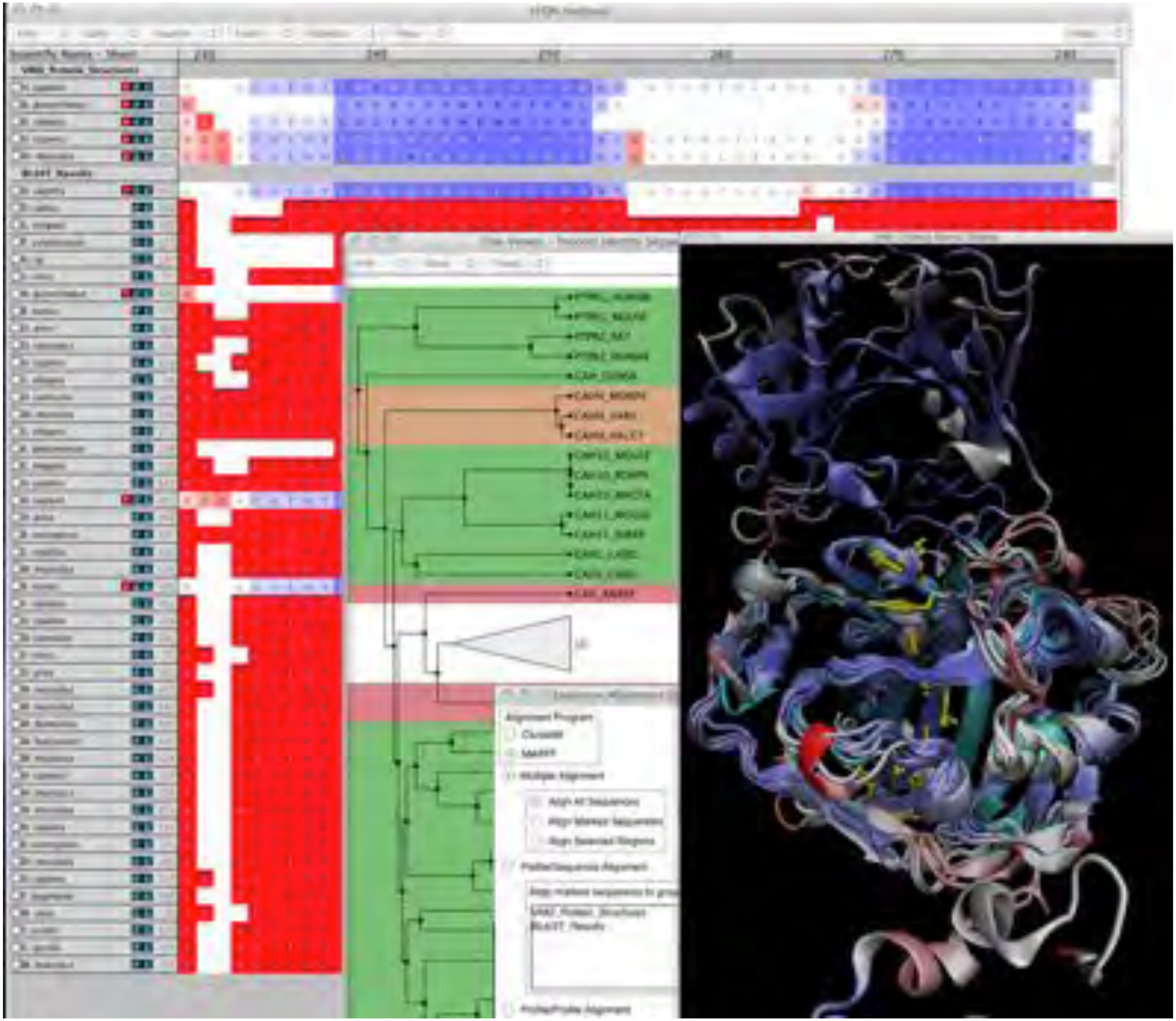
MultiSeq



Sequence Viewer



Structure, Sequence and Phylogenetic Analysis with VMD



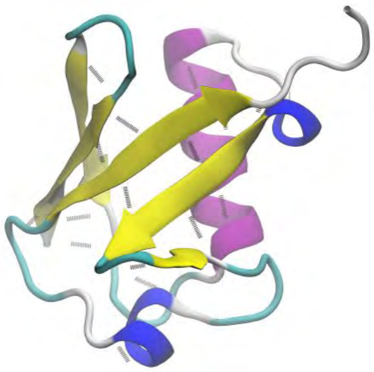
VMD Handles Volumetric Data

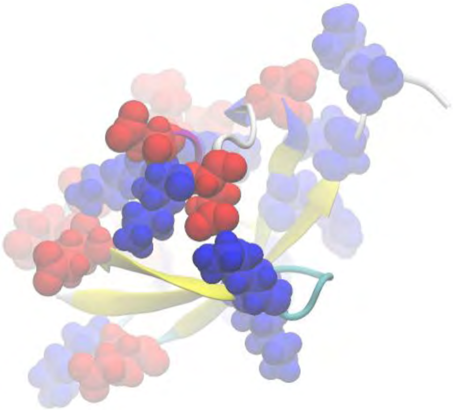
electron density
from QM/MM
calculation
Martinez, Stanford

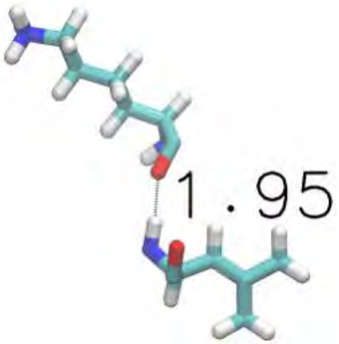
Cryo-EM map of the *E. coli* ribosome at 6.7-Å resolution

cryo-EM density

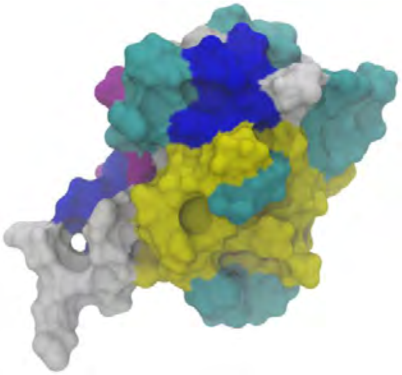
VMD Determines Physical Properties

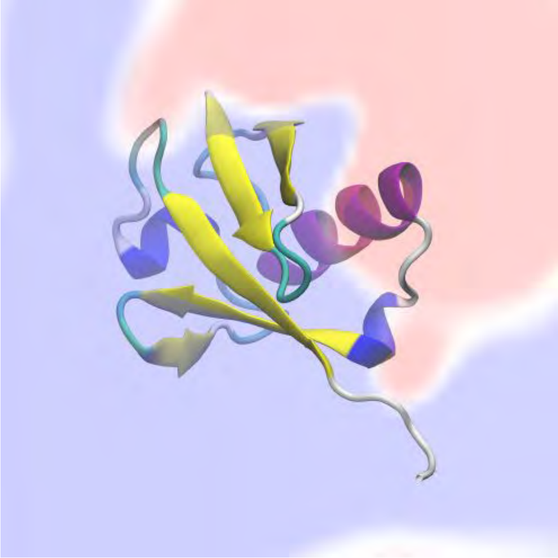

hydrogen bonds


salt bridges



distances


SASA


electrostatics

- SASA
- secondary structure
- interaction surfaces
- hydrogen bonds
- salt bridges
- electrostatics
- distances
- angles
- dihedrals

