Advances In Biomolecular Simulation with NAMD and VMD

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http://www.ks.uiuc.edu/Research/gpu/

http://www.ks.uiuc.edu/Research/namd/

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

Pawsey Supercomputing Centre

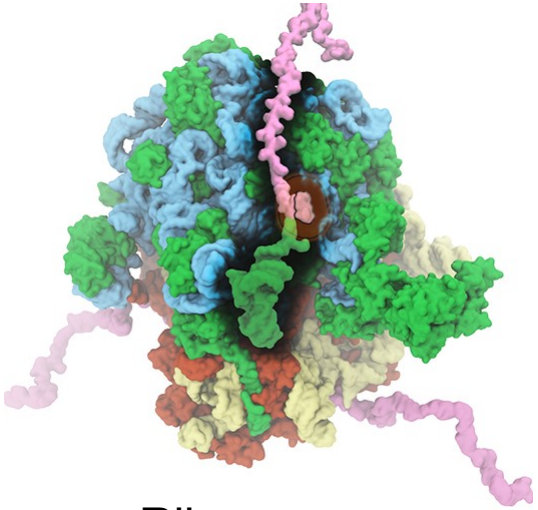
Kensington, WA, Australia, Thursday April 18th, 2018

NAMD & VMD: Computational Microscope

Enable researchers to investigate systems described at the atomic scale

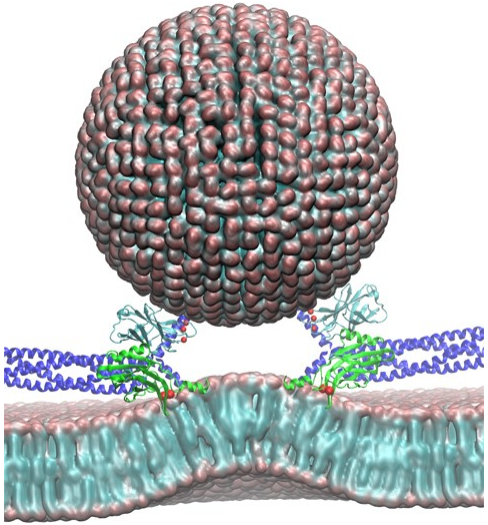
NAMD - molecular dynamics simulation

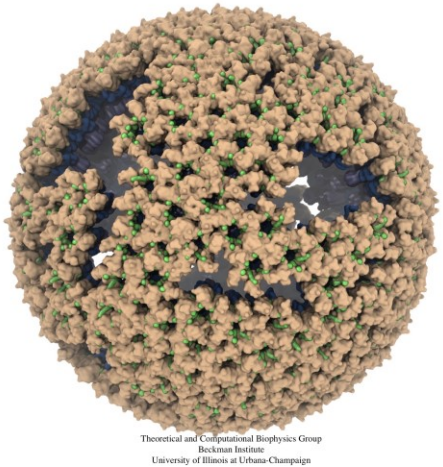
VMD - visualization, system preparation and analysis



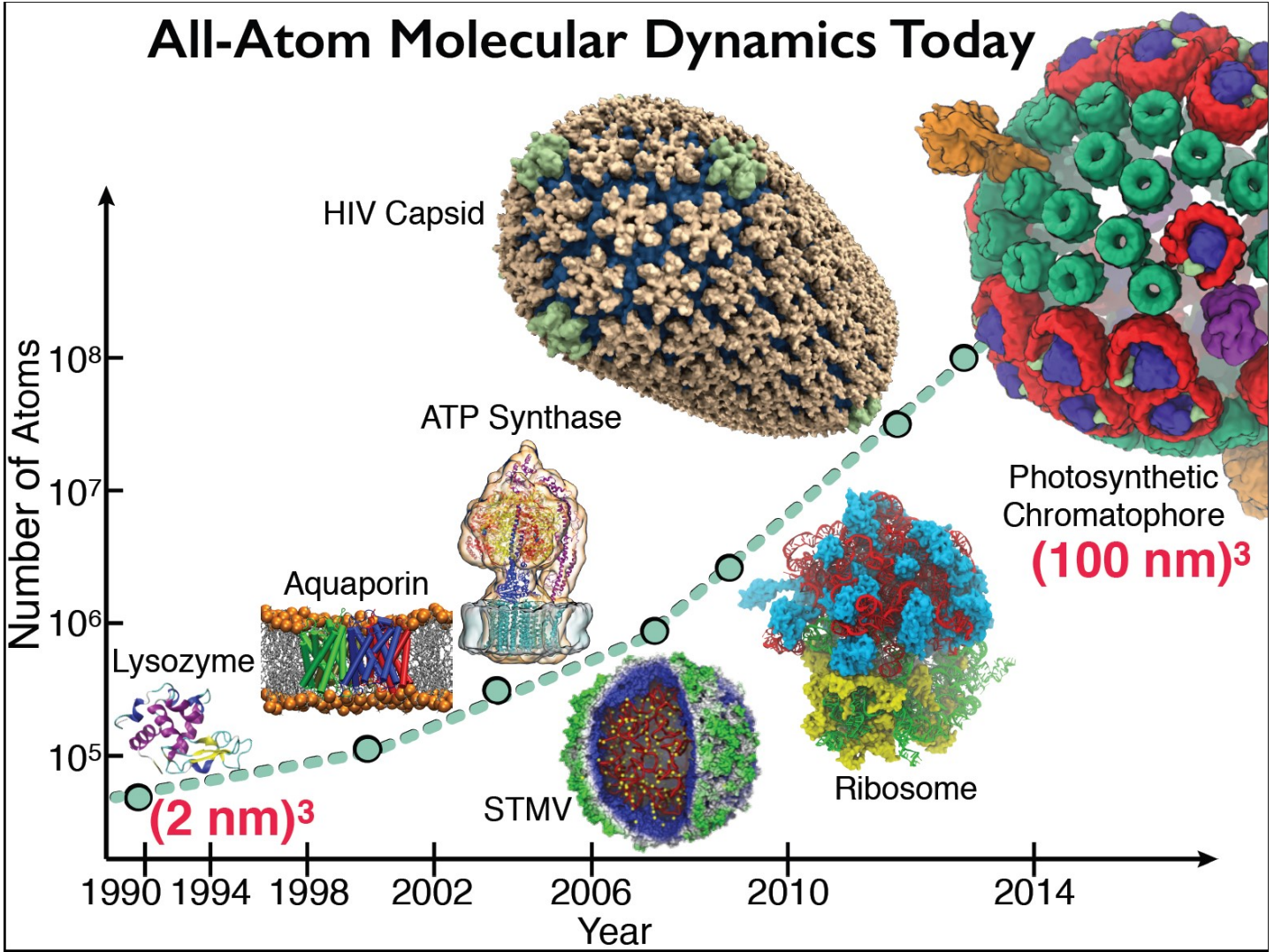
Ribosome

Neuron

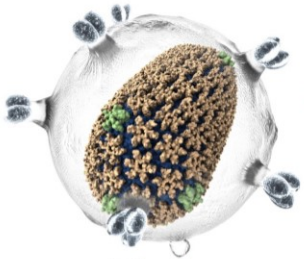




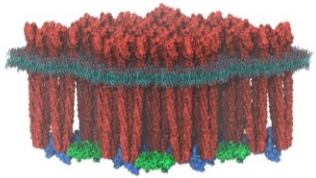
Virus Capsid


All-Atom Molecular Dynamics Today
HIV Capsid
ATP Synthase
Aquaporin
Lysozyme
STMV
Ribosome
Photosynthetic Chromatophore
(100 nm)3
(2 nm)3
Number of Atoms
10^8
10^7
10^6
10^5
1990
1994
1998
2002
2006
2010
2014
Year

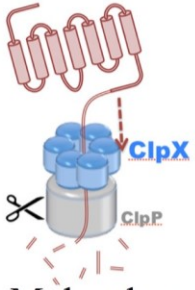
Petascale Simulations Driving NAMD/VMD Development



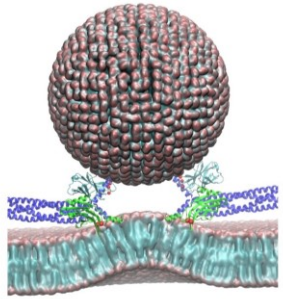
Viral Infection



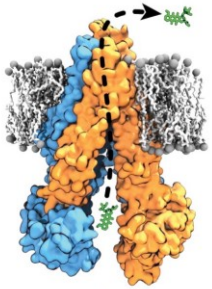
Symbiont Bacteria



Molecular Motors



Neurons and Synapses



Membrane Transporters

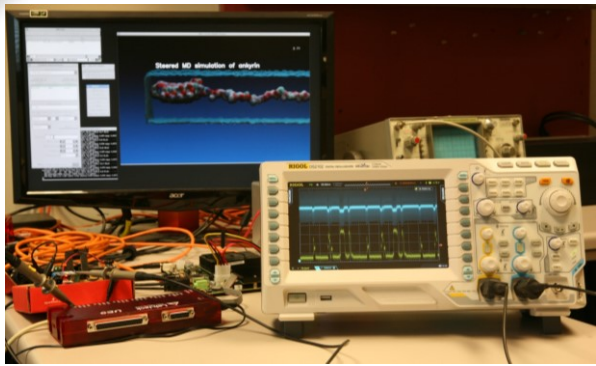
NCSA ORNL	Blue Waters (4,228 XK7 nodes) Titan (18,688 XK7 nodes)	AMD Opteron + K20X Kepler GPU	16 CPU cores / GPU
TACC	Stampede 2 (4200 KNL nodes, 1736 Skylake nodes)	Intel Knights Landing Intel Xeon Skylake	68 CPU cores 48 CPU cores
ORNL	Summit (~4600 nodes)	2 IBM Power9 + 6 Tesla V100 GPUs	7 CPU cores / GPU

Technology Opportunities and Collaborations

- Supercomputer Centers, Cray, IBM
  - GPU accelerated supercomputing
  - **In-situ and remote visualization technologies**
- NVIDIA
  - **GPU computing**
  - **Performance profiling and optimization**
  - **Ray tracing**
  - **In-situ and remote visualization**
  - **HPC/AI containers and clouds**
- Intel
  - **CPU vectorization and sw optimization**
  - **Ray tracing**
  - **Non-volatile memory systems**
- Amazon
  - Cloud deployment of VMD/NAMD, related tools
- Universities:
  - **T. Ertl, U. Stuttgart: visualization algorithms**
  - G. Fiorin, J. Henin, Toni Giorgino, collective variables
  - W. Sherman, Indiana U.: VR HMDs, visualization

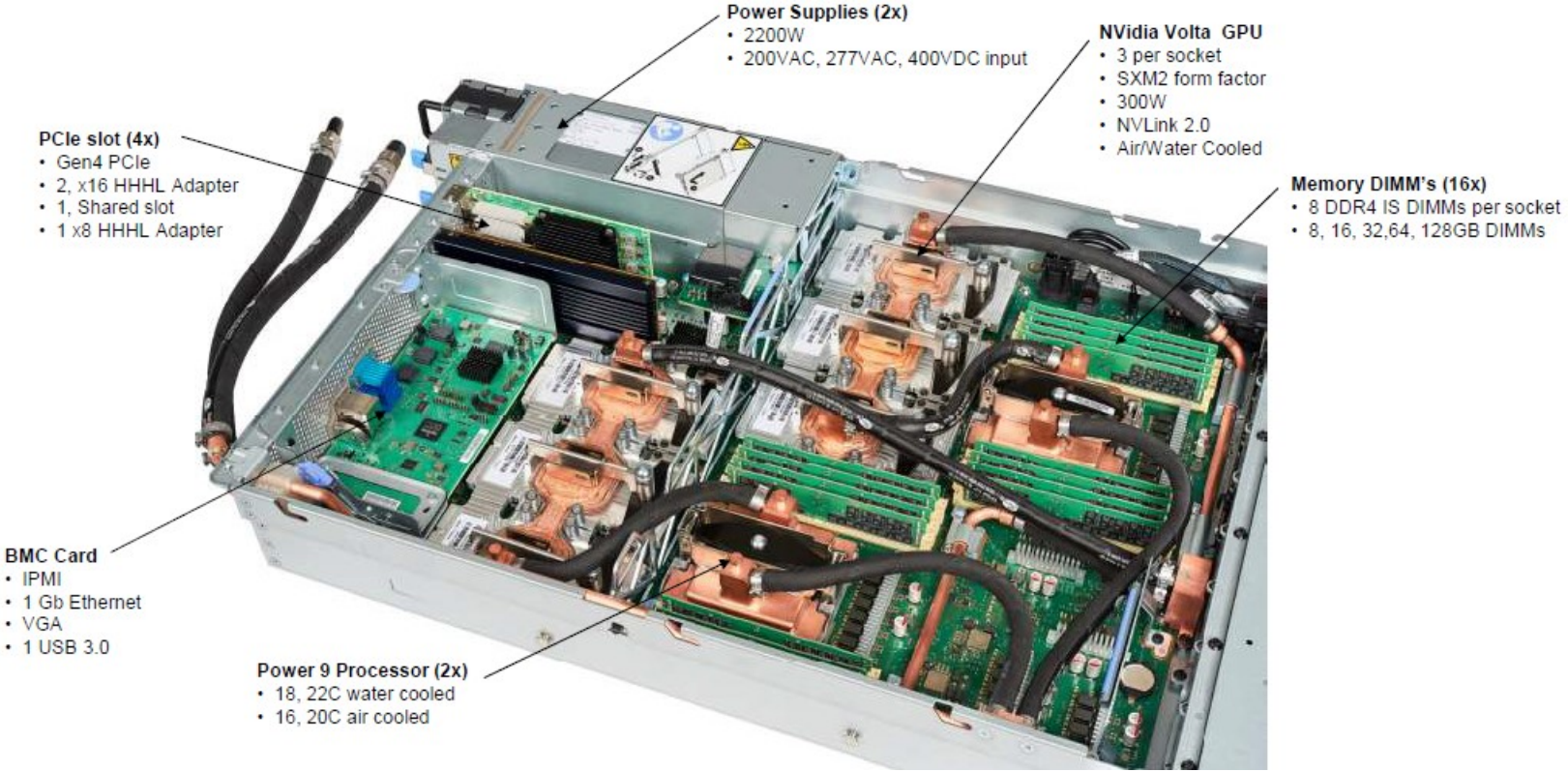
VR HMDs, 6DoF input devices

GPU computing,
Ray tracing,
Remote viz.

