

VMD Plugin Highlights

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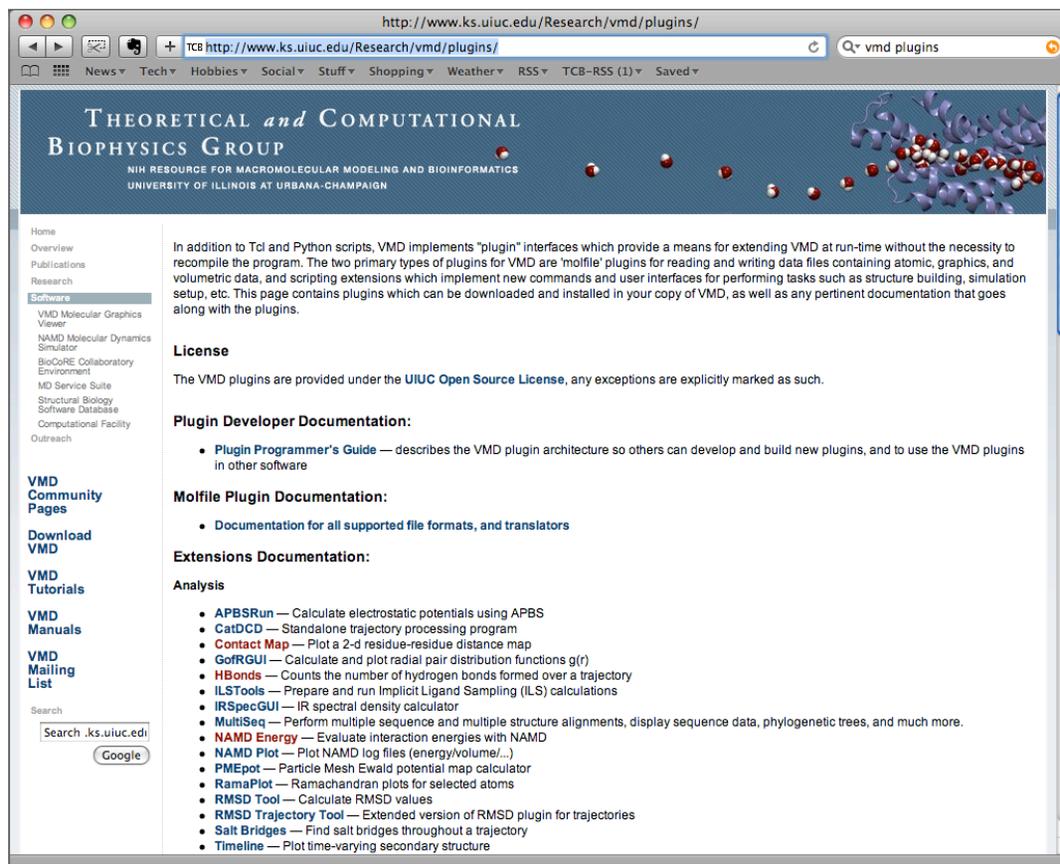
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NIH Resource for Biomolecular Modeling and Bioinformatics
<http://www.ks.uiuc.edu/>

Beckman Institute, UIUC

Plugins: The Molecular Modeling Toolbox

- Extensive library of plugins comes with VMD: See Extensions Menu
- Some are text only, many have text and graphical modes
- Write your own in Tcl/Tk
- Third-party plugins