- RMSD
- RMSF
- interaction energies
- forces
- free energy profiles
- normal modes

Trajectory Graphics/Analysis with VMD

VMD Plugin: Timeline

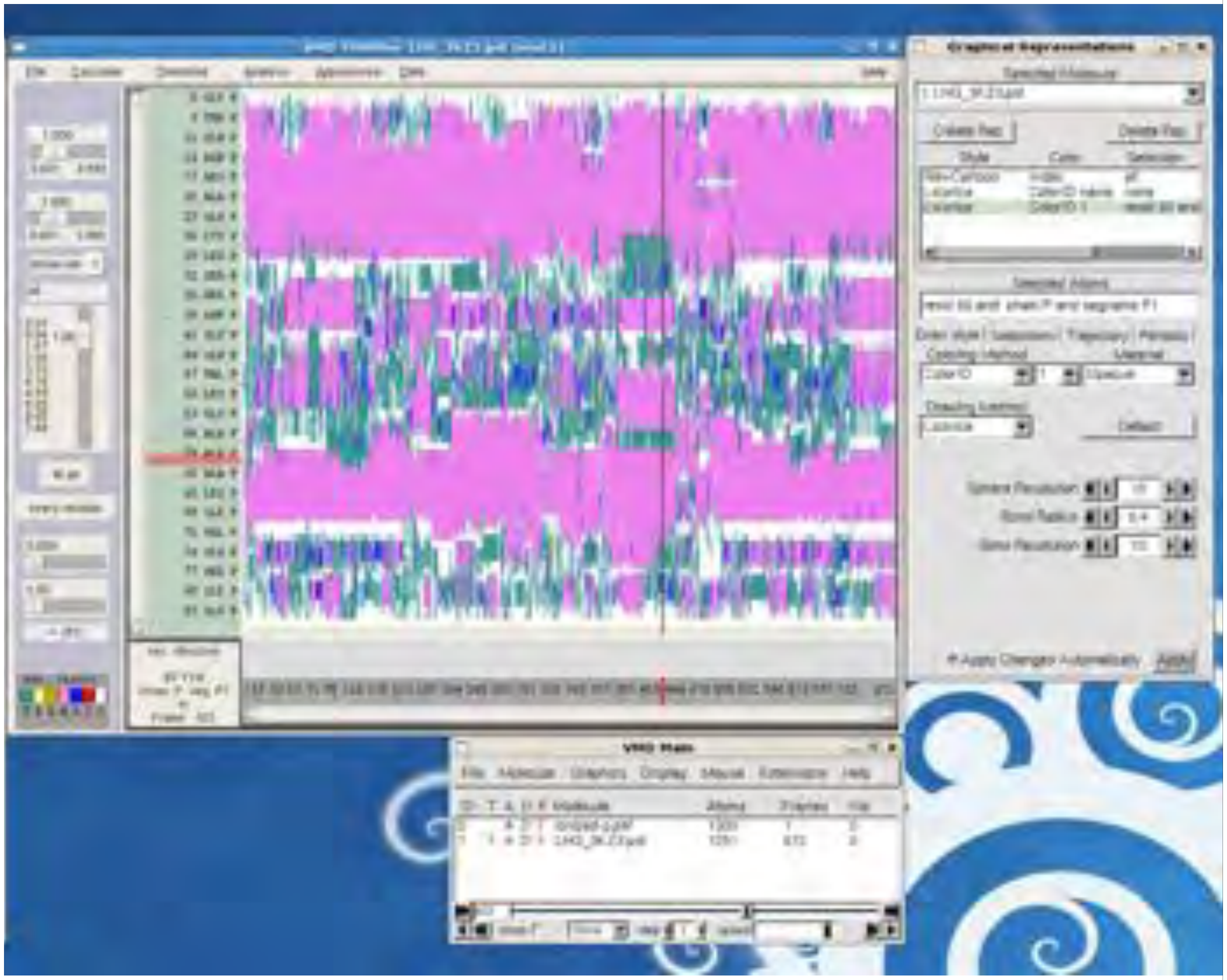
plugin to analyze MD trajectories for events

plot properties, e.g. RMSD, secondary structure, hydrogen bonds, for each residue across a trajectory

Example: protein folding

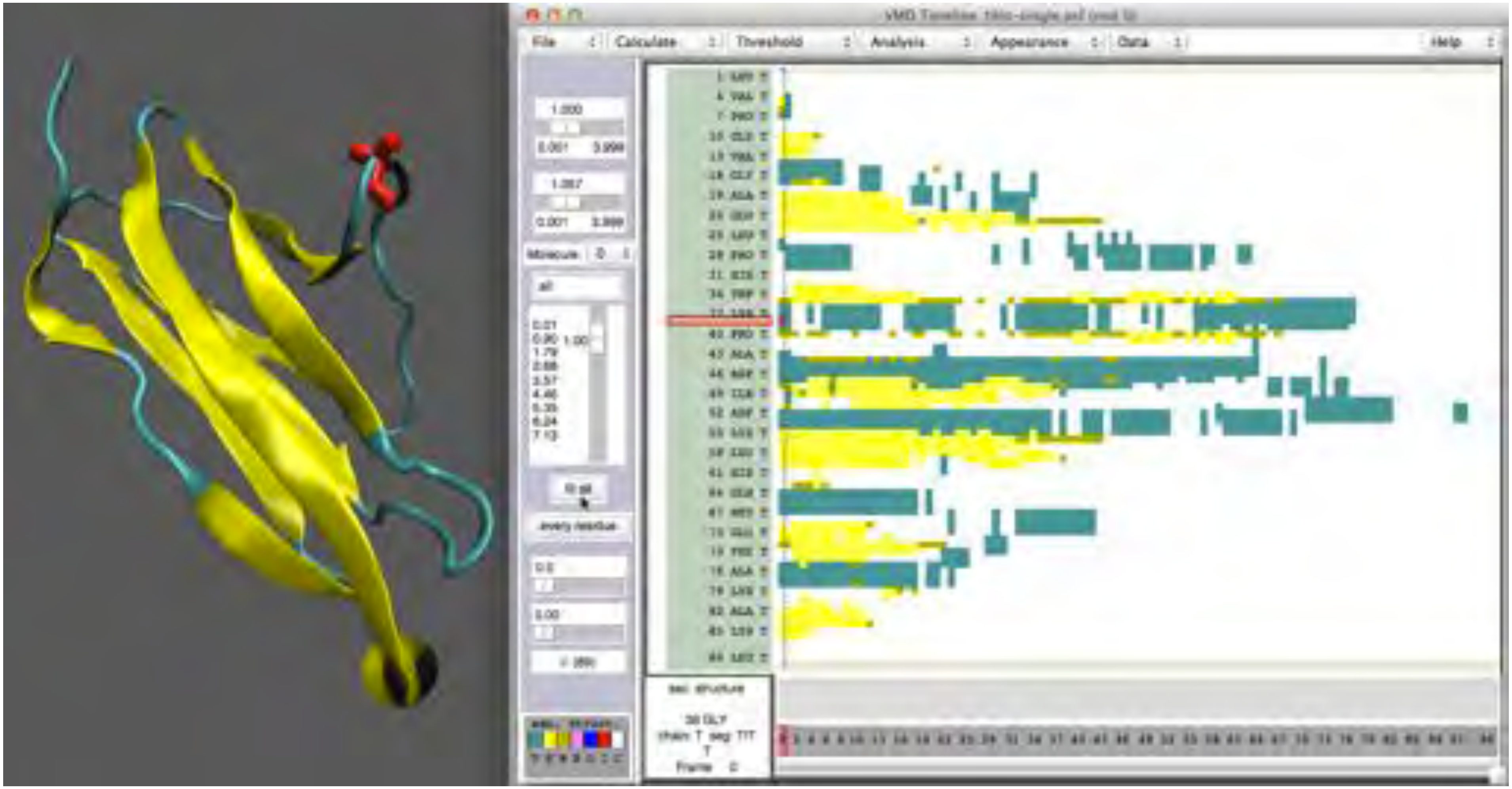
lambda repressor (2012)
80 amino acids, 100 μs

Journal of Physical Chemistry Letters, 3:1117-1123, 2012. *Proceedings of the National Academy of Sciences, USA*, In press, 2013.