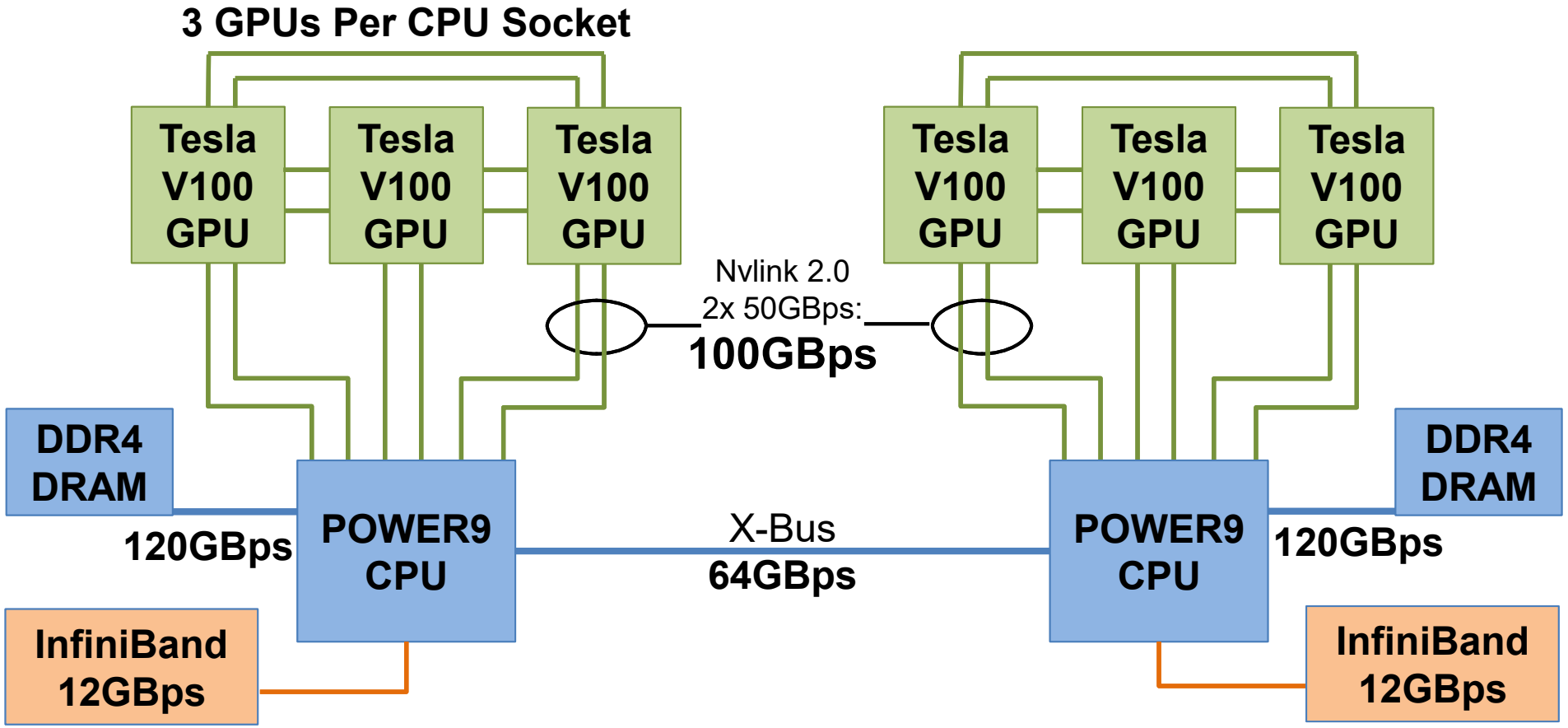


Energy efficiency: ARM+GPU

IBM AC922 w/ 6 GPUs



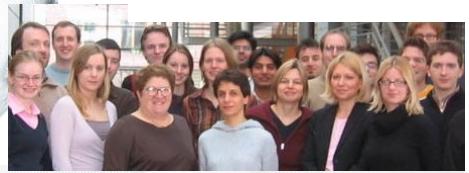
IBM AC922 Summit Node

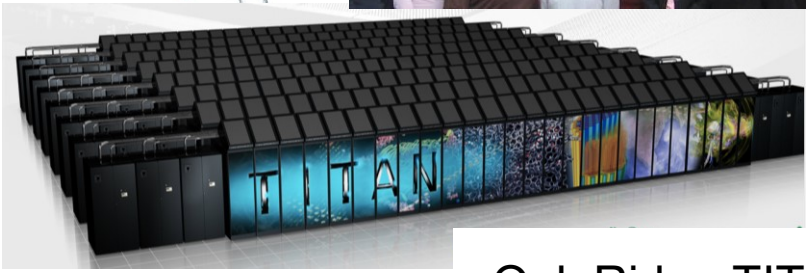


NAMD Highlights

- **Over 12,600 citations of NAMD**
- One program available on all platforms.
  - Desktops and laptops – setup and testing
  - Linux clusters – affordable local workhorses
  - Supercomputers – free allocations on XSEDE
  - Blue Waters – sustained petaflop/s performance
  - GPUs – from desktop to supercomputer
- User knowledge is preserved across platforms.
  - No change in input or output files.
  - Run any simulation on **any number of cores**.
- Available free of charge to all.

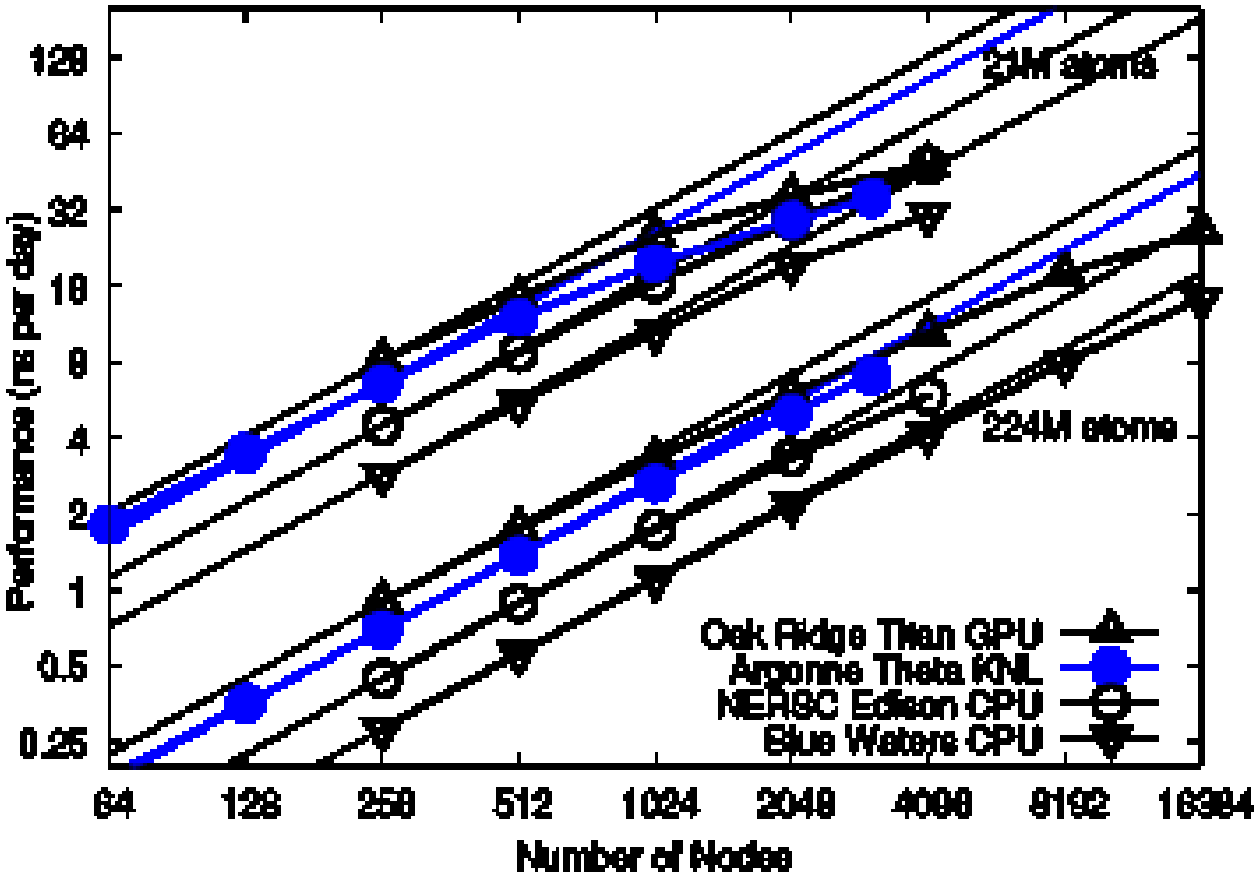
Hands-On Workshops



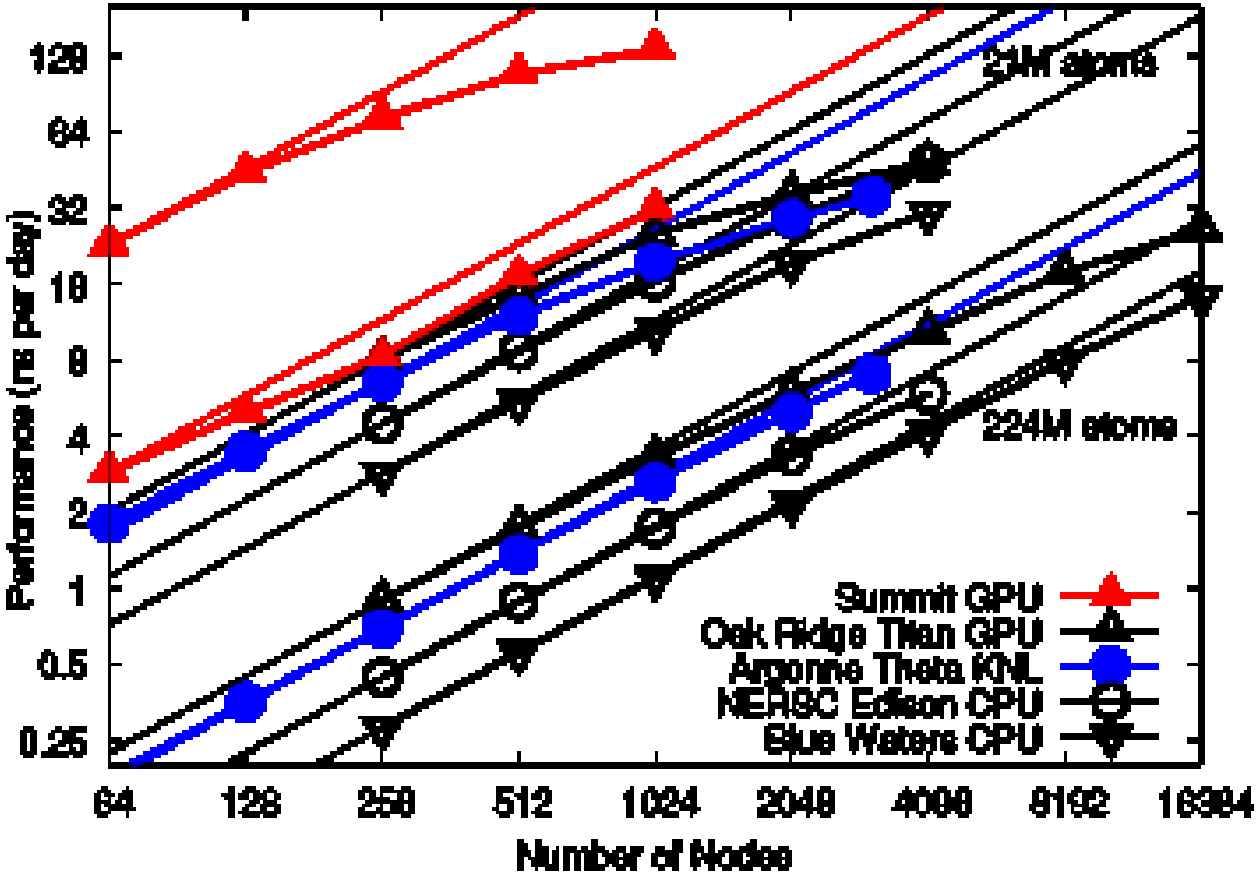


Oak Ridge TITAN

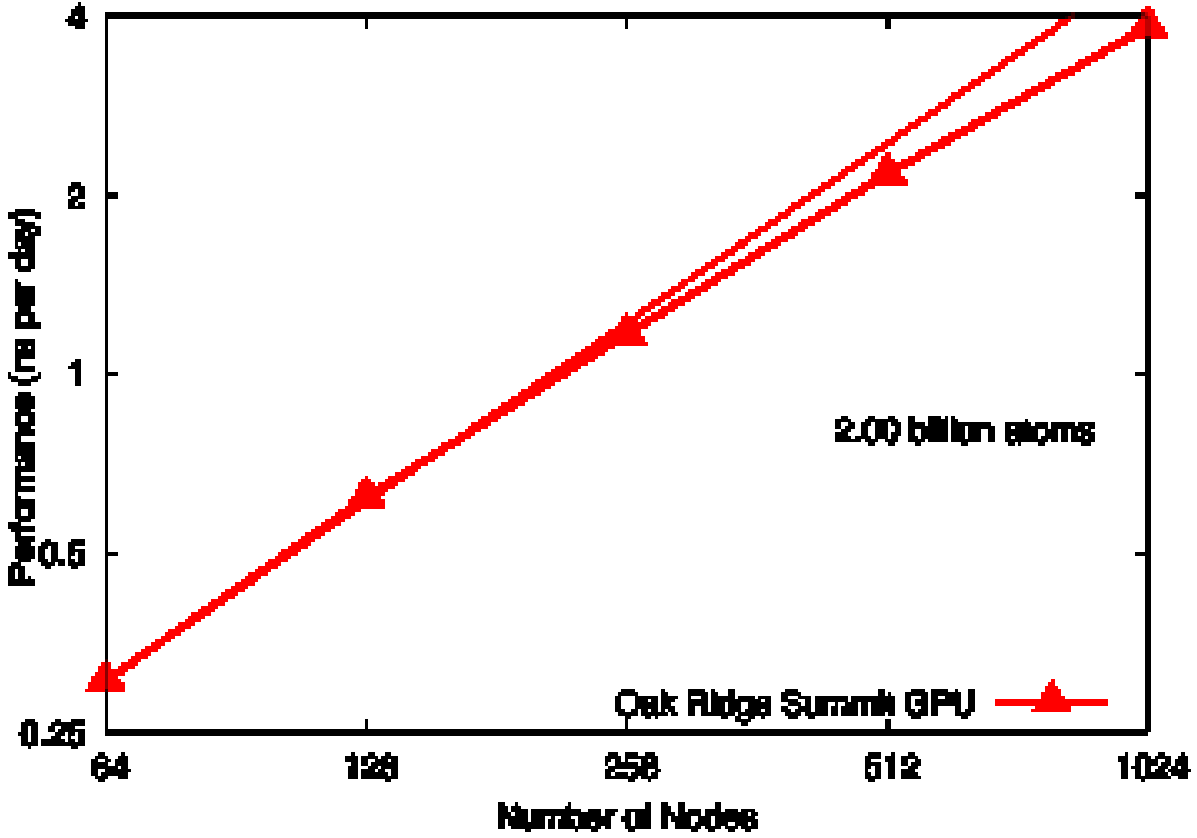
NAMD Now Runs on Summit



NAMD Now Runs on Summit



NAMD 2 Billion Atom Benchmark



Upcoming NAMD 2.13 Release

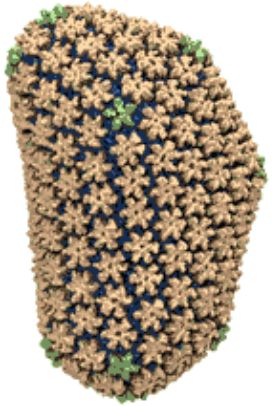
- NAMD 2.13 beta will soon be released
- Improved GPU support
  - Introducing CUDA kernels for offloading (almost) entire force calculation
    - Bonds, angles, dihedrals, impropers, crossterms, exclusions
  - Better GPU device management, especially for multiple GPUs per node
- Support for system sizes up to 2 billion atoms
  - Internal fixes for data structure setup and file I/O
  - Extend system preparation tools (combine Psfgen with substructure assembly)
  - Enables simulation of initial protocell model