<http://www.ks.uiuc.edu/Research/vmd/plugins/>
vmd-l@ks.uiuc.edu

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



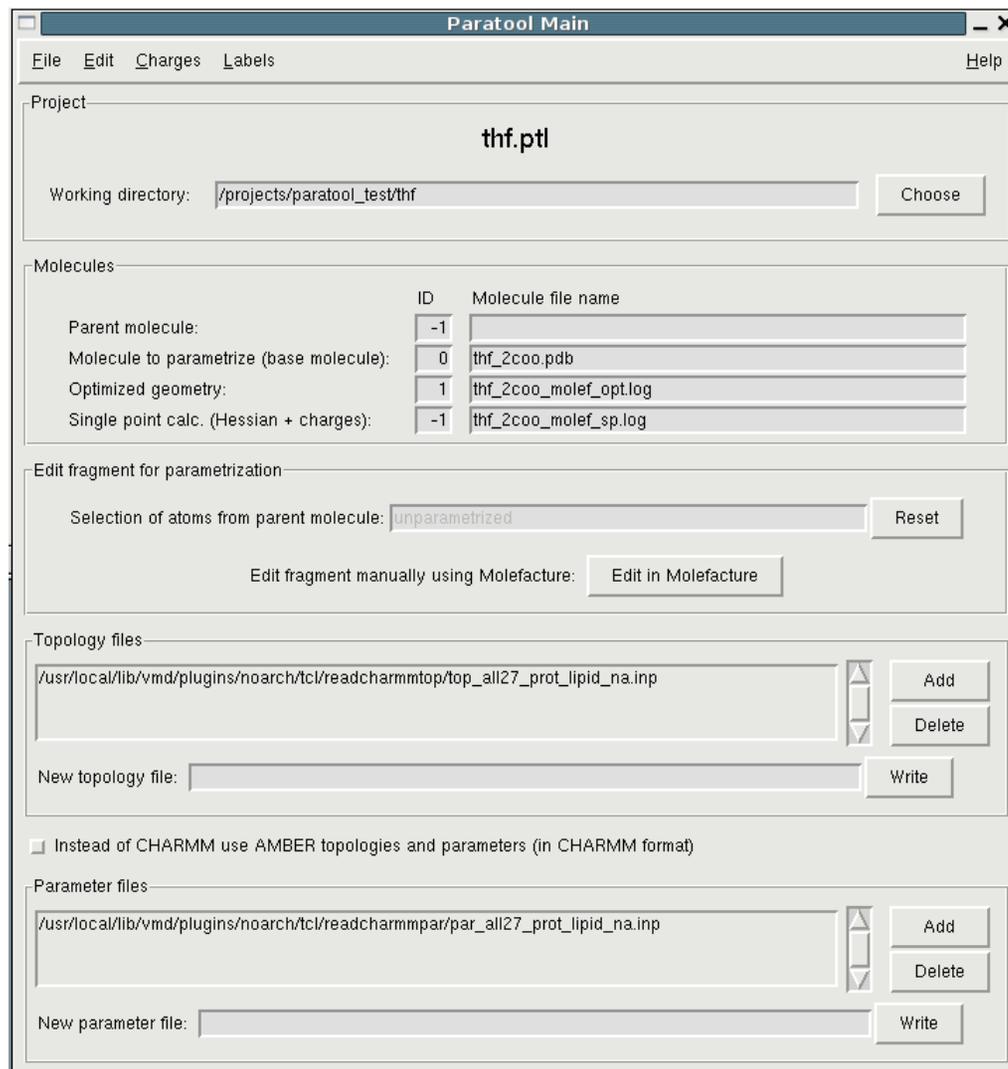
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Build a molecule

- Molefacture — small structure builder
- Inorganic Builder — Build devices
- MergeStructs — Merge multiple structures
- Paratool — Calculation of force field parameters
- CGTools — Transform structures between coarse-grain and all-atom representations



Prepare the System

- PSFgen — Build structures for use with NAMD
- AutoPSF — Automatic PSF structure building tool
- Solvate — Add water to a structure
- AutoIonize — Add sodium or chlorine ions to a structure for simulation

AutoPSF

Help

Input and Output Files

Molecule: 0: 1ubq Output basename: 1ubq_autopsf

Topology files

/Projects/vmd/pub/linux/lib/vmd186b2/plugins/noarch/to1

Add

Delete

Load input files

Selections to include in PSF/PDB

Everything Protein Nucleic Acid

Other:

Guess and split chains using current selections

Chains Identified

Name	Length	Index	Range	Nter	Cter	Type
P1	76	1-	602	NTER	CTER	Prot
O1	58	603-	660	none	none	Other

Add a new chain

Edit chain

Delete chain

Create chains

Patches

Patch	Segid:Resid	Segid:Resid
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Add patch