VMD Session 2:
trajectory of villin head piece

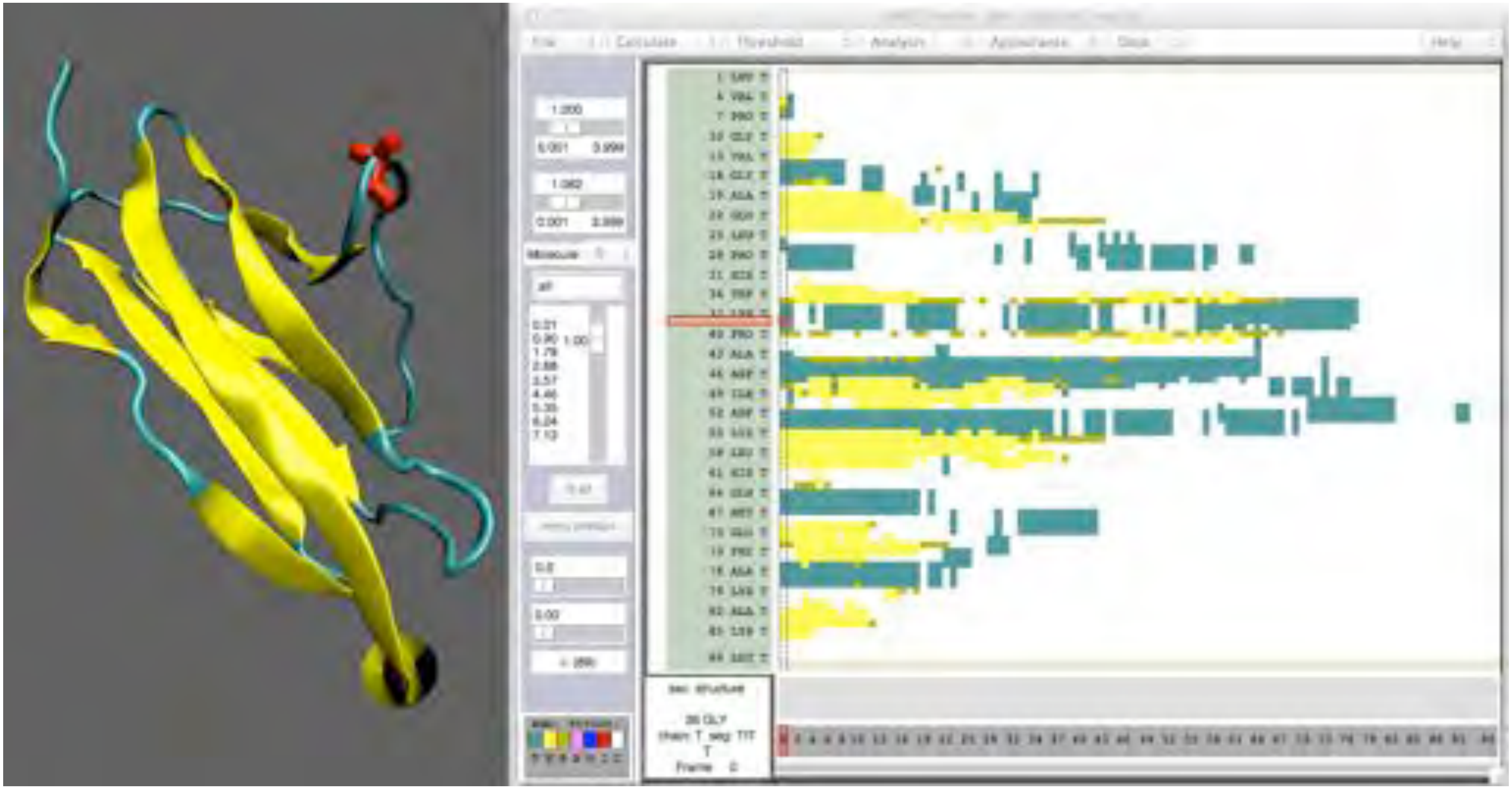
Timeline: a graphing and analysis tool to identify events in an MD trajectory



🟦 Beta turn 🟨 Extended beta 🟩 Isolated bridge ☐ None (coil)

secondary structure during titin domain extension

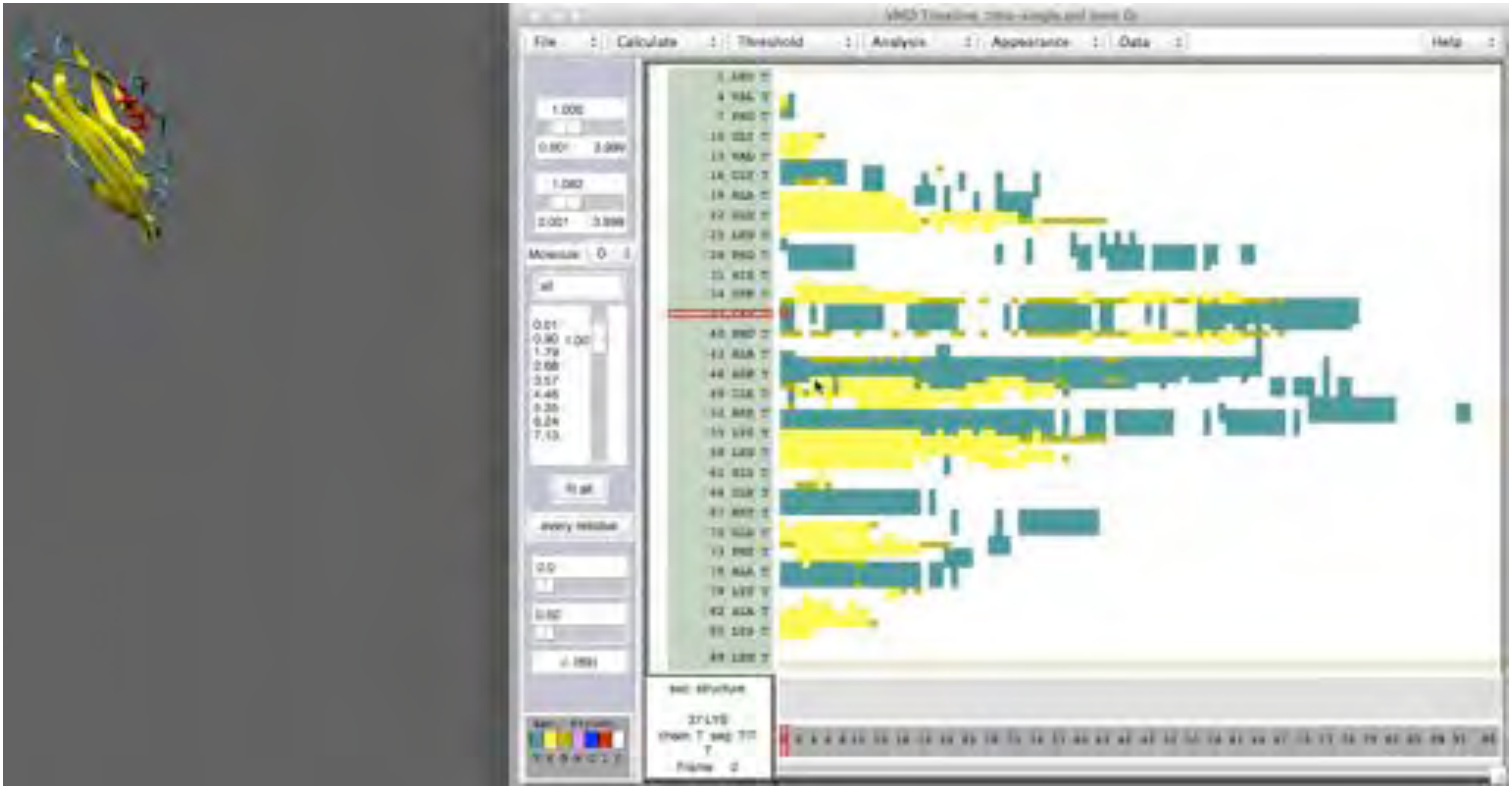
Timeline: a graphing and analysis tool to identify events in an MD trajectory