NAMD 2.13 Advanced Simulation Features

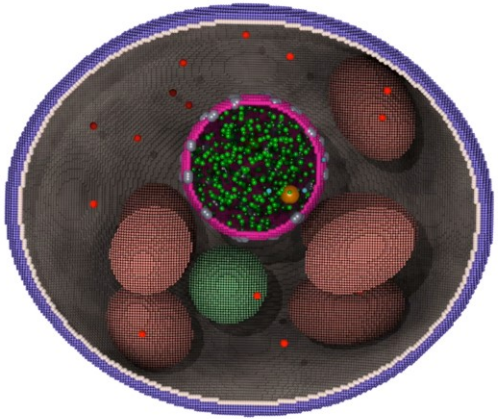
- Hybrid Quantum Mechanics / Molecular Mechanics simulation
  - Precise QM calculations for regions such as active sites of enzymes
  - Combined with fast classical calculation for the rest of a biomolecular system
  - **Interfaces support MOPAC (semi-empirical) and ORCA (*ab-initio*/DFT)**
  - **M. Melo, R. Bernardi, et al. *Nature Methods*, 2018.**
- Constant-pH Molecular Dynamics simulation
  - Study changes in protonation states of molecules in response to a pH buffer
- REST2 (Replica Exchange Solute Tempering) simulations
  - Enhanced sampling, more efficient than traditional temperature exchange
  - Implemented by rescaling force field parameters - immediate GPU support

VMD – “Visual Molecular Dynamics”

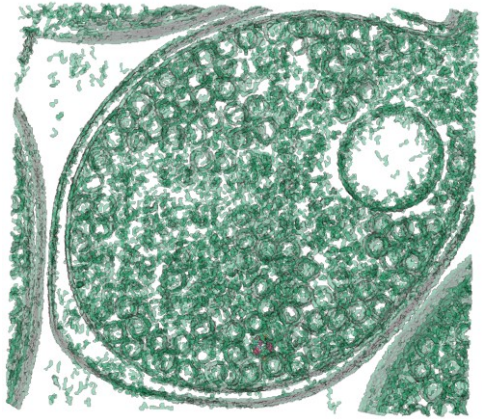
- Unique capabilities:
  - Trajectories are fundamental to VMD
  - Support for very large systems, now reaching billions of particles
  - Extensive GPU acceleration
  - Parallel analysis/visualization with MPI
- Visualization and analysis of:
  - Molecular dynamics simulations
  - “Particle” systems and whole cells
  - Cryo-EM densities, volumetric data
  - Quantum chemistry calculations
  - Sequence information



MD Simulations

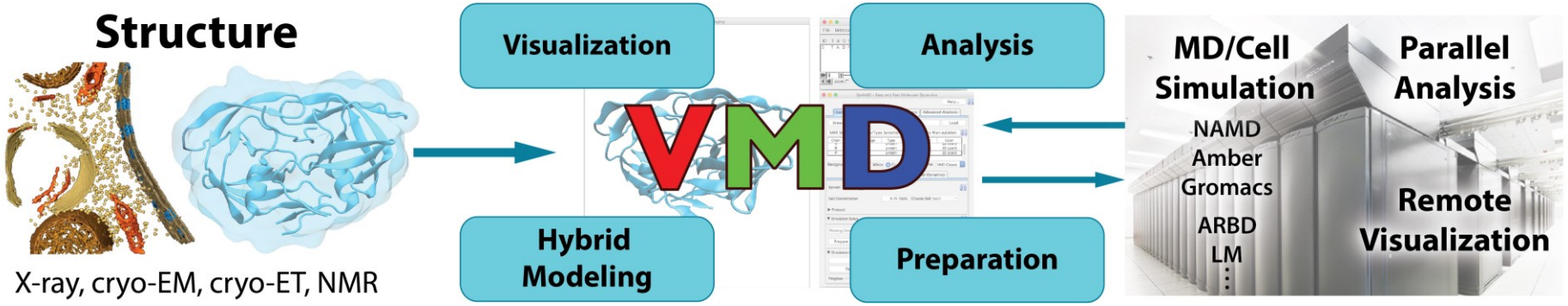


Cell-Scale Simulation



Integrate w/ Cryo-EM/ET

VMD: Building A Next Generation Modeling Platform



- Provide tools for simulation preparation, visualization, and analysis
  - Reach cell-scale modeling w/ all-atom MD, coarse grained, Lattice Microbes
  - Improved performance, visual fidelity, exploit advanced technologies (GPUs, VR HMDs)
- Enable hybrid modeling and computational electron microscopy
  - Load, filter, process, interpret, visualize multi-modal structural information
- Connect key software tools to enable state-of-the-art simulations
  - Support new data types, file formats, software interfaces
- Openness, extensibility, and interoperability are VMD hallmarks
  - Reusable algorithms made available in NAMD, for other tools

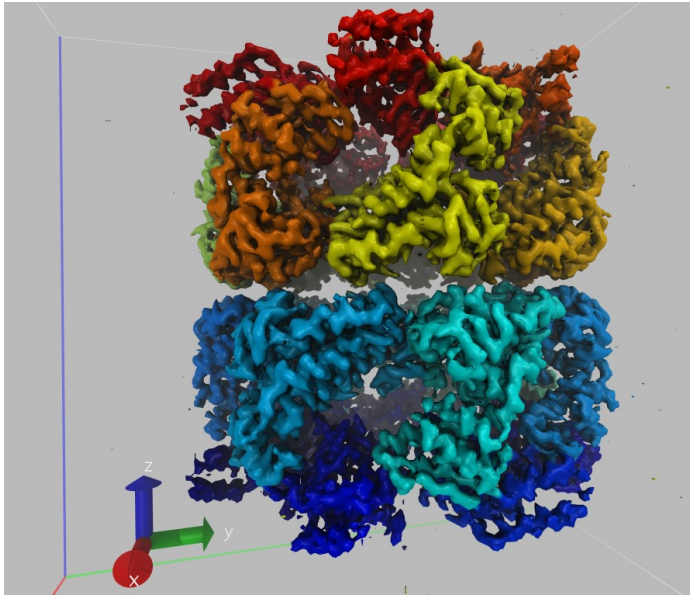
Upcoming VMD 1.9.4 Release, Foundation for Future

24,600 VMD Citations

1.9.3: 63,000 users, 9,965 NIH (Nov'16)

1.9.4 pre-releases: 12,500 users (Jul'17)

- VMD 1.9.4 beta release next month
- Support for ORNL Summit
- Many visualization and analytical advances:
  - **GPU-accelerated density map segmentation**
  - **Multi-billion voxel tomograms and density maps**
  - **QM/MM visualization improvements**
  - NanoShaper: molecular surfaces, cavity calc.
  - Many ray tracing advances
- New, updated, user-contributed plugins:
  - **QwikMD simulation prep/analysis: QM/MM**
  - **ffTK force field parameterization: RESP calcs**
  - BFEE– Binding free energy estimator
  - ParseFEP – Analyze NAMD free energy calculations



GPU Density Map Segmentation

Recent Publications:

- **NAMD goes quantum: An integrative suite for hybrid simulations. Nature Methods, 2018.**
- **Challenges of Integrating Stochastic Dynamics and Cryo-Electron Tomograms in Whole-Cell Simulations. JPCB, 2017**

Selected VMD Plugins: Center Developed, and User Developed

Analysis

- APBSRun
- CatDCD
- Contact Map
- GofRGUI
- HeatMapper
- ILSTools
- IRSpecGUI
- MultiSeq
- NAMD Energy
- NAMD Plot
- NetworkView
- NMWiz
- ParseFEP
- PBCTools
- PMEpot
- PropKa GUI
- RamaPlot
- RMSD Tool
- RMSD Trajectory Tool
- RMSD Visualizer Tool
- Salt Bridges
- Sequence Viewer
- Symmetry Tool
- Timeline
- TorsionPlot
- VolMap

Modeling

- AutoIonize
- AutoPSF
- Chirality
- Cionize
- Cispeptide
- CGTools
- Dowser
- ffTK
- Inorganic Builder
- MDFF
- Membrane
- Merge Structs
- Molefacture
- Mutator
- Nanotube
- Psfgen
- RESPTool
- RNAView
- Solvate
- SSRestraints
- Topotools

Visualization

- Clipping Plane Tool
- Clone Rep
- DemoMaster
- Dipole Watcher
- Intersurf
- Navigate
- NavFly
- MultiMolAnim
- Color Scale Bar
- Remote
- Palette Tool
- ViewChangeRender
- ViewMaster
- Virtual DNA Viewer
- VMD Movie Maker

Simulation

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

Collaboration

- Remote Control

Data Import and Plotting

- Data Import
- Multiplot
- PDBTool
- MultiText

Externally Hosted Plugins and Extensions

- Check sidechains
- MultiMSMS
- Interactive Essential Dynamics
- Mead Ionize
- Clustering Tool
- iTrajComp
- Swap RMSD
- Intervor
- SurfVol
- vmdICE

75 MolFile I/O Plugins:
structure, trajectory, sequence, and density map

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

QwikMD: Guided MD Simulation and Training
See live demo during lab tour!

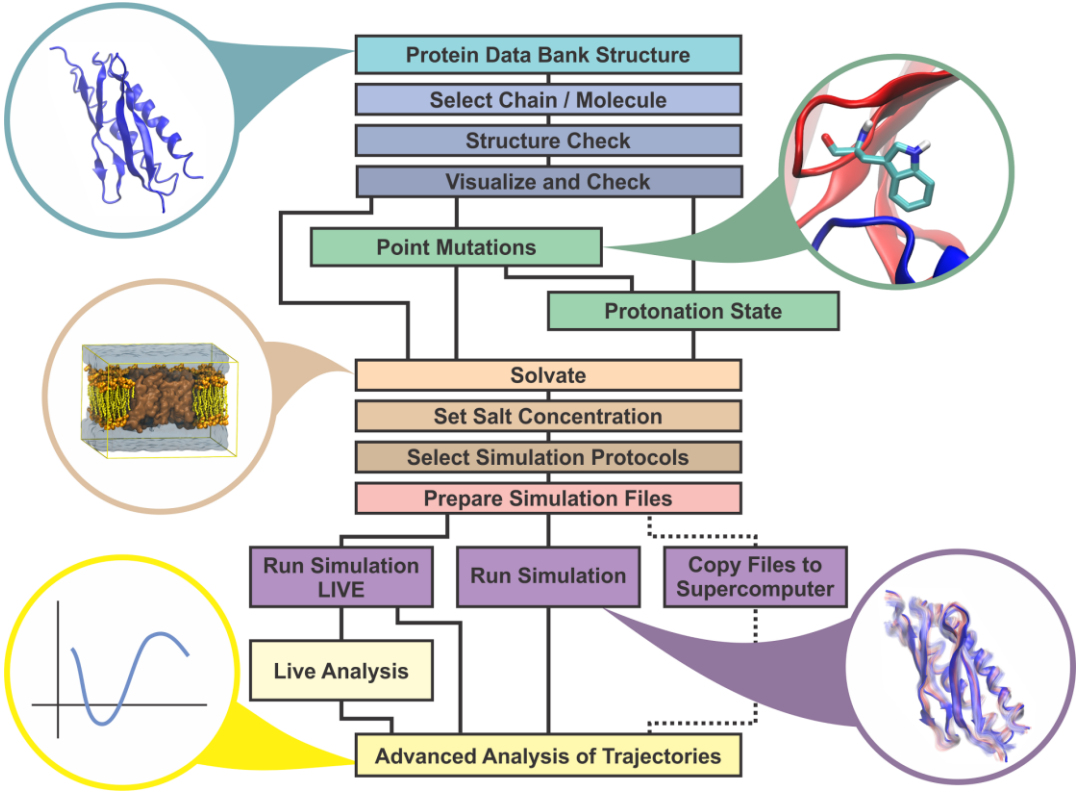
Smooths initial learning curve (non-expert users)

Training: used in 4 Center workshops to-date

Speed up tedious simulation preparation tasks (expert users)

Reproducibility: detailed log of all steps

Interactive preparation, simulation, and analysis



Ribeiro, et al. QwikMD - Integrative Molecular Dynamics Toolkit for Novices and Experts. ***Sci. Rep***. 6, 26536, 2016

Trajectory and Large System Analysis and Visualization on GPUs, Clusters, and Supercomputers

VMD Petascale Visualization and Analysis

- Analyze/visualize large trajectories too large to transfer off-site:
  - User-defined parallel analysis operations, data types
  - Parallel rendering, movie making
- Supports GPU-accelerated Cray XK7 nodes for both visualization and analysis:
  - **GPU accelerated trajectory analysis w/ CUDA**
  - **OpenGL and GPU ray tracing for visualization and movie rendering**
- Parallel I/O rates up to **275 GB/sec** on 8192 Cray XE6 nodes – can read in **231 TB in 15 minutes!**

Parallel VMD currently available on:

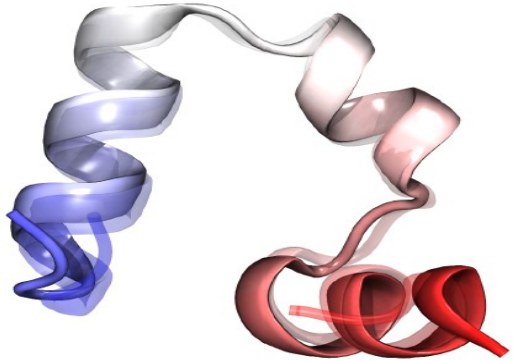
ORNL Titan, NCSA Blue Waters, Indiana Big Red II, CSCS Piz Daint, and similar systems