Delete patch

Apply patches and finish PSF/PDB

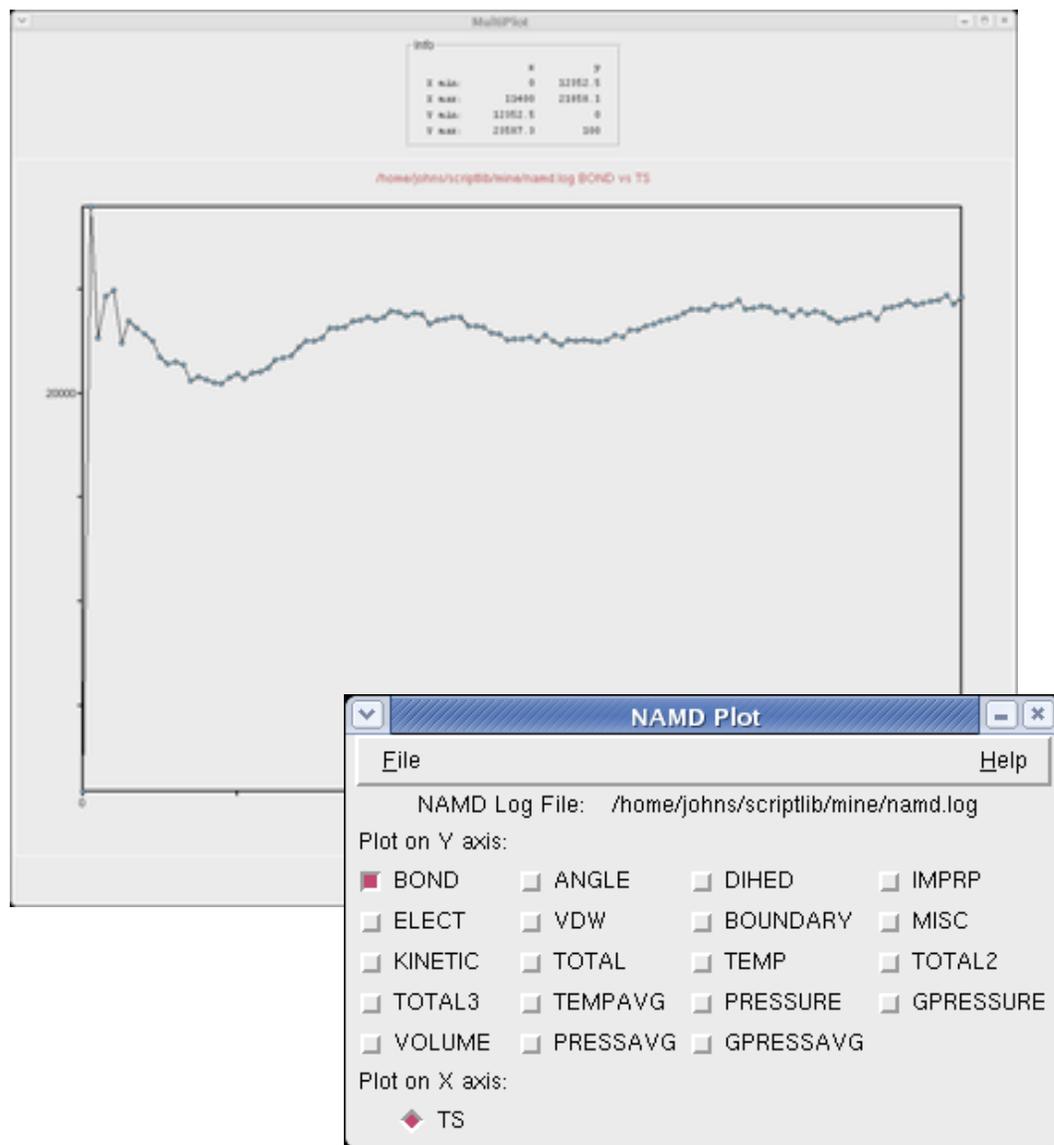
Extras: Solvate Ionize Regen

Reset Autopsf

I'm feeling lucky

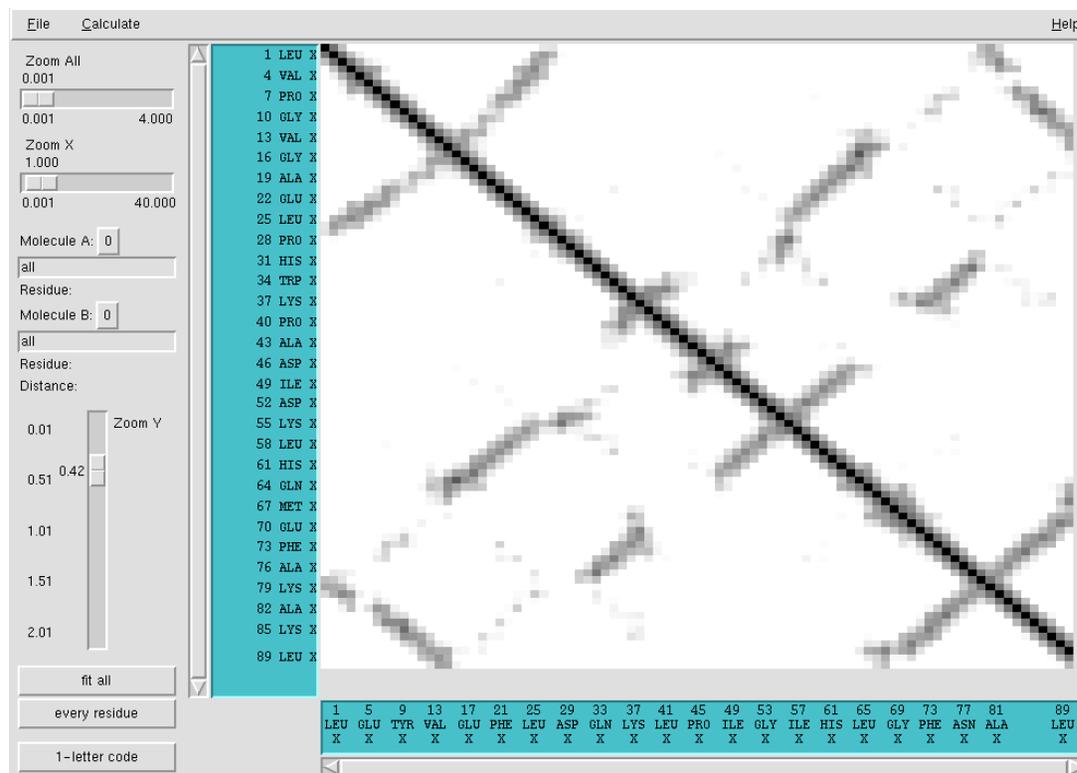
Post-Processing

- TkConsole — A better console
- CatDCD — Trajectory processing
- PBCTools — Tools for manipulating simulation data with periodic boundary conditions
- NAMD Plot — Plot NAMD log output
- RamaPlot — Ramachandran plots
- RMSD Trajectory Tool — Calculate RMSD values for trajectories