■ Beta turn ■ Extended beta ■ Isolated bridge □ None (coil)

secondary structure during titin domain extension

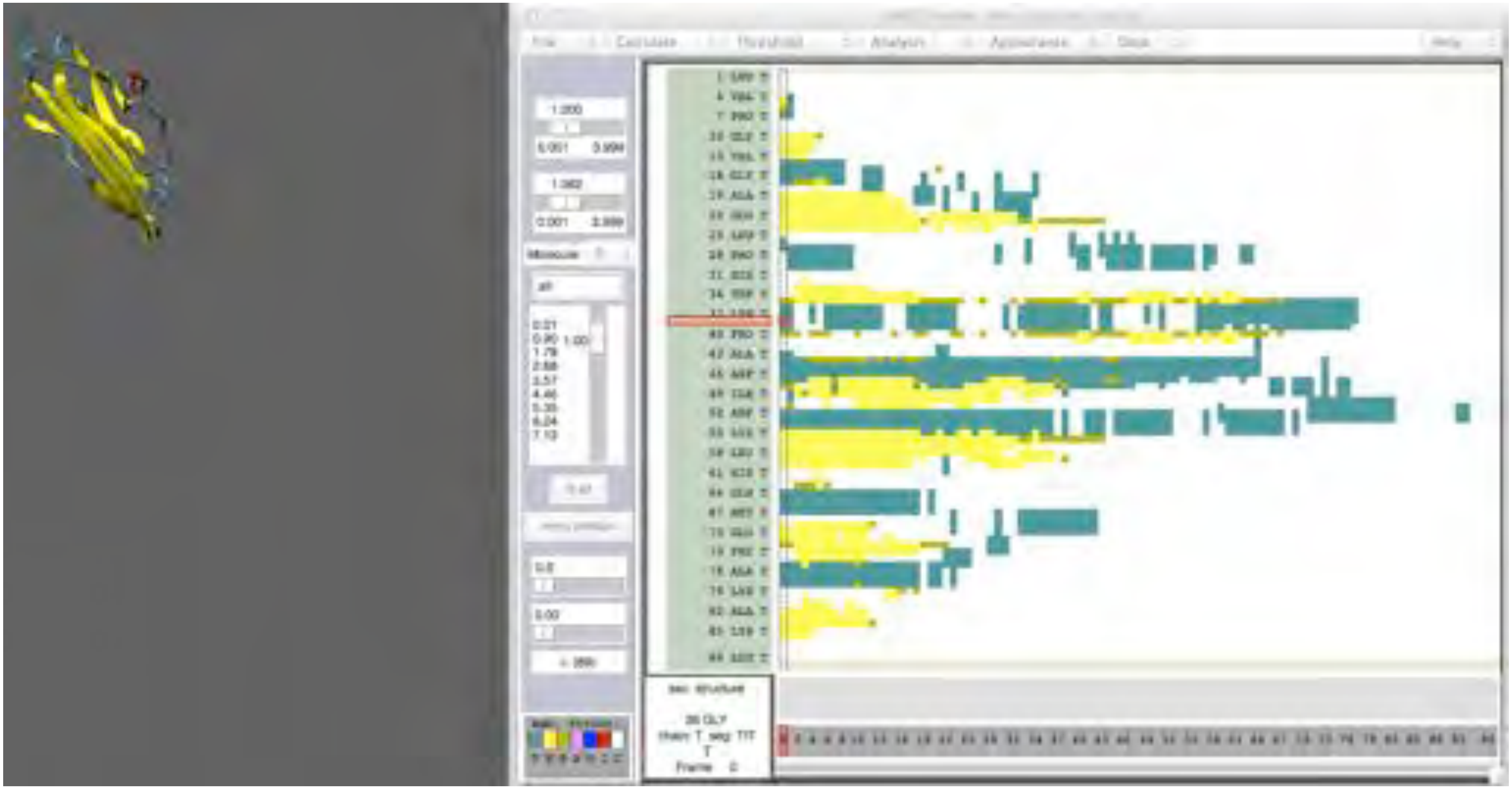
Timeline: a graphing and analysis tool to identify events in an MD trajectory



🟦 Beta turn 🟨 Extended beta 🟩 Isolated bridge ⬜ None (coil)

secondary structure during titin domain extension

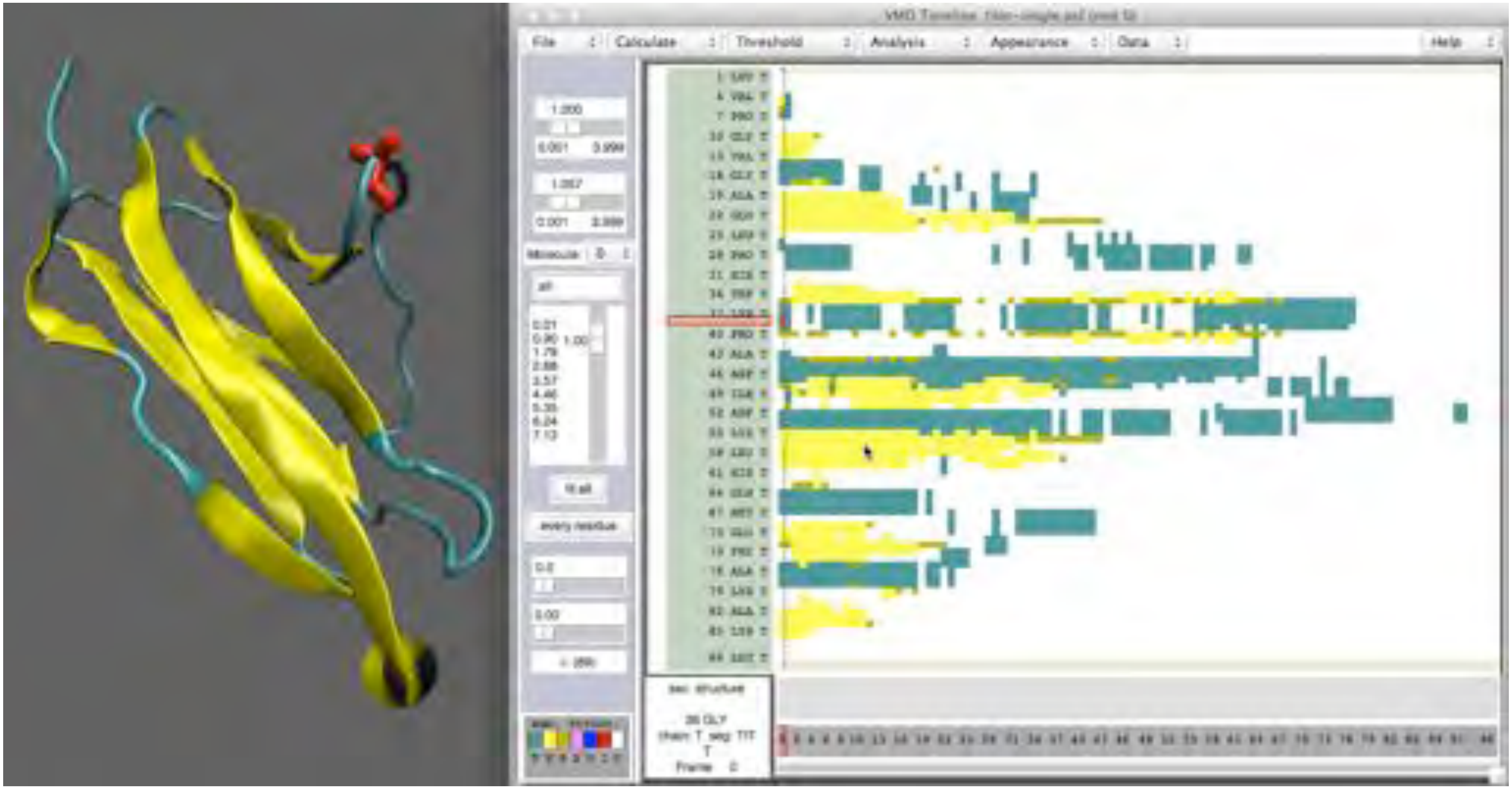
Timeline: a graphing and analysis tool to identify events in an MD trajectory