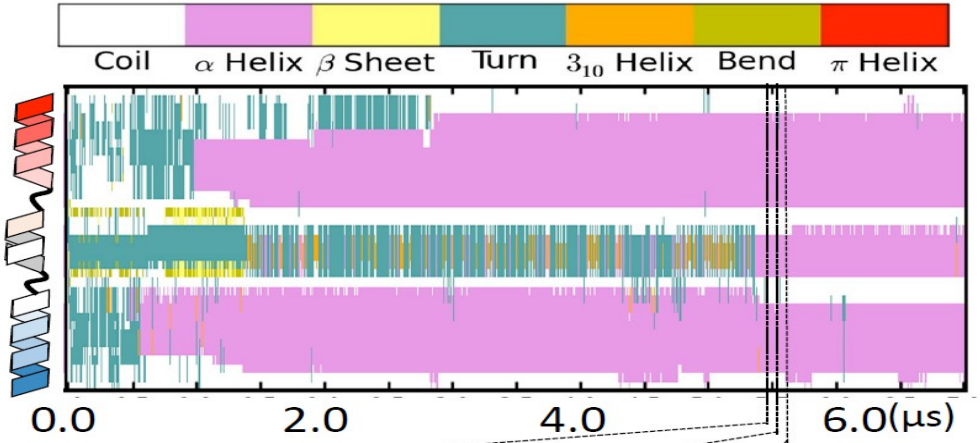
NCSA Blue Waters Hybrid Cray XE6 / XK7
22,640 XE6 dual-Opteron CPU nodes
4,224 XK7 nodes w/ Telsa K20X GPUs

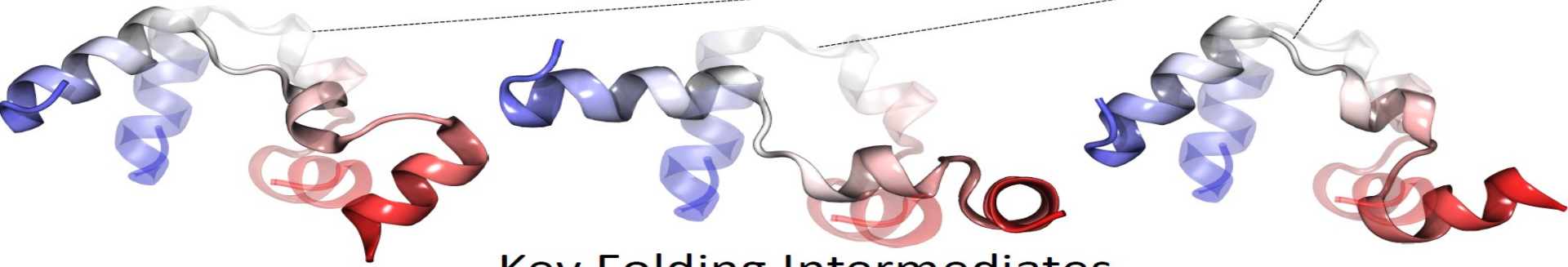
Folding Dynamics of Villin Headpiece Unveiled

6.9μs folding simulation of 30K atoms: 380GB trajectory

Schulten et al. *Biophys J* **94**:L75, 2008, **97**: 2009



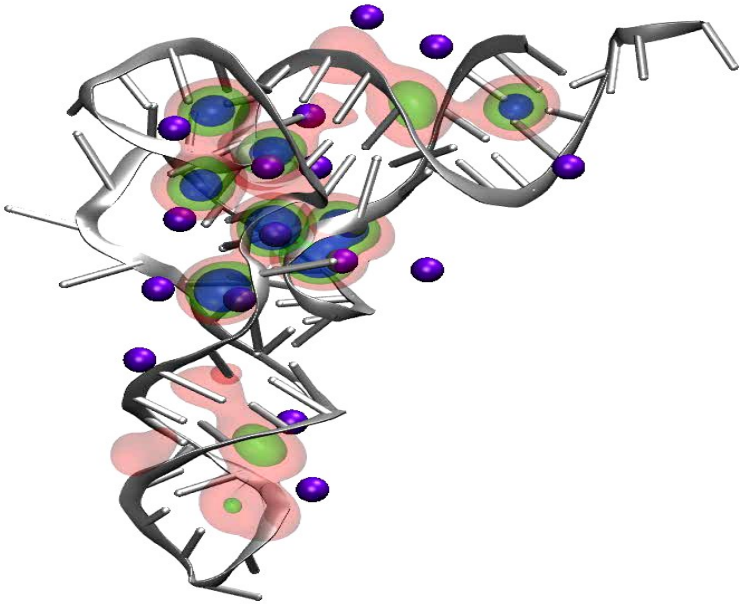




Key Folding Intermediates

Time-Averaged Volumetric Properties

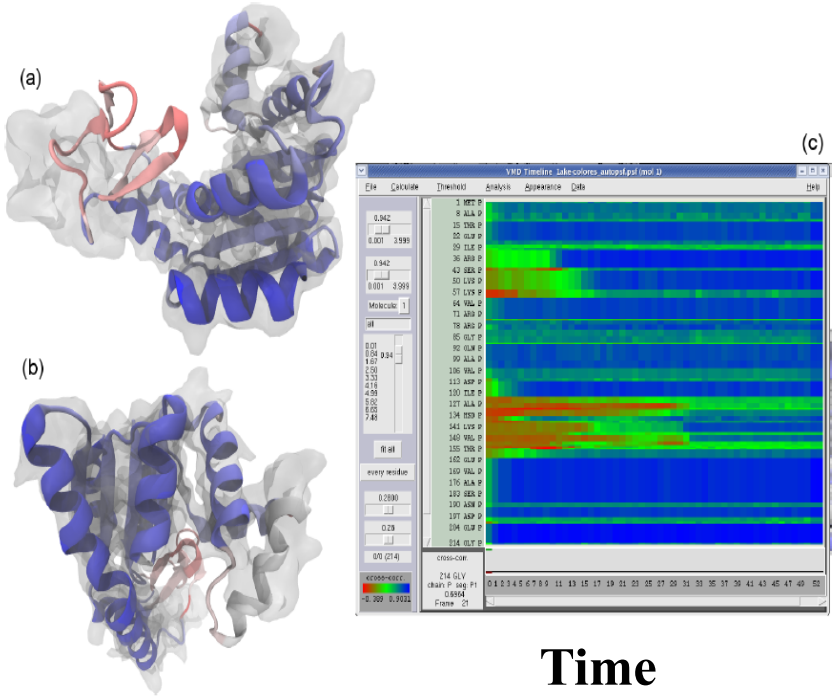
- Compute density, distance, occupancy, potential maps for a frame or averaged over a trajectory
- Example: display binding sites for diffusively bound ions as probability density isosurfaces



tRNA magnesium ion occupancy: VMD volmap plugin

Interactive and Parallel Analysis

- New graphical interfaces for batch and interactive exploration, calculation
  - User interactions drive analysis focus with progressive refinement of details
  - Interactive in-situ analysis of running simulations
- Enabled by GPU acceleration, parallel computing on desktops, clouds, clusters
- Incorporate VMD analysis functions into NAMD, and other software



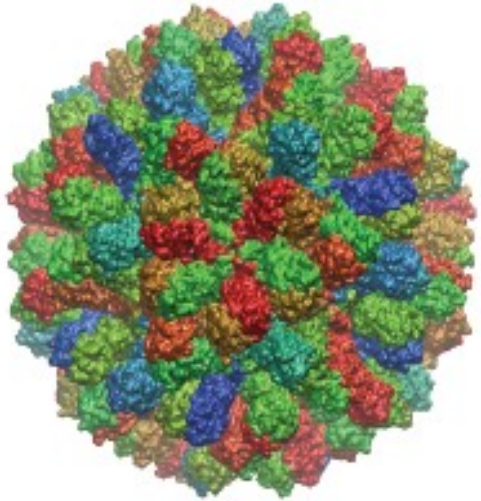
MDFF Cross Correlation Analysis

Regions with poor fit **Regions with good fit**

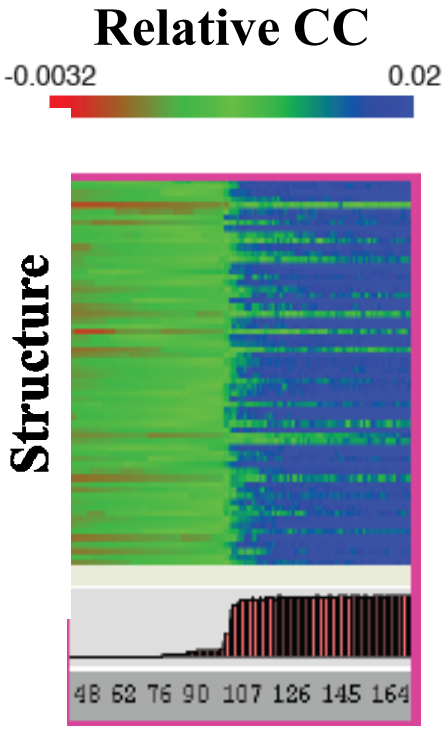
Parallel MDFF Cross Correlation Analysis on Cray XK7

Rabbit Hemorrhagic Disease Virus (RHDV)	
Traj. frames	10,000
Structure component selections	720
Single-node XK7 (projected)	336 hours (14 days)
128-node XK7	3.2 hours 105x speedup
2048-node XK7	19.5 minutes 1035x speedup

Calculation of 7M CCs would take **5 years** using serial CPU algorithm!



RHDV colored by relative CC



Stone et al., Faraday Discuss., 169:265-283, 2014.

VMD Tesla V100 Cross Correlation Performance

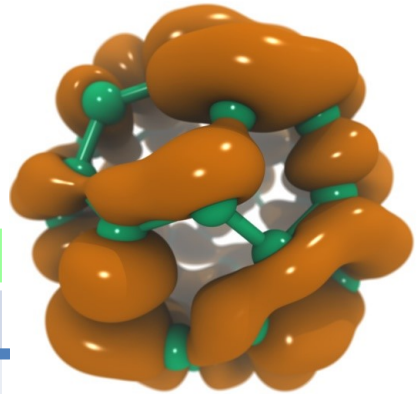
Rabbit Hemorrhagic Disease Virus: 702K atoms, 6.5Å resolution

VMD on Volta GPUs now **~9x faster** than Kepler GPUs

Application and Hardware platform	Runtime, Speedup vs. Chimera,		VMD+GPU
Chimera Xeon E5-2687W (2 socket) [1]	15.860s,	1x	
VMD-CUDA IBM Power8 + 1x Tesla K40 [2]	0.488s,	32x	**0.9x**
VMD-CUDA Intel Xeon E5-2687W + 1x Quadro K6000 [1,2]	0.458s,	35x	**1.0x**
VMD-CUDA Intel Xeon E5-2698v3 + 1x Tesla P100	0.090s,	176x	**5.1x**
VMD-CUDA IBM Power8 “Minsky” + 1x Tesla P100	0.080s,	198x	**5.7x**
VMD-CUDA Intel Xeon E5-2697Av4 + 1x Tesla V100	**0.050s,**	317x	**9.2x**
VMD-CUDA IBM Power9 “Newell” + 1x Tesla V100	**0.049s,**	**323x**	**9.3x**

[1] GPU-Accelerated Analysis and Visualization of Large Structures Solved by Molecular Dynamics Flexible Fitting. J. E. Stone, R. McGreevy, B. Isralewitz, and K. Schulten. Faraday Discussions 169:265-283, 2014.
[2] Early Experiences Porting the NAMD and VMD Molecular Simulation and Analysis Software to GPU-Accelerated OpenPOWER Platforms. J. E. Stone, A.-P. Hynninen, J. C. Phillips, K. Schulten. International Workshop on OpenPOWER for HPC (IWOPH'16), LNCS 9945, pp. 188-206, 2016.

VMD Tesla V100 Performance for C_{60} Molecular Orbitals, 516x519x507 grid



Hardware platform		Runtime,	Speedup
IBM Power8 (ORNL 'crest') + 1x Tesla K40 [1]		3.49s,	**1.0x**
Intel Xeon E5-2697Av4	**+ 1x Tesla V100 [2]**	**0.610s,**	**5.7x**
Intel Xeon E5-2697Av4	**+ 2x Tesla V100 [2]**	**0.294s,**	**11.8x**
Intel Xeon E5-2697Av4	**+ 3x Tesla V100 [2]**	**0.220s,**	**15.9x**
IBM Power9 "Newell"	**+ 1x Tesla V100**	**0.394s,**	**8.8x**
IBM Power9 "Newell"	**+ 2x Tesla V100**	**0.207s,**	**16.8x**
IBM Power9 "Newell"	**+ 3x Tesla V100**	**0.151s,**	**23.1x**
IBM Power9 "Newell"	**+ 4x Tesla V100**	**0.130s,**	**26.8x**

NVLink perf. boost

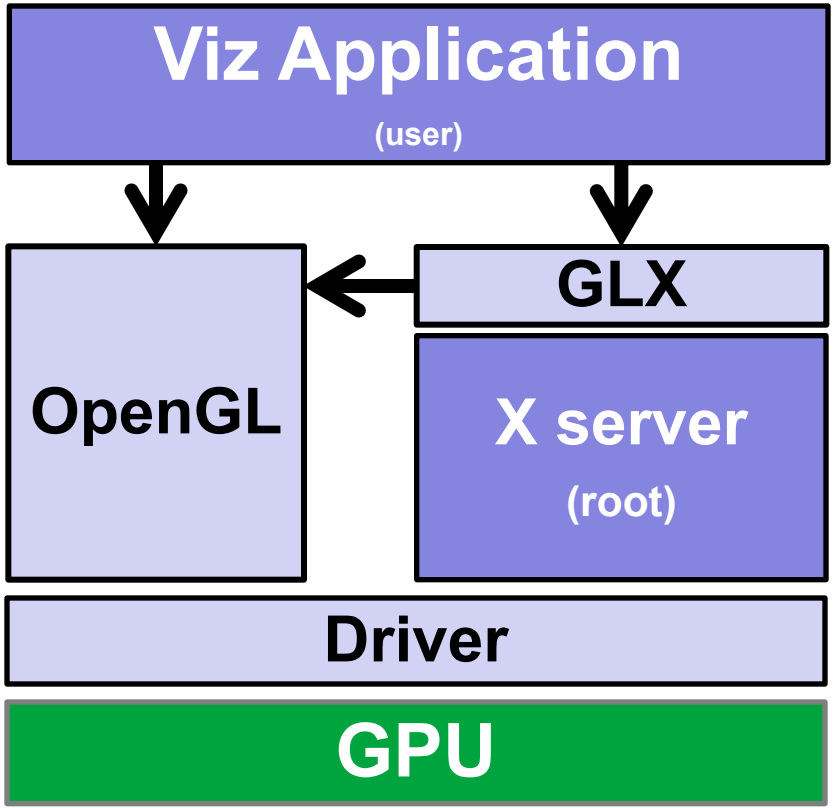
[1] Early Experiences Porting the NAMD and VMD Molecular Simulation and Analysis Software to GPU-Accelerated OpenPOWER Platforms. J. E. Stone, A.-P. Hynninen, J. C. Phillips, K. Schulten. International Workshop on OpenPOWER for HPC (IWOPH'16), LNCS 9945, pp. 188-206, 2016.

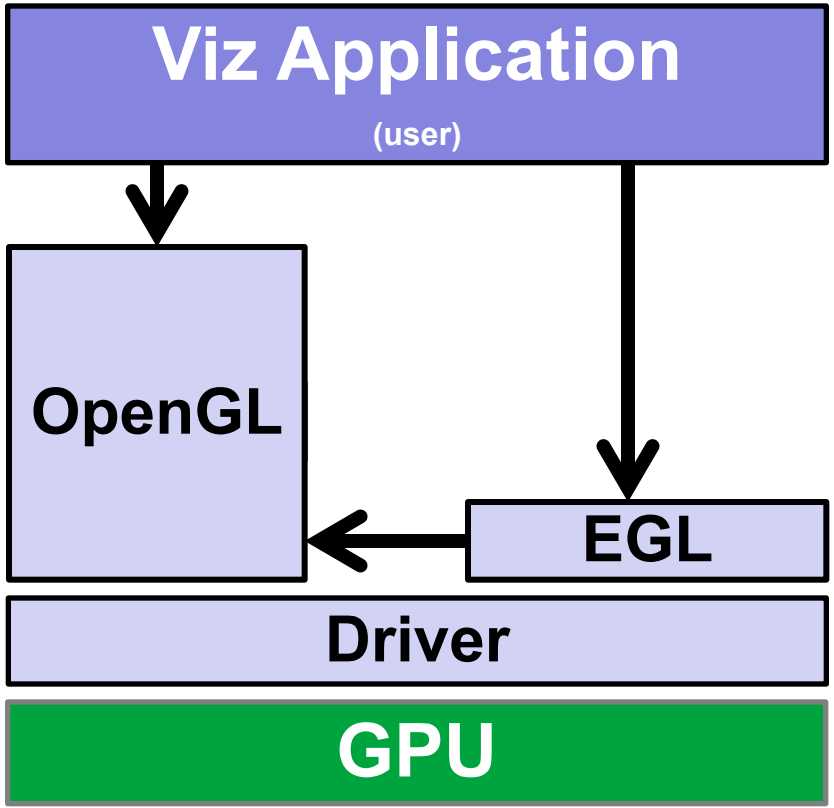
[2] NAMD goes quantum: An integrative suite for hybrid simulations. Melo et al., Nature Methods, 2018.

VMD Off-Screen Rendering w/ EGL

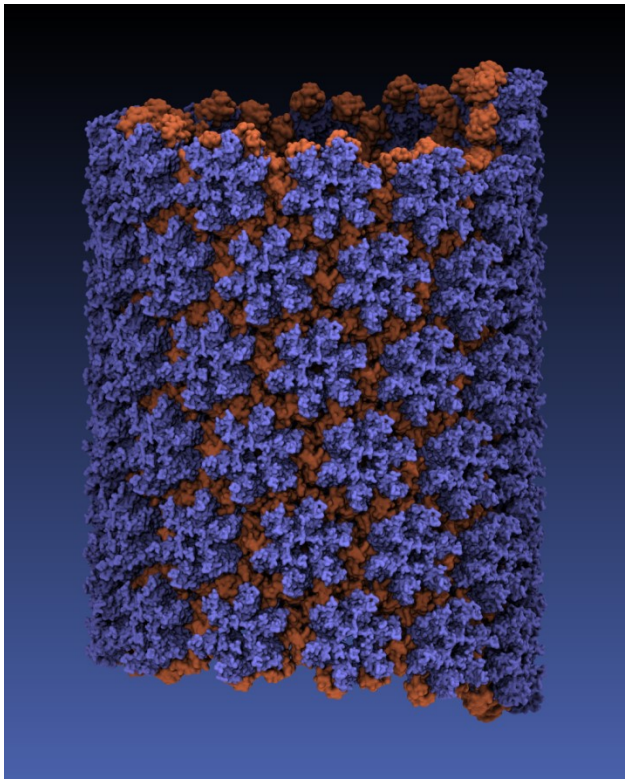
- Containers+Cloud+Workstations with recent NVIDIA drivers
- VMD on HPC systems w/ latest GPUs:
  - Cray XC50, CSCS Piz Daint
  - **ORNL Summit in progress now**
  - IBM OpenPOWER, drivers 375.66 and later support both GLX and EGL

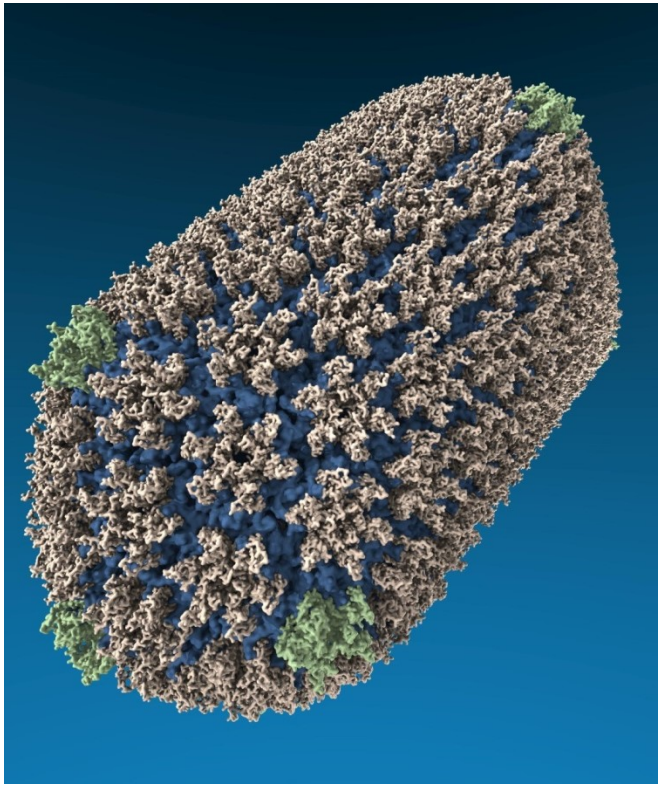
OpenGL: GLX vs. EGL





VMD “QuickSurf” Representation, Ray Tracing

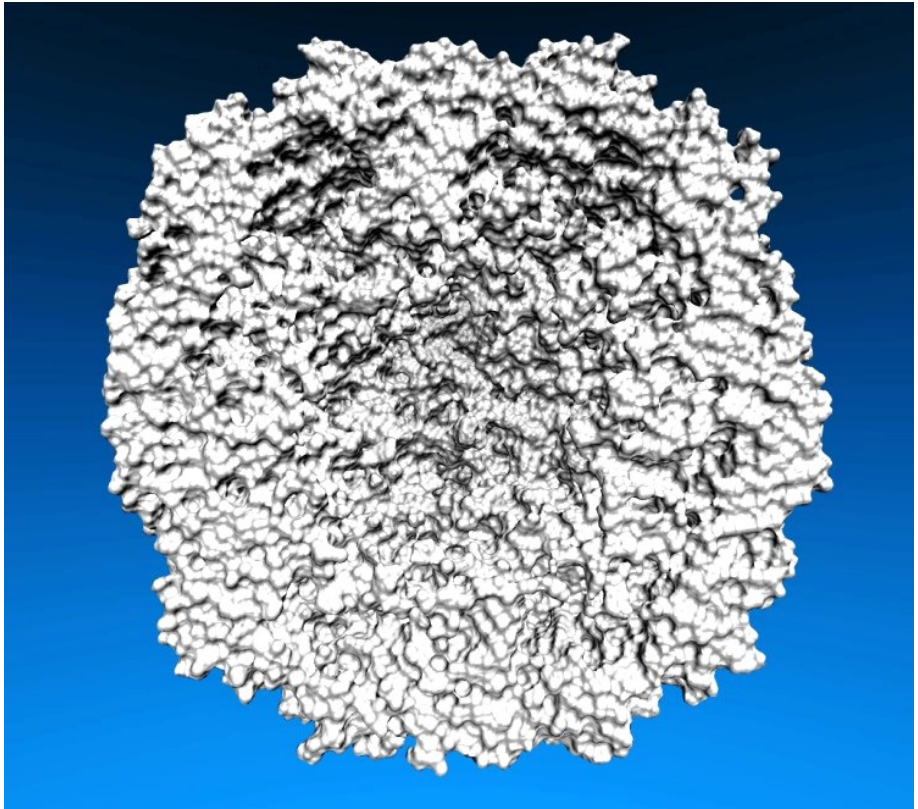




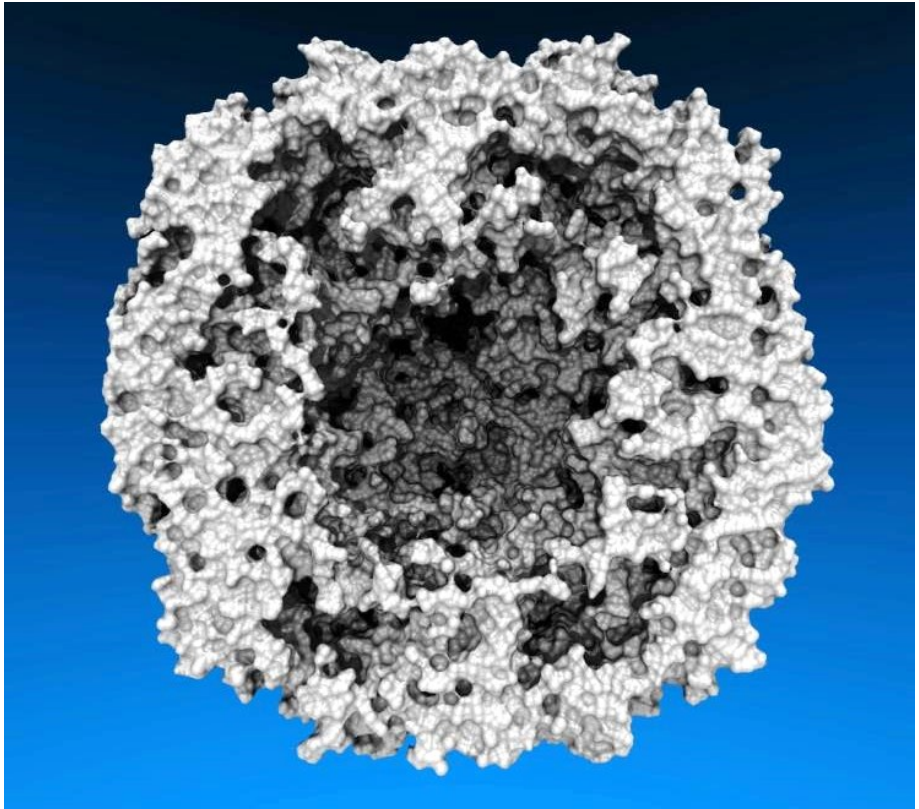
All-atom HIV capsid simulations w/ up to 64M atoms on Blue Waters

Interactive Ray Tracing, Lighting Comparison: STMV Capsid

Two lights, no shadows (e.g. as used by OpenGL)

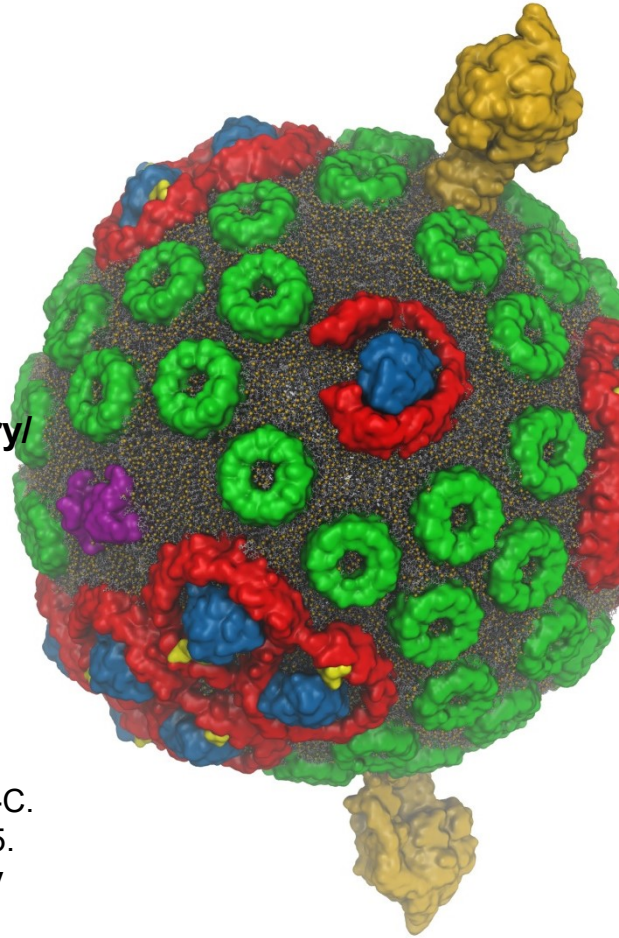


Ambient occlusion lighting and shadows w/ RT



VMD w/ OptiX 5

- Interactive RT on laptops, desktops, and cloud
- Large-scale parallel rendering: in situ or post hoc visualization
- Remote RT on NVIDIA GPU clusters
- Stereoscopic panoramic and full-dome projections
- Omnidirectional VR for YouTube, VR HMDs
- **GPU memory sharing via NVLink on Quadro GP100, Tesla P100**
- **VMD+OptiX 5, NVIDIA NGC container: https://ngc.nvidia.com/registry/**
- **In-progress:**
  - **OptiX denoising support: fast turnaround w/ AO, DoF, etc**
  - **Denoising to enable practical use of path tracing in VMD**



VMD/OptiX GPU Ray Tracing of all-atom Chromatophore w/ lipids.

GPU-Accelerated Molecular Visualization on Petascale Supercomputing Platforms. J. E. Stone, K. L. Vandivort, and K. Schulten. UltraVis'13, pp. 6:1-6:8, 2013.

Visualization of Energy Conversion Processes in a Light Harvesting Organelle at Atomic Detail. M. Sener, et al. SC'14 Visualization and Data Analytics Showcase, 2014.

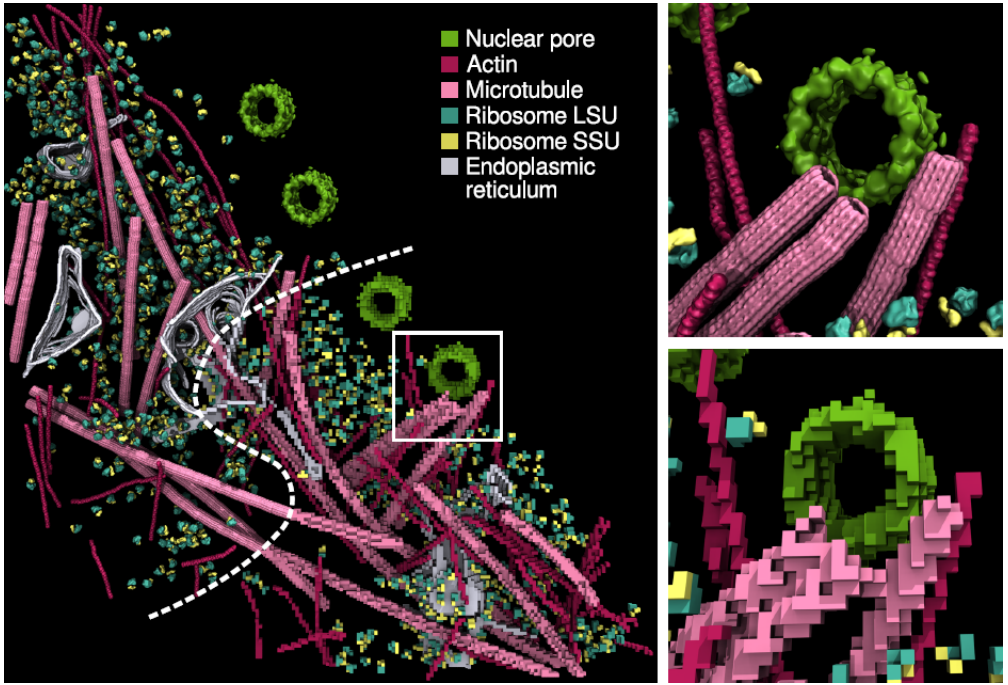
Chemical Visualization of Human Pathogens: the Retroviral Capsids. J. R. Perilla, B.-C. Goh, J. E. Stone, and K. Schulten. SC'15 Visualization and Data Analytics Showcase, 2015.

Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing. J. E. Stone et al., J. Parallel Computing, 55:17-27, 2016.

Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering J. E. Stone, W. R. Sherman, and K. HPDAV, IPDPSW, pp. 1048-1057, 2016.

Interactive Ray Tracing of Cells

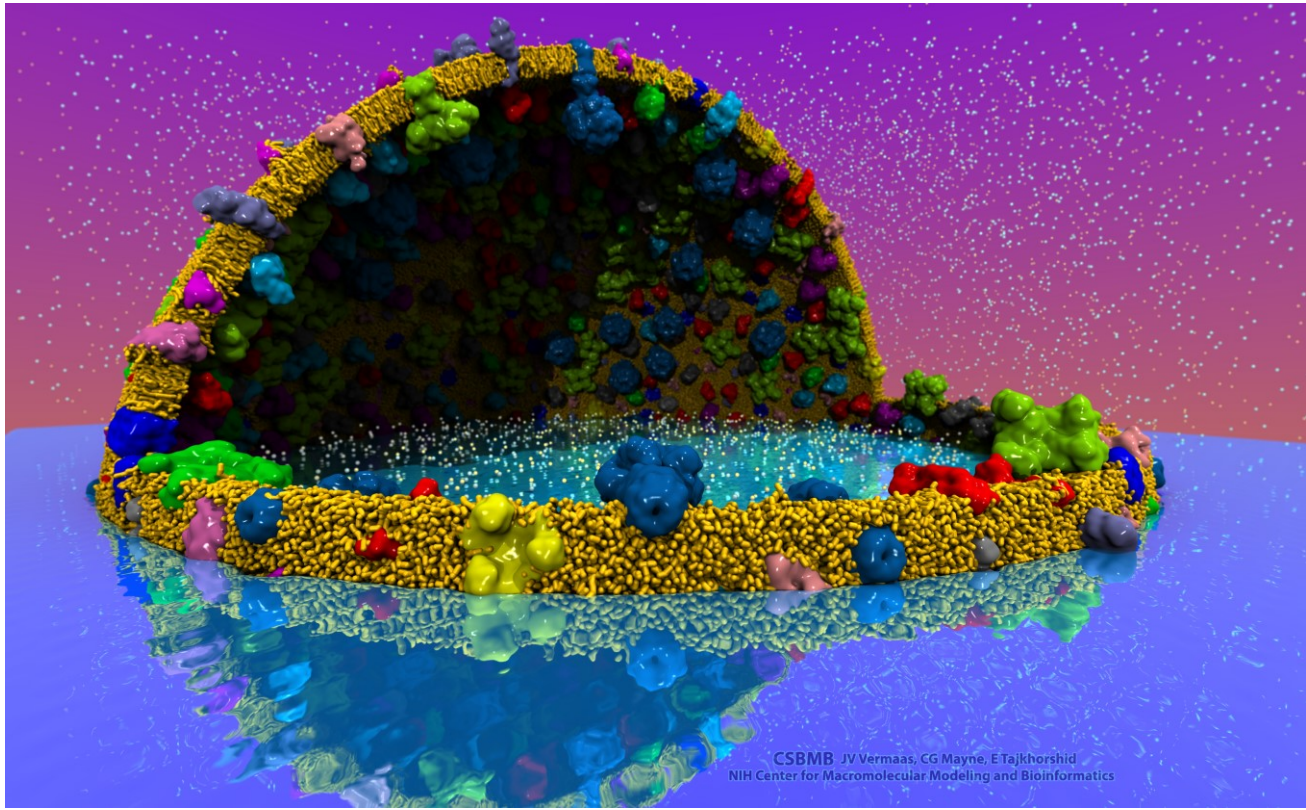
- High resolution cellular tomograms, **billions of voxels**
- Even isosurface or lattice site graphical representations involve ~100M geometric primitives
- 24GB Quadro M6000s used for interactive RT of cellular tomograms of this size
- **Quadro GP100 / GV100 GPUs benefit from OptiX support for NVLink and distribution of scene data across multiple GPUs**



Earnest, et al. J. Physical Chemistry B, 121(15): 3871-3881, 2017.

Proto-Cell Rendered with VMD+OptiX

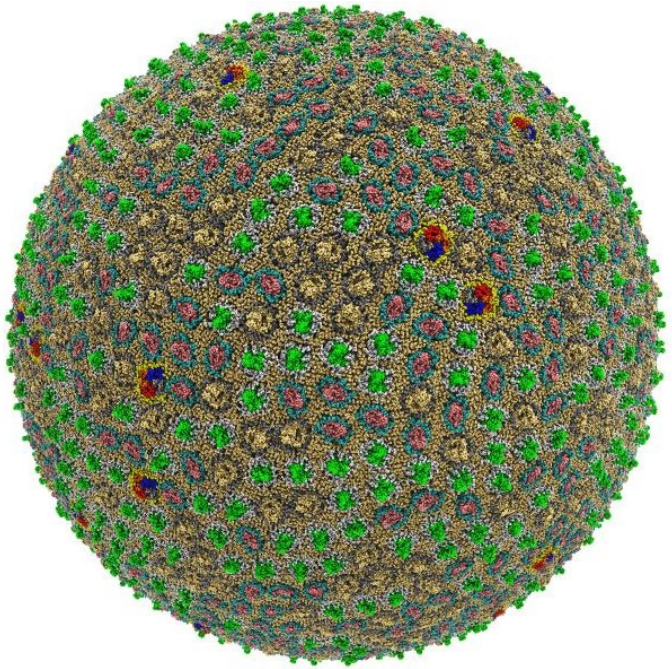
- 113M particles
- 1,397 copies of 14 different membrane proteins
- Preparing for simulations on pre-exascale computers



Preparation, Visualization, Analysis of Cell-Scale Simulations

- Support for large memory (TB), up to **2 billion atoms per "molecule" now**
- Interactive viz. w/ OpenGL/EGL, Vulkan
- Interactive ray tracing on CPUs and GPUs
- Remote visualization w/ video streaming
- New file formats, compression, out-of-core, and non-volatile memory technologies
- Parallel analysis, visualization w/ MPI

- 200 nm spherical envelope
- Membrane with ~50% occupancy by proteins
- 63M atoms in envelope model



Challenges of Integrating Stochastic Dynamics and Cryo-electron Tomograms in Whole-cell Simulations. Earnest, et al. J. Physical Chemistry B, 121(15): 3871-3881, 2017.

Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing. J.E. Stone, …, K. Schulten, J. Parallel Computing, 55:17-27, 2016.

High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL. J.E. Stone, ..., K. Schulten. IEEE High Performance Data Analysis and Visualization, IPDPSW, pp. 1014-1023, 2016.

VMD Atomic Detail Visualization of Cellular Architecture with Instancing

- VMD 1.9.4 supports instancing of graphical representations associated with molecules
- Exploit **VBO caching** in OpenGL to eliminate host-GPU geometry transfers
- **OptiX instancing** of geometry buffers to minimize GPU memory footprint for cell-scale scenes w/ atomic structures

Making Our Research Tools Easily Accessible

- Docker “container” images available in NVIDIA NGC registry
  - Users obtain Docker images via registry, download and run on the laptop, workstation, cloud, or supercomputer of their choosing
  - **https://ngc.nvidia.com/registry/**
  - **https://ngc.nvidia.com/registry/hpc-vmd**

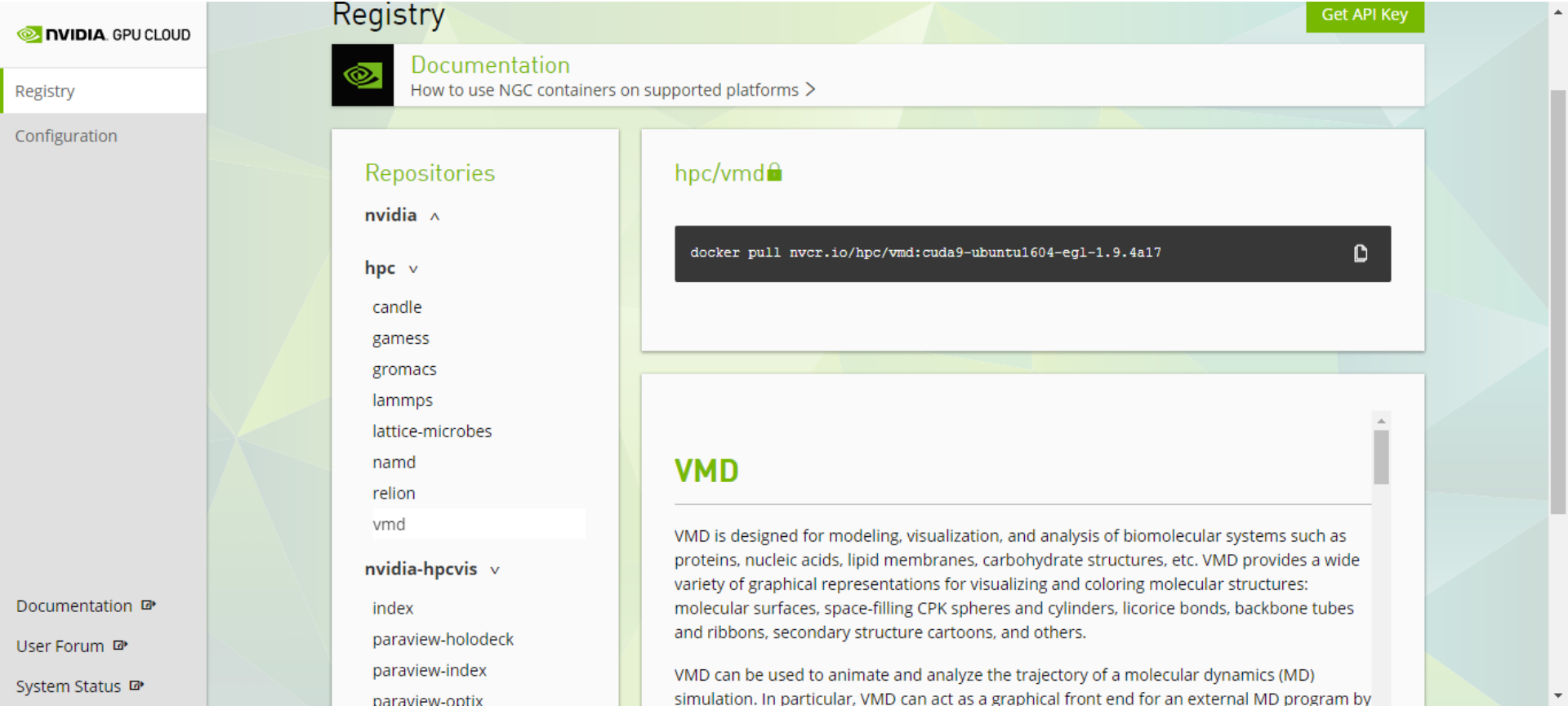
- Cloud based deployment
  - Full virtual machines (known as “AMI” in Amazon terminology)
  - Amazon AWS EC2 GPU-accelerated instances:
    http://www.ks.uiuc.edu/Research/cloud/

Clusters, Supercomputers

Workstations,
Servers,
Cloud

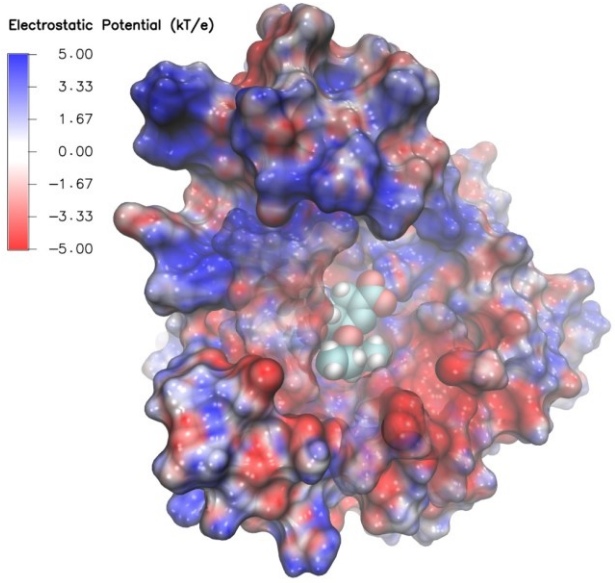
Molecular dynamics-based refinement and validation for sub-5 Å cryo-electron microscopy maps. Abhishek Singharoy, Ivan Teo, Ryan McGreevy, John E. Stone, Jianhua Zhao, and Klaus Schulten. *eLife*, 10.7554/eLife.16105, 2016. (66 pages).
QwikMD-integrative molecular dynamics toolkit for novices and experts. Joao V. Ribeiro, Rafael C. Bernardi, Till Rudack, John E. Stone, James C. Phillips, Peter L. Freddolino, and Klaus Schulten. *Scientific Reports*, 6:26536, 2016.
High performance molecular visualization: In-situ and parallel rendering with EGL. John E. Stone, Peter Messmer, Robert Sisneros, and Klaus Schulten. *2016 IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW)*, pp. 1014-1023, 2016.

VMD / NAMD / LM, NGC Containers



VMD OptiX/EGL NGC Container

- **https://ngc.nvidia.com/registry/**
- **CUDA-accelerated** viz+analysis
- **EGL off-screen rendering** – no windowing system needed
- **OptiX high-fidelity GPU ray tracing** engine built in
- All dependencies included
- **Easy to deploy on a wide range of GPU accelerated platforms**



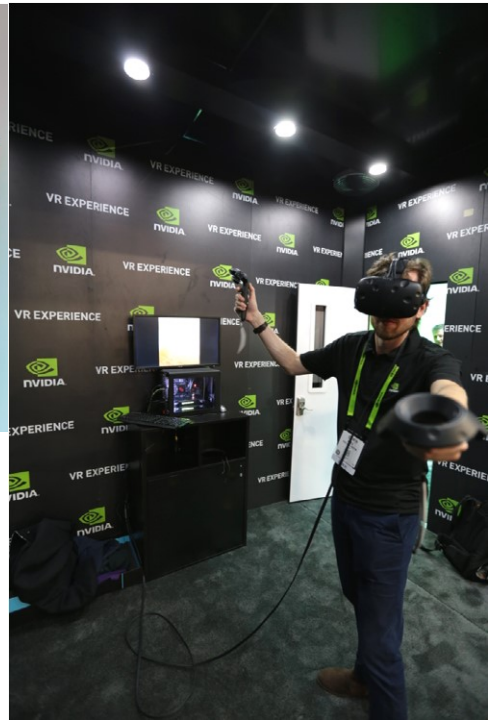
High performance molecular visualization: In-situ and parallel rendering with EGL. J. E. Stone, P. Messmer, R. Sisneros, and K. Schulten. *2016 IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW)*, pp. 1014-1023, 2016.

VMD VR Progress

Ongoing Work:
- Khronos OpenXR
- NVIDIA VR plugin for use w/ game engines

VMD VR ray tracing:
Google Cardboard [1]
Remote VR Viz. [2]

VR user interaction with VMD models in **room-scale VR** with NVIDIA



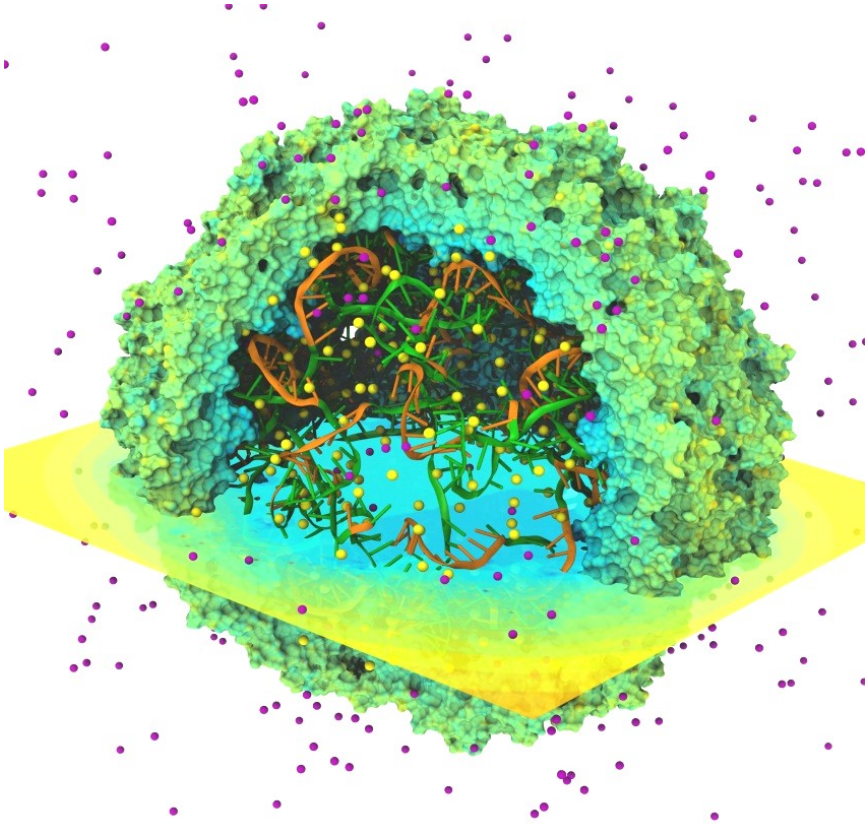
VMD Chromatophore Demo, NVIDIA VR Room @ Supercomputing

[1] Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing. Stone et al., J. Parallel Computing, 55:17-27, 2016.
[2] Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering. J.E. Stone, W.R. Sherman, K. Schulten. IEEE HPDAV (IPDPSW), pp. 1048-1057, 2016.

VMD Visualization Concepts

Biomolecular Visualization Challenges

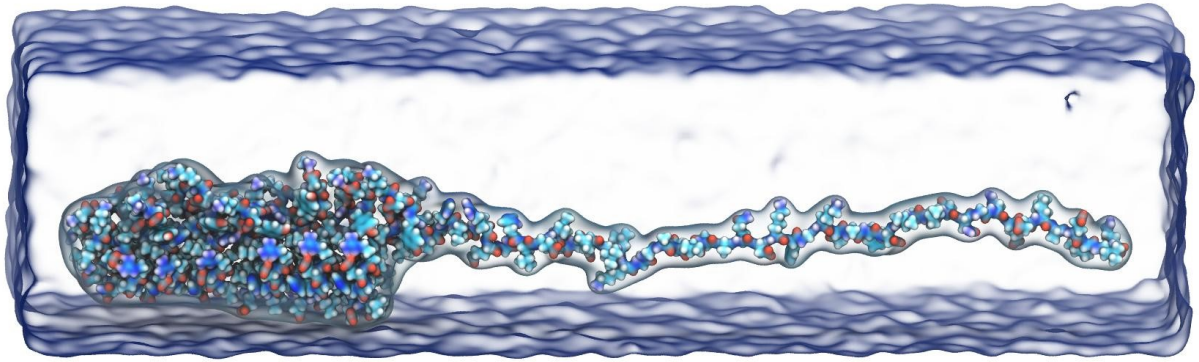
- Geometrically complex scenes
- Spatial relationships important to see clearly: fog, shadows, AO helpful
- Often show a mix of structural and spatial properties
- Time varying!



Structure Visualization

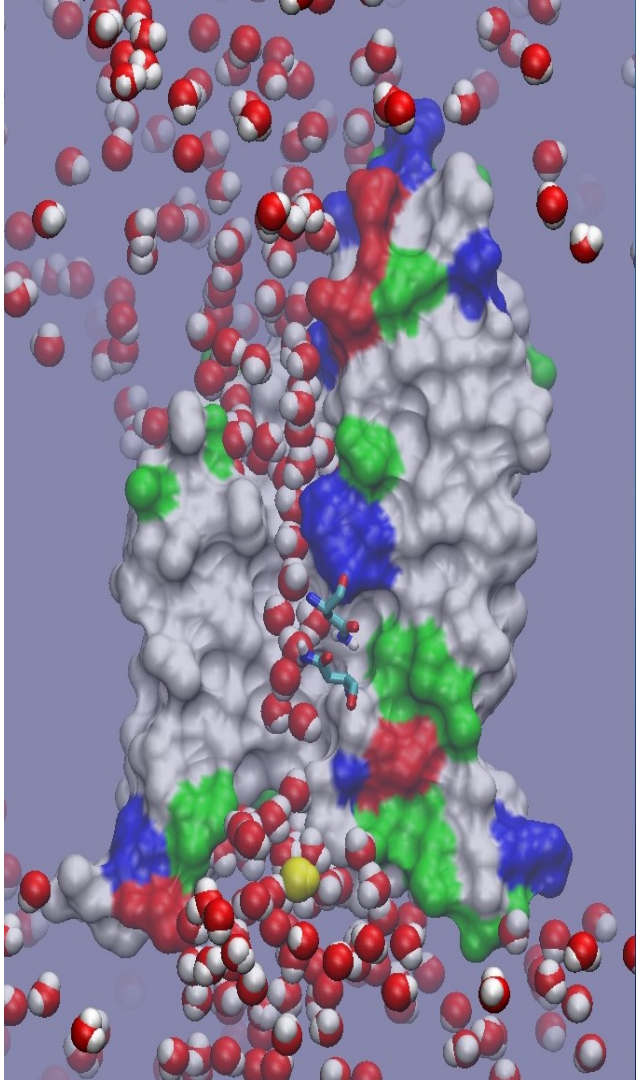
Molecular representations provide different levels of abstraction, atomic detail vs. higher level organizational information

- Atoms, VdW spheres, bonds, ball-stick, …
- Molecular orbitals (quantum chemistry)
- Molecular surfaces
- Coarse-grained “beads”
- Ribbons, secondary structure, “cartoon” reps, RNA/DNA



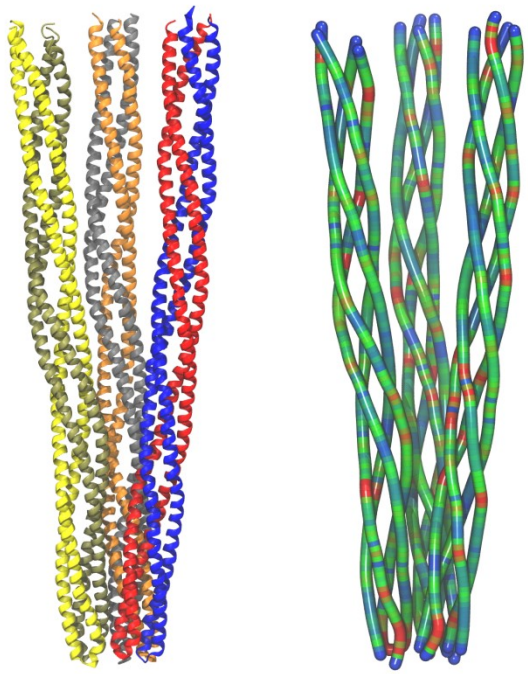
Selection, Filtering

- Most viz tools allow interactive visual picking, menu-driven selections of structure components to display or operate on
- VMD also extensively uses a text-based selection language (think google):
  - “water within 10 of protein and z > 0”
  - Allows selection on user-defined fields
  - ***Promotes synergy between interactive and scripting interfaces***
  - Works very well when dealing with huge time-varying structures



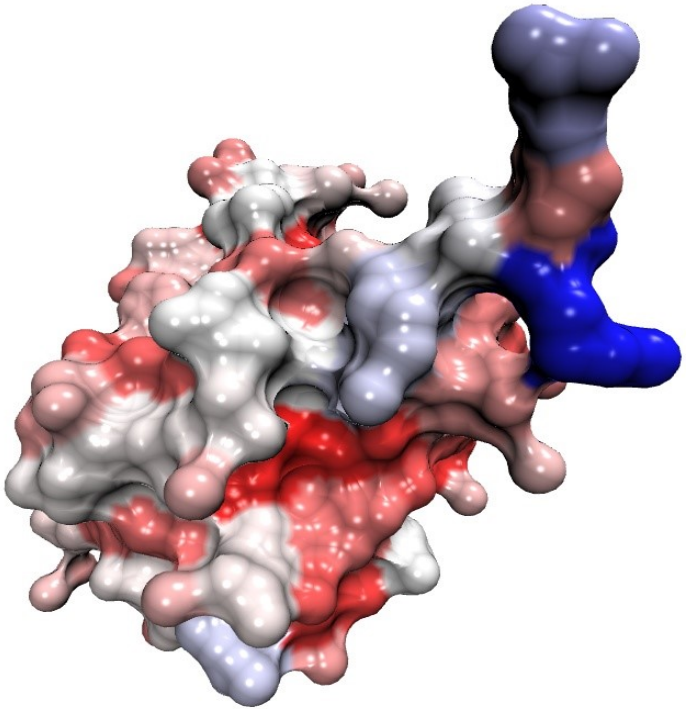
Computed Properties

- Smoothing of thermal noise
- Secondary structure
- Hydrogen bonds, salt bridges
- Forces, energies, stress, strain
- Time averaging of electrostatic fields, occupancy maps
- Quality-of-fit cross correlation with cryo-EM density maps
- Normal modes, principal component analysis, essential dynamics
- Cluster simulation trajectory timesteps by structural similarity

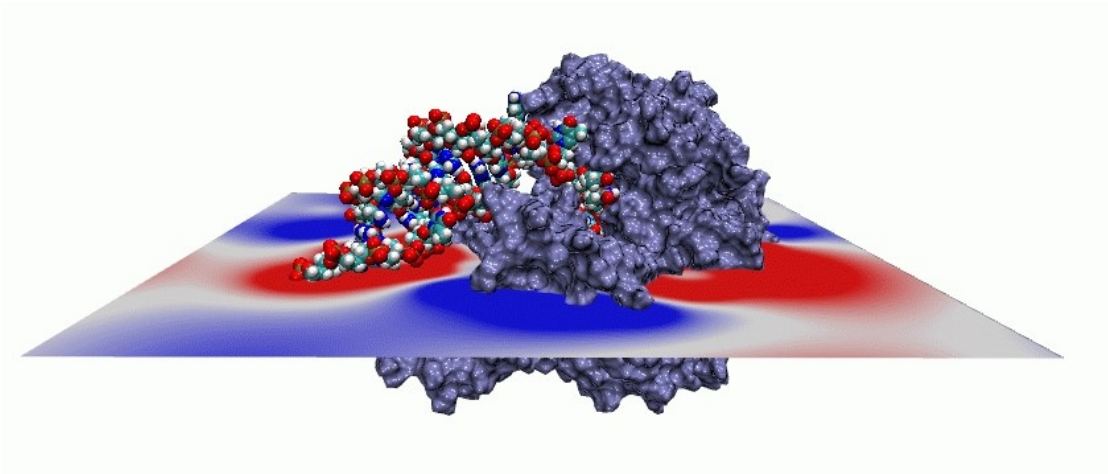


Chemoreceptor trimer-of-dimers analysis with Bendix plugin in VMD

Display of Computed Properties on Structures

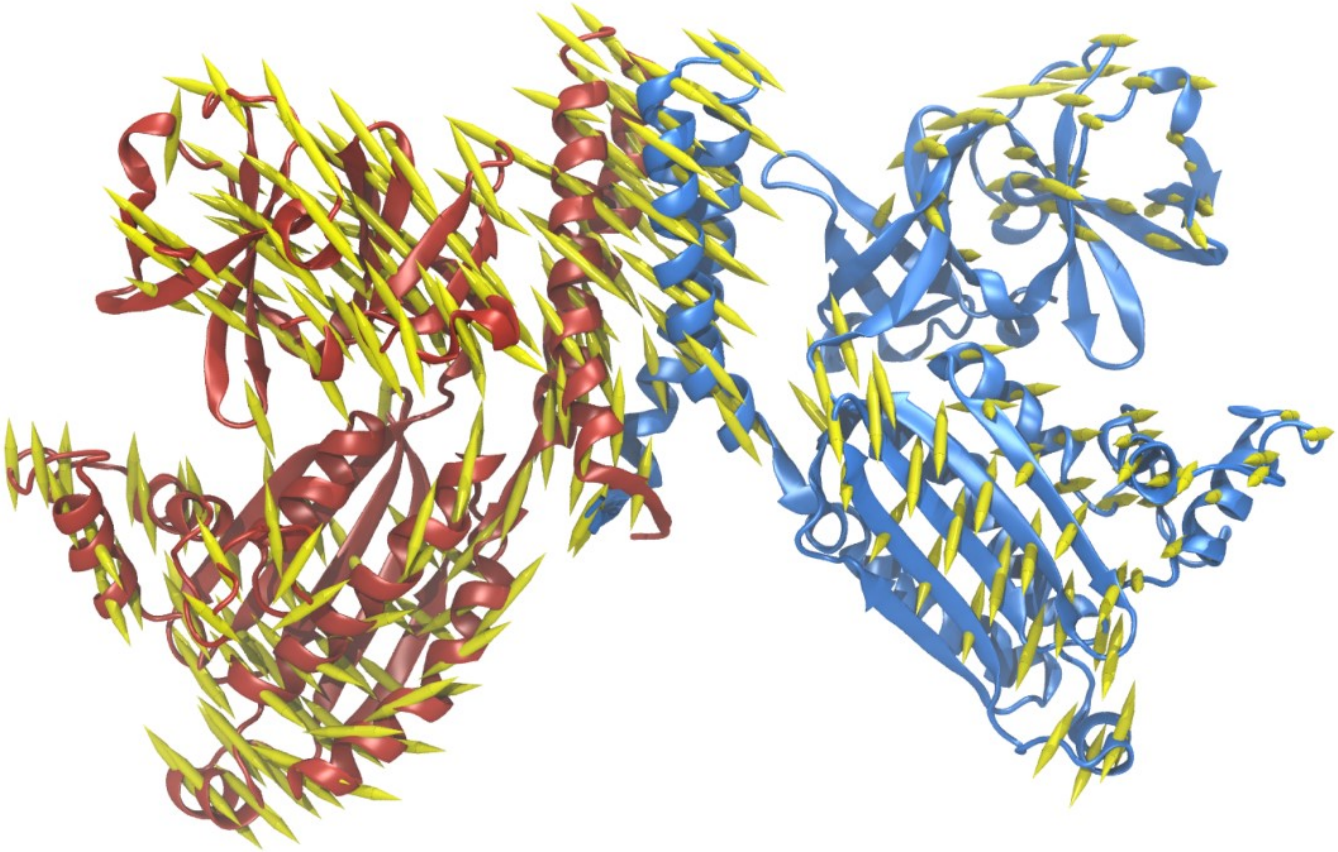


Per-residue solvent-accessible surface area of Ubiquitin



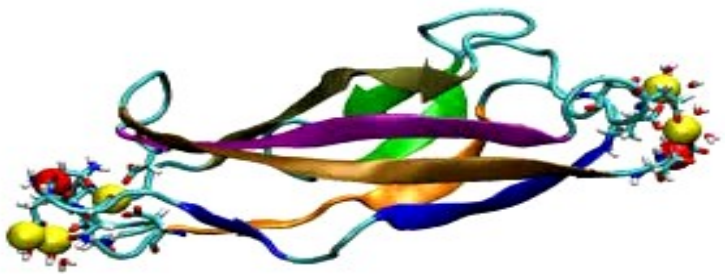
PME electrostatic potential contour for a helicase on a volumetric slice plane

CheA kinase PCA: first principal component porcupine plot



Visualization of Molecular Dynamics

- Molecular dynamics simulations save trajectories of atomic coordinates as simulated time progresses
- Researchers study trajectories by analyzing force profiles, energies, structural changes, etc.
- **Visualization selections, graphics, structure properties recomputed for each trajectory timestep!**

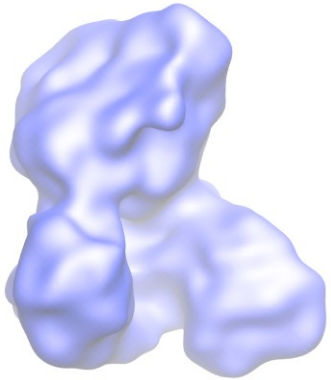


Petascale Computing - A Key Instrument for Life Science

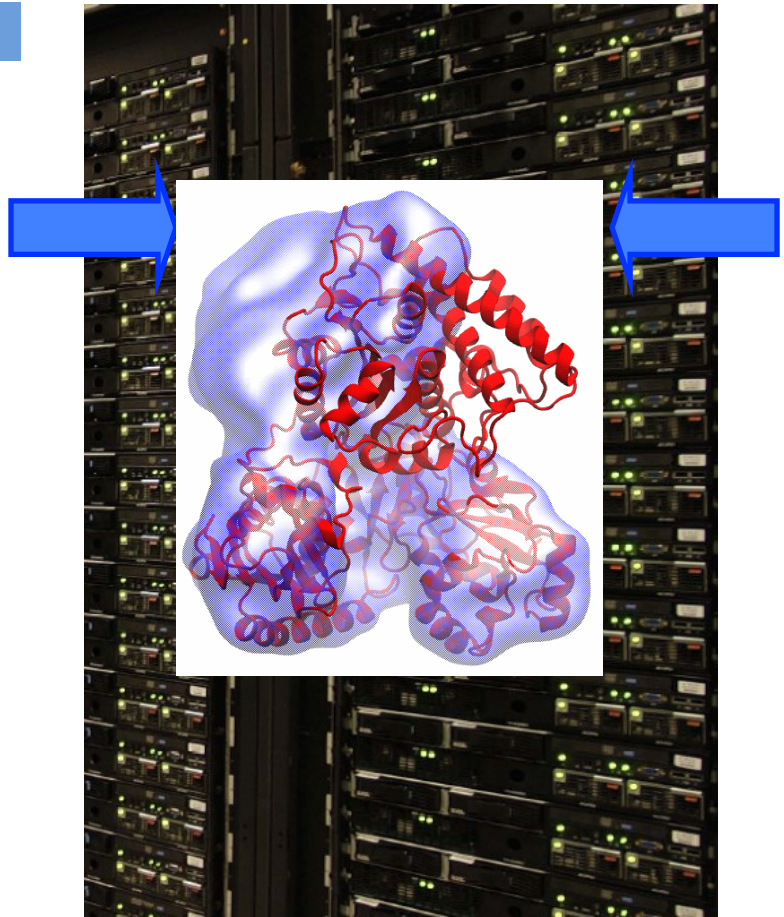
MDFF Solves Structures from X-ray Crystallography and Cryo-EM

Electron microscopy

FEI microscope

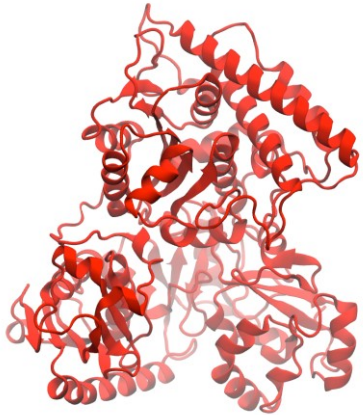


Electron density of protein in action at low resolution



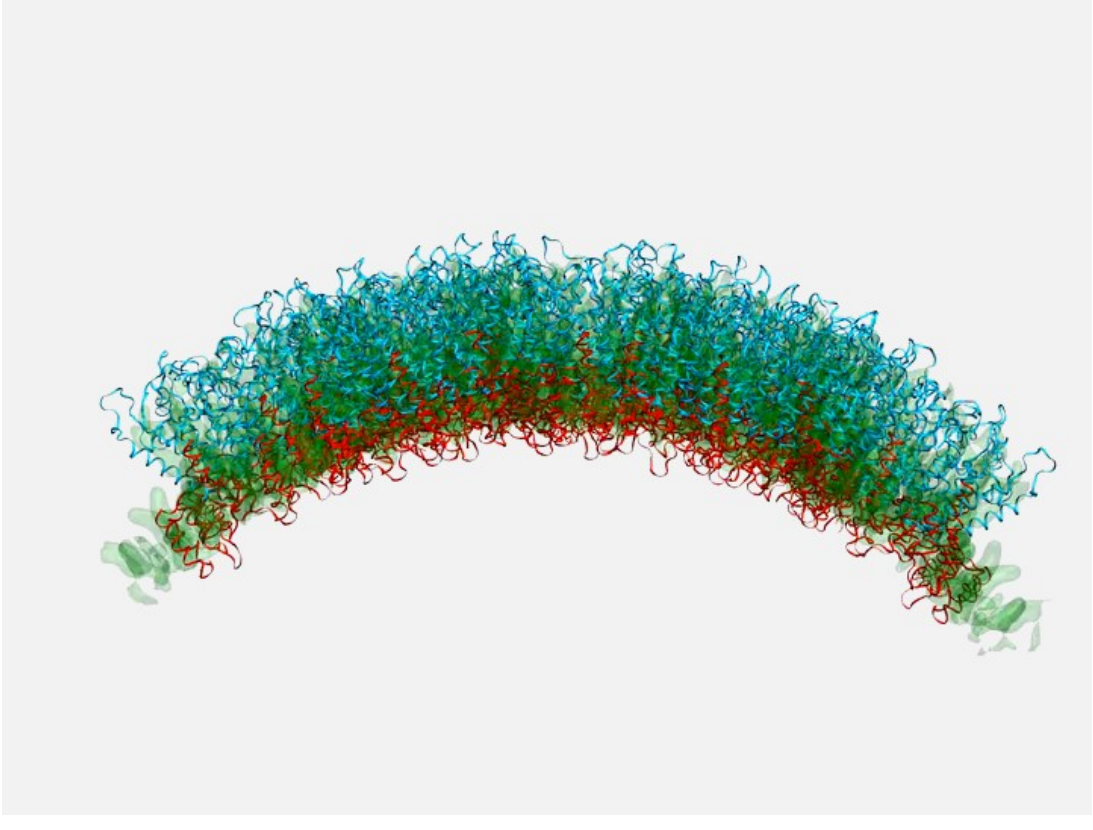
X-ray crystallography

APS at Argonne



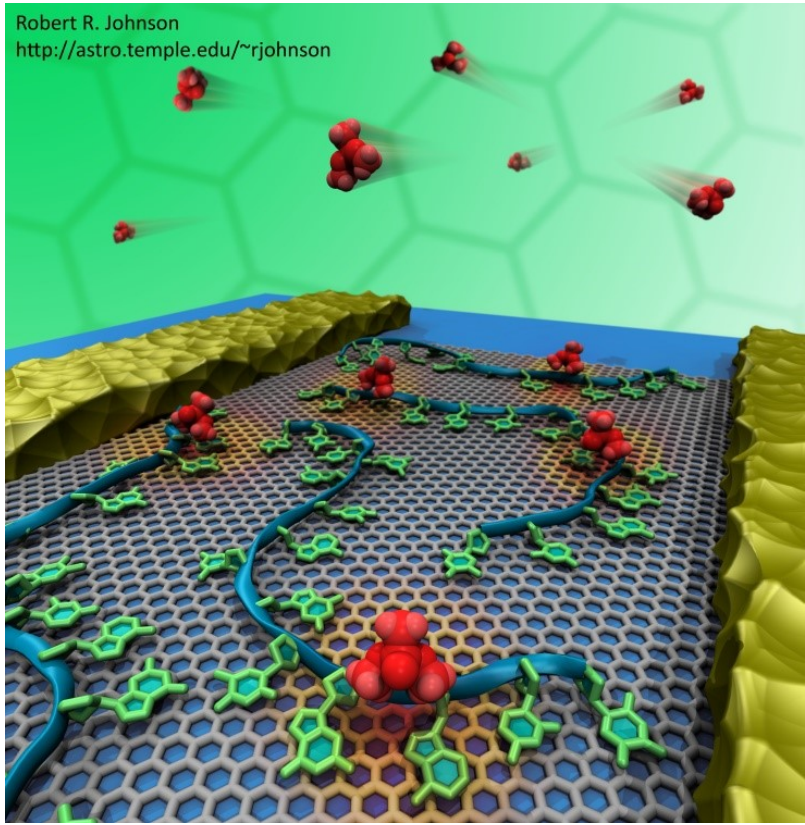
Ideal protein structure at high resolution
Acetyl – CoA Synthase

Hexamer of hexamers HIV capsid substructure Molecular Dynamics Flexible Fitting (MDFF) simulation. All-atom structure fitting into cryo-EM density map.



Ray Tracing in VMD

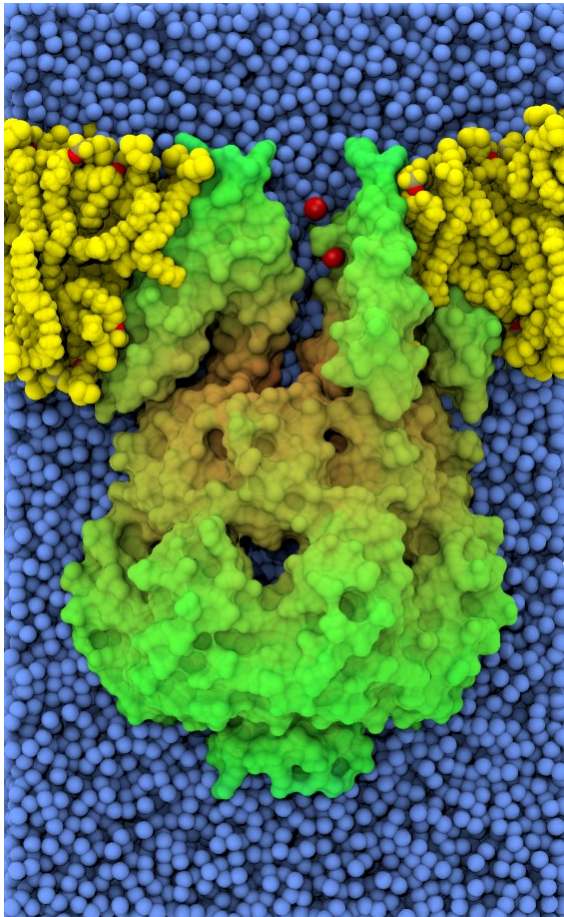
- Support for ray tracing of VMD molecular scenes began in 1995
- Tachyon parallel RT engine interfaced with VMD (1999)
- Tachyon embedded as an internal VMD rendering engine (2002)
- Built-in support for large scale parallel rendering (2012)
- Refactoring of VMD to allow fully interactive ray tracing as an alternative