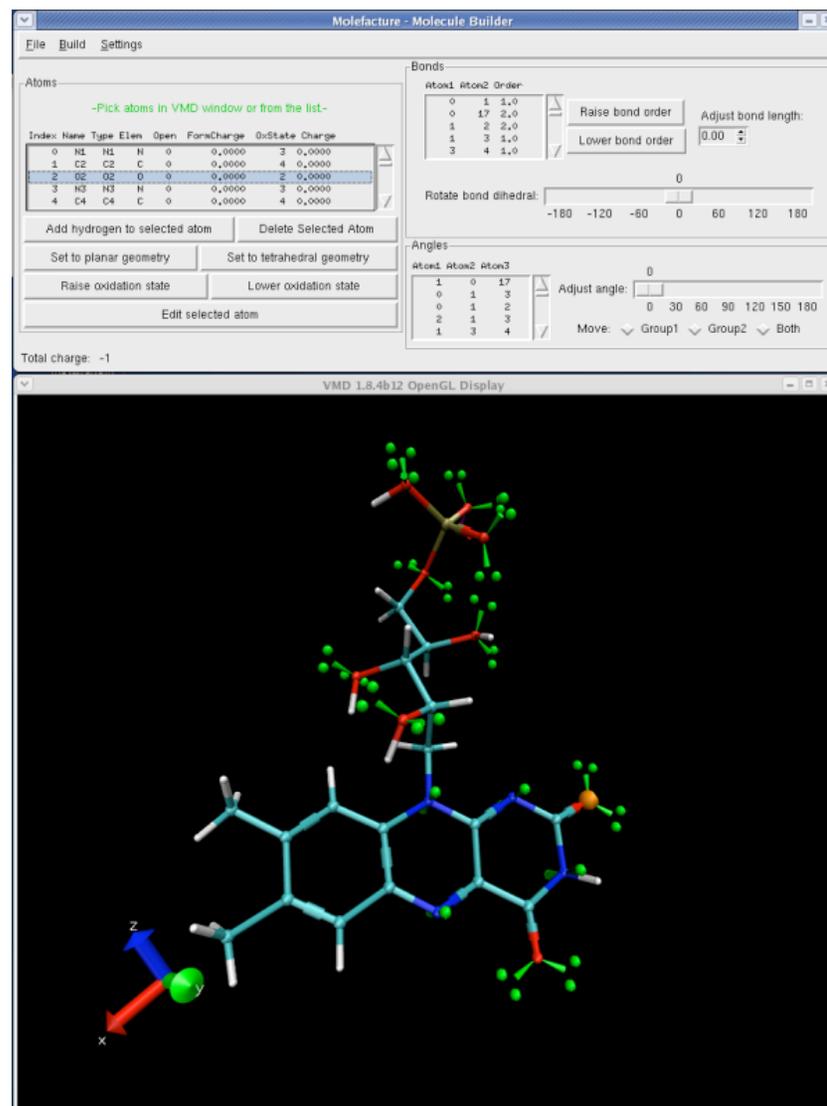
Analysis

- Contact Map — Plot a 2-d residue-residue distance map
- HBonds — Counts hydrogen bonds formed over a trajectory
- Salt Bridges — Find salt bridges throughout a trajectory
- NAMD Energy — Evaluate interaction energies
- PMEpot — Particle Mesh Ewald potential map calculator
- Timeline — Plot time-varying secondary structure



Molefactory: Assemble small molecules

- Edit molecules
- Add, delete, or manipulate their structure at atomic level
- Build new components from a library of common fragments.