🟦 Beta turn   🟨 Extended beta   ■ Isolated bridge   ☐ None (coil)

secondary structure during titin domain extension

Timeline: a graphing and analysis tool to identify events in an MD trajectory



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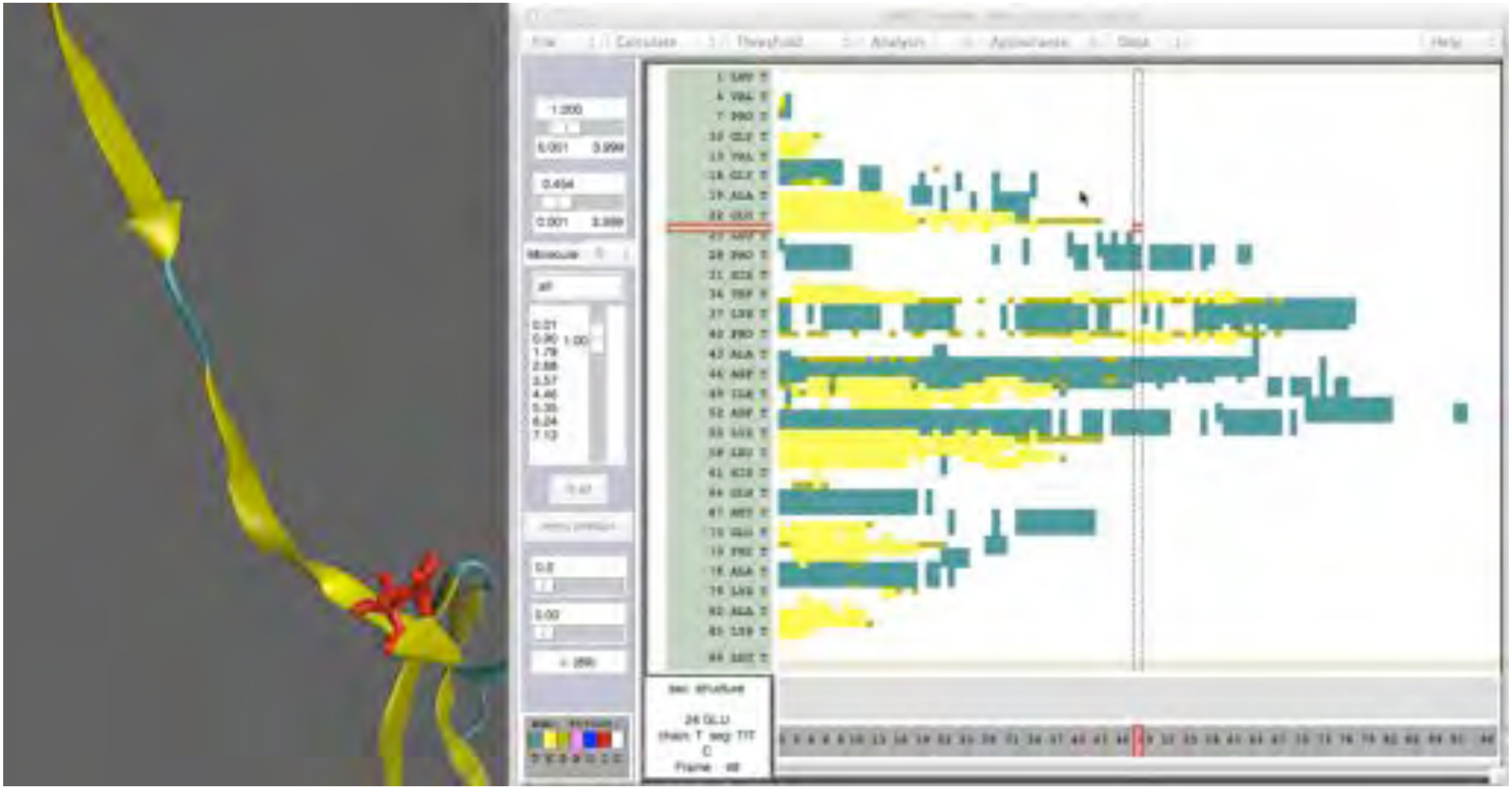

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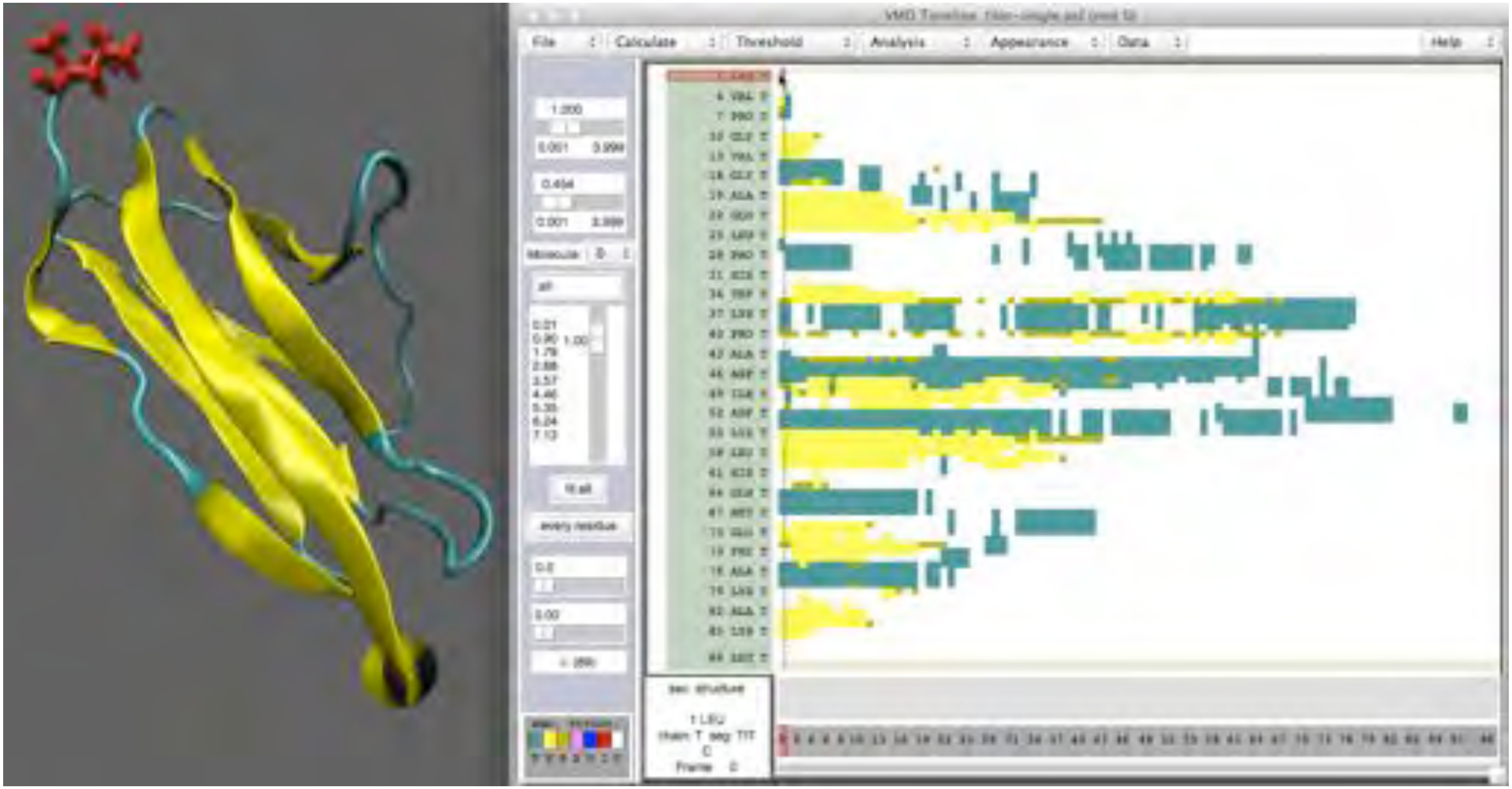


🟦 Beta turn 🟨 Extended beta 🟩 Isolated bridge ☐ None (coil)

secondary structure during titin domain extension

VMD Plugins: extensible analysis

Modeling Plugins

- AutoIonize
- AutoPSF
- Chirality
- Cispeptide
- CGTools
- Dowser
- FFTK
- Inorganic Builder
- MDFF
- Membrane Builder
- MergeStructs
- Molefacture
- Mutator
- Nanotube
- Paratool
- Psfgen
- Solvate
- SSRestraints
- Topotools

Analysis Plugins

- APBSRun
- CatDCD
- Contact Map
- GofRGUI
- HBonds
- ILSTools
- IRSpecGUI
- MultiSeq
- NAMDEnergy
- NAMDPlot
- NetworkView
- NMWiz
- ParseFEP
- PropKaGUI
- RamaPlot
- RMSD Tool
- RMSD Trajectory Tool
- RMSD Visualizer Tool
- Salt Bridges
- Sequence Viewer
- Symmetry Tool
- Timeline
- VolMap

Visualization Plugins

- Clipping Plane Tool
- Clone Rep
- Dipole Watcher
- Intersurf
- Navigate
- NavFly
- MultiMolAnim
- Color Scale Bar
- Remote
- Palette Tool
- ViewChangeRender
- Viewmaster
- Virtual DNA Viewer
- VMDMovie

Simulation Plugins

- AutoIMD
- IMDMenu
- NAMD GUI
- NAMD Server
- QMTool

Data Plugins

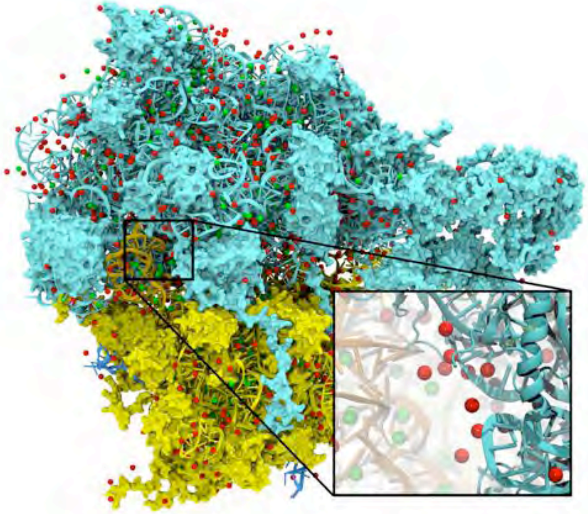
- Data Import
- Multiplot
- PDBtool
- MultiText

Other Plugins

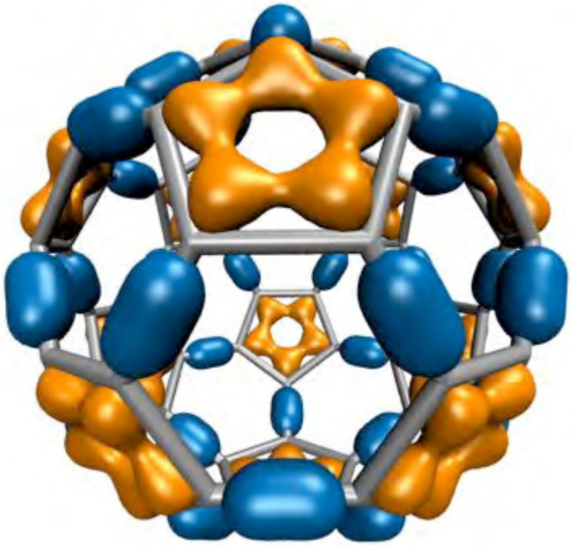
- AtomEdit
- DemoMaster
- ExecTool
- Hesstrans
- Optimization
- PBCTools
- RESPTool
- RNAview
- SignalProc
- TkCon

http://www.ks.uiuc.edu/Research/vmd/plugins/

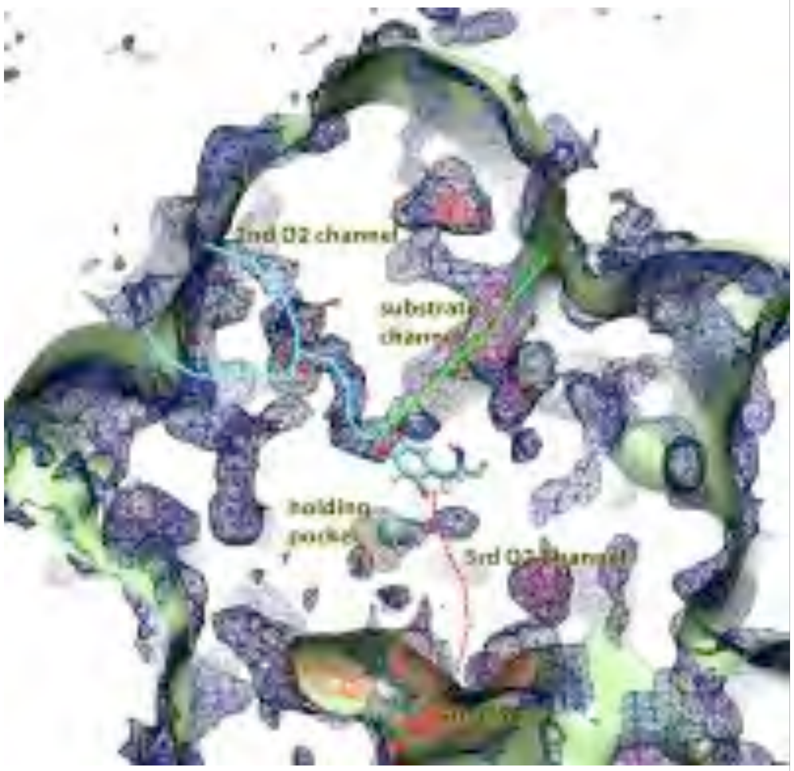
VMD the Compute Engine



Electrostatic field calculation, ion placement: factor of 20x to 44x faster

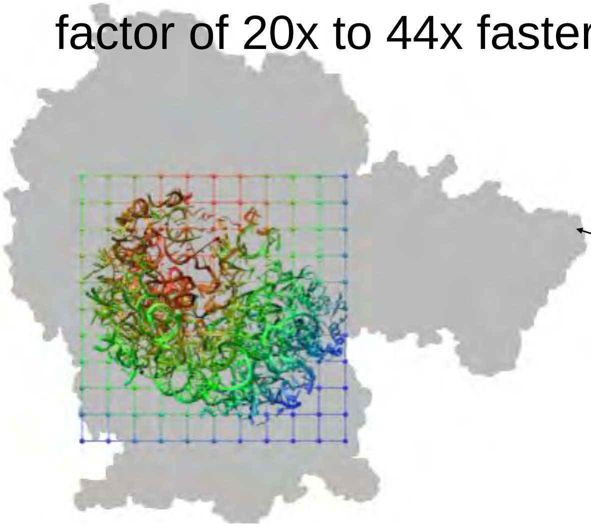


Molecular orbital calculation and display: factor of 120x faster



Imaging of gas migration pathways in proteins with implicit ligand sampling:

factor of 20x to 30x faster



Parallel analysis on GPUs

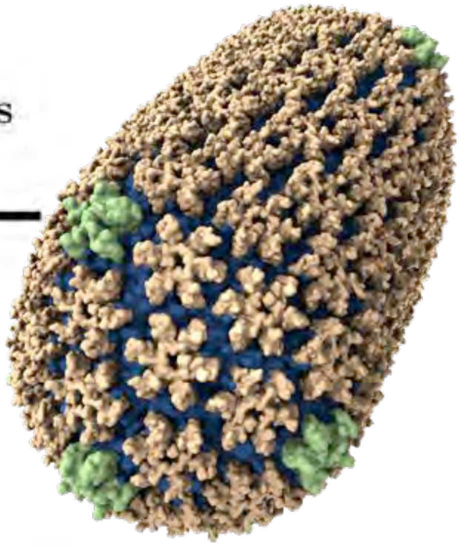
VMD is first bio-software that is optimized for power consumption!

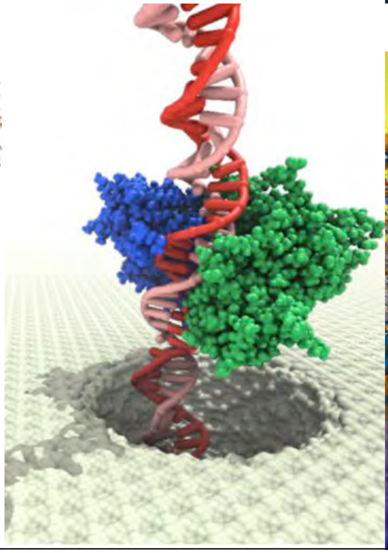
VMD the Artist

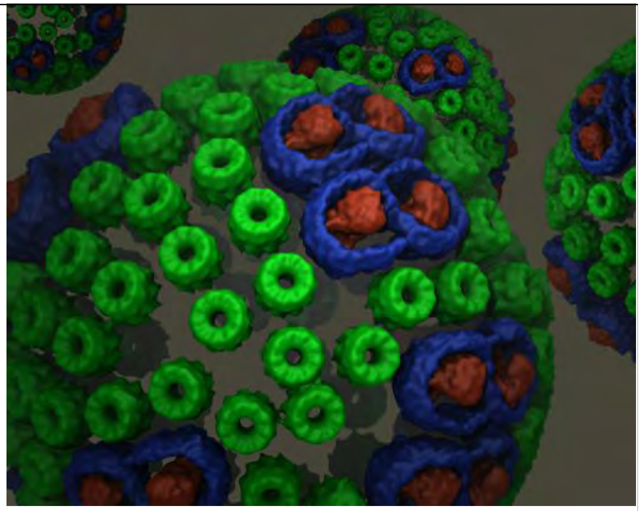
Publication-quality images and movies

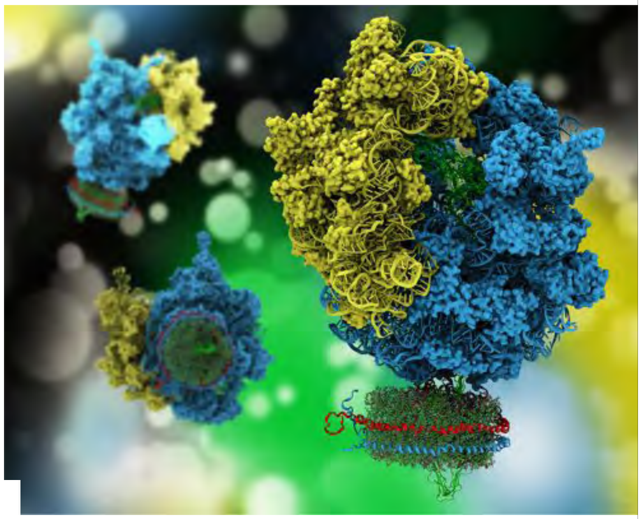
University of Illinois at Urbana-Champaign
Beckman Institute for Advanced Science and Technology
Theoretical and Computational Biophysics Group
Computational Biophysics Workshop

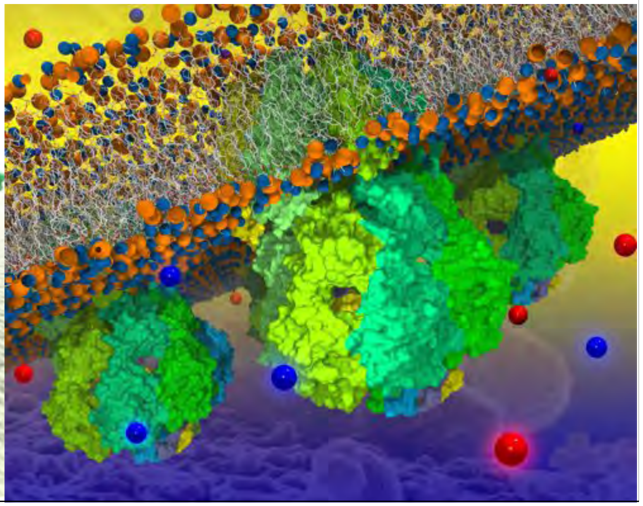
VMD Images and Movies
Tutorial





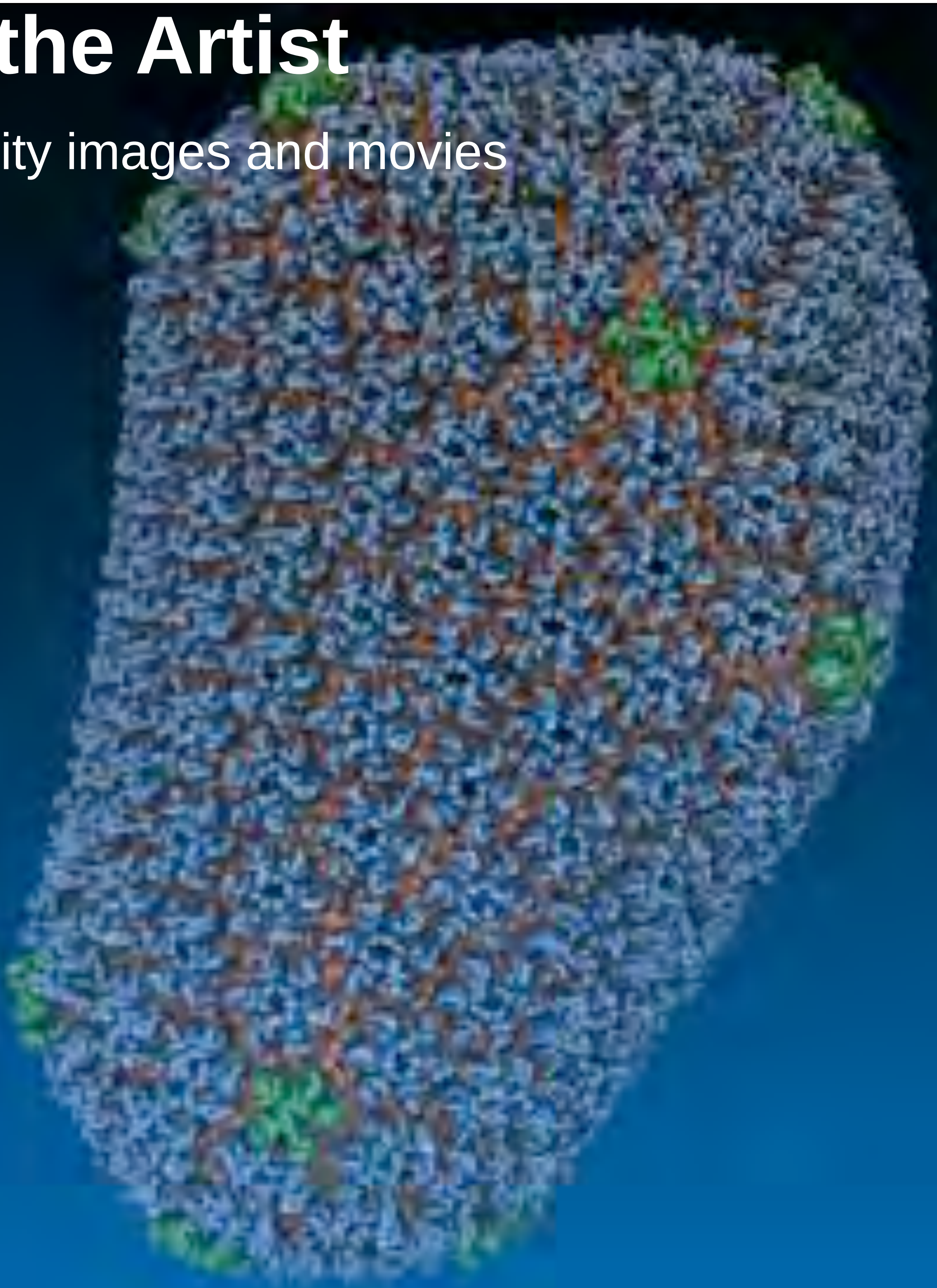






VMD the Artist

Publication-quality images and movies



Section from “Life on Earth” and chromatophore movie

VMD Session 3:
exchanging .vmd file
of photosynthetic chromatophore
for joint viewing

VMD 1.9.1 Released Feb. 4, 2012

Key Features

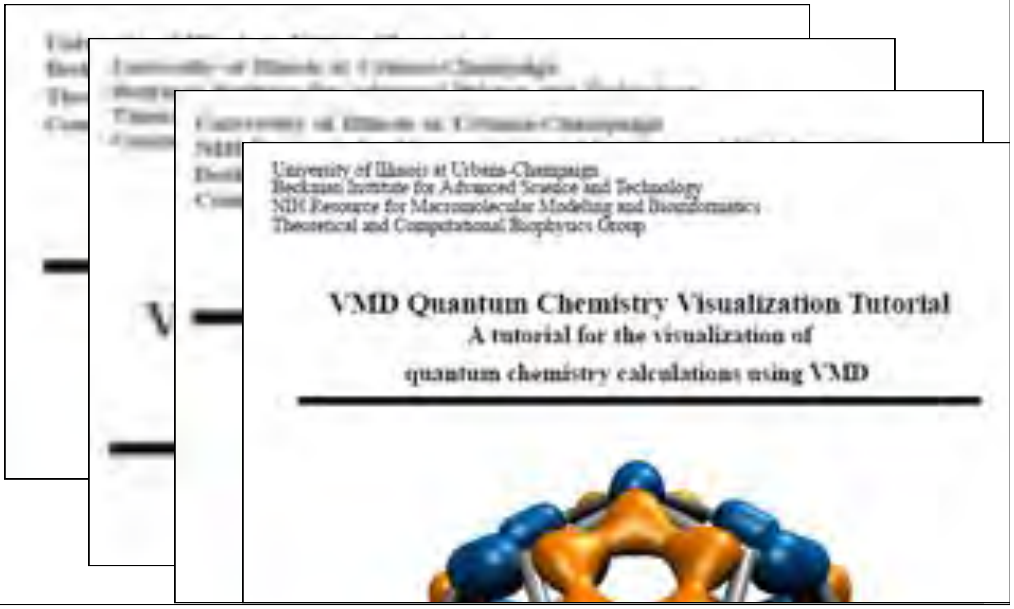
- New **NetworkView** plugin for study of allostery, signaling networks
- New **Force Field Toolkit (ffTK)** assists with CHARMM parameter development
- New "**QuickSurf**" surface representation
- New **user-contributed plugins**:
  - Normal Mode Wizard
  - PropKa interface
  - RMSD Trajectory Tool
  - "Heat map" plotting
  - Many others…

NetworkView: tRNA anti-codon w/ ligand in GluRS active site

VMD and NAMD Work Together

- Over 212,000 registered VMD users
  - 18% (39,000) are NIH-funded
  - Over 49,000 have downloaded multiple VMD releases
- Over 8,000 citations
- User community runs VMD on:
  - MacOS X, Unix, Windows operating systems
  - Laptops, desktop workstations
  - Clusters, supercomputers

- VMD user support efforts:
  - 20,000 emails, 2007-2011
  - Develop and maintain VMD tutorials and topical mini-tutorials; 11 in total
  - Periodic user surveys



University of Illinois at Urbana-Champaign
Beckman Institute for Advanced Science and Technology
NIH Resource for Macromolecular Modeling and Bioinformatics
Theoretical and Computational Biophysics Group

VMD Quantum Chemistry Visualization Tutorial

A tutorial for the visualization of quantum chemistry calculations using VMD

The Biomedical Technology Research Center (BTRC) for Macromolecular

Achievements Built on People

- 5 faculty members (2 physics, 1 chemistry, 1 biochemistry, 1 computer science);
- 8 developers; 1 system admin.; 17 post docs; 46 graduate students; 3 administrative staff (assistant director, grants coordinator, training and dissemination)
- Funding/support from NIH and National Science Foundation

Beckman Institute, Urbana, Illinois