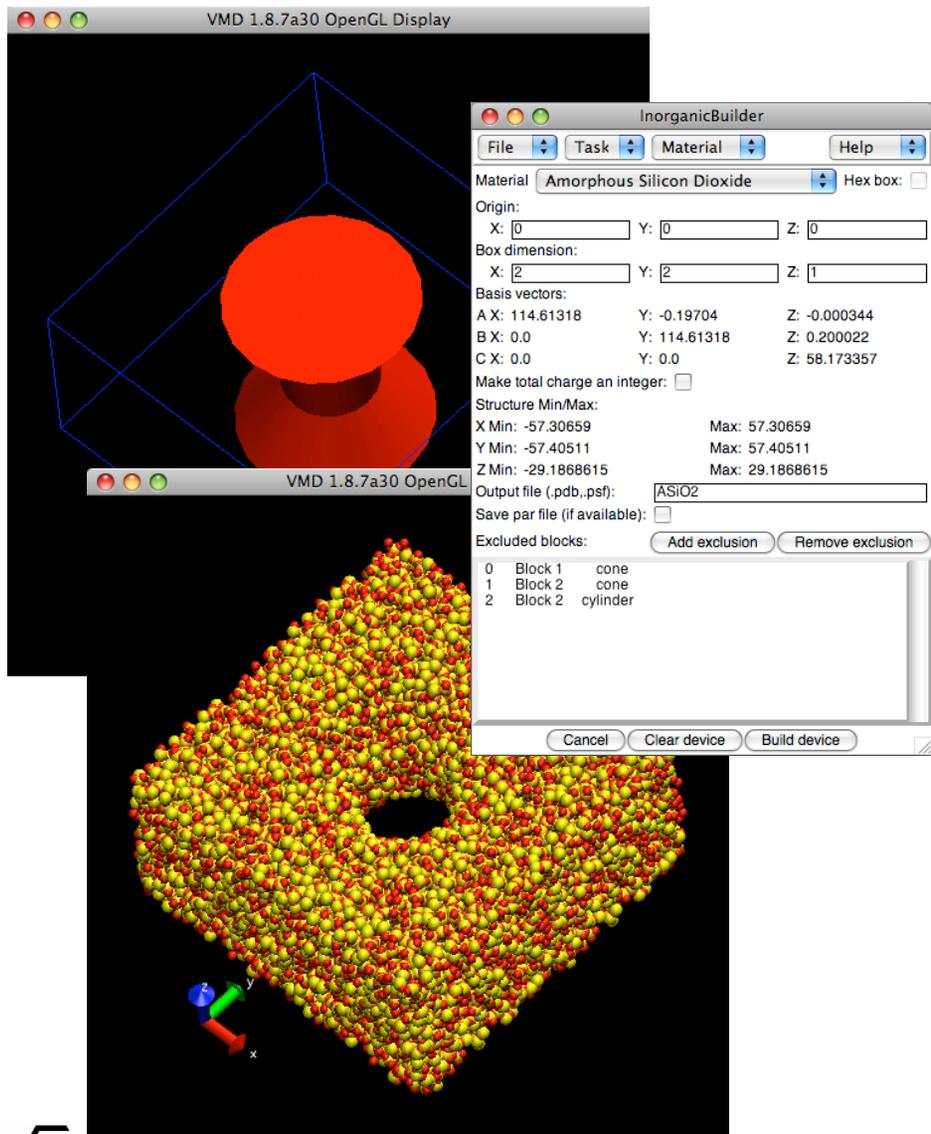


Inorganic Builder: Build nanodevice models

Goal: Provide a fast way to build device models for evaluating prototype designs

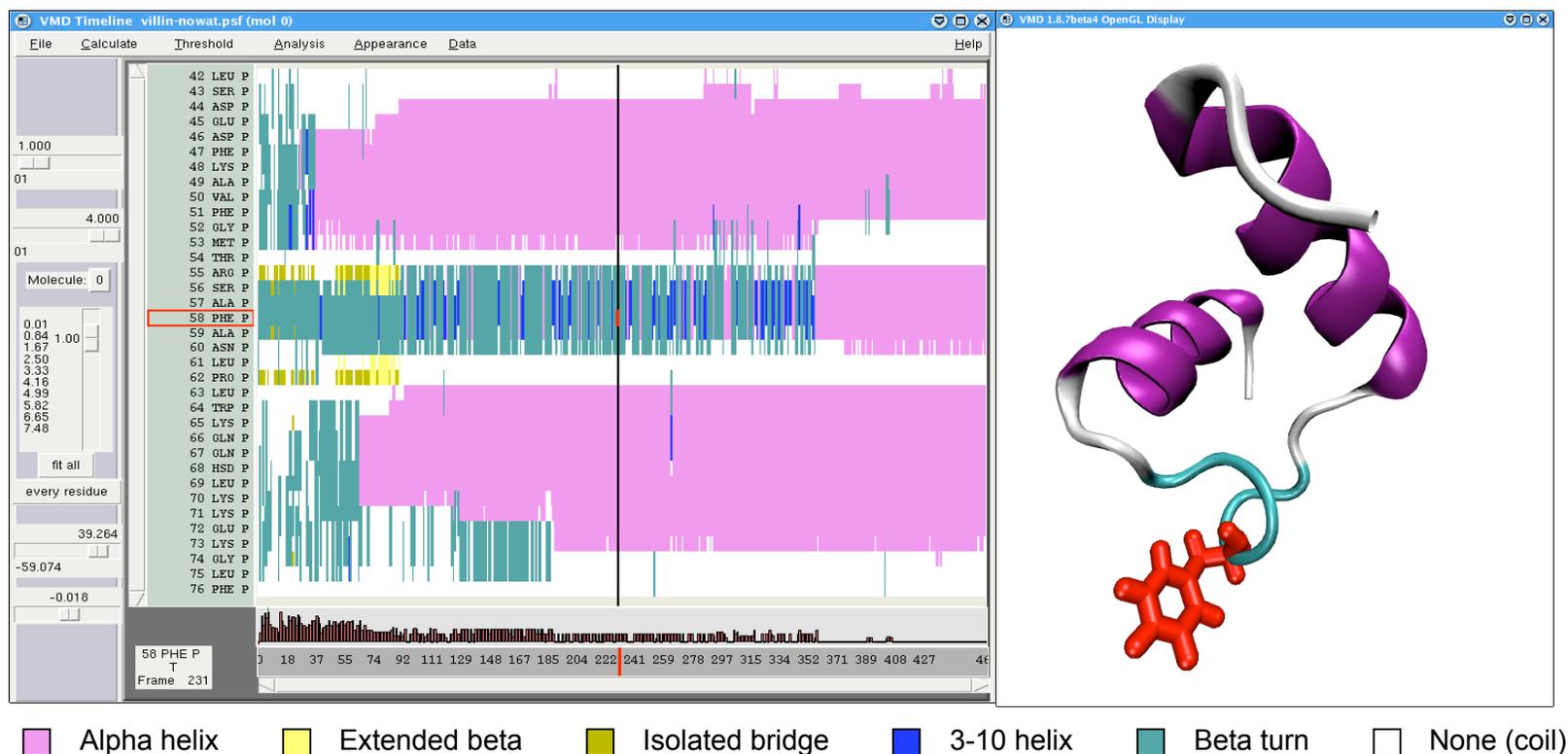
InorganicBuilder Plugin

- Design device model geometry
- Bond search: type/distance based
- Extract surface atoms
- Add biomolecules
- Solvate model
- Library of common materials
- Extensible material list



Timeline: a tool to locate events in MD trajectories

Events during 7 μ s villin headpiece folding



Per-residue secondary structure: villin headpiece folding from a fully denatured state.
7 μ s simulation; 654 atoms; over 1 million frames to examine

VMD Timeline plug-in: graphing and analysis tool to identify events in an MD trajectory

- a single picture shows changing properties across entire structure, entire trajectory.
- explore time vs. attribute (per-residue or per-selection) linked to molecular structure
- many analysis methods available; user-extendable

End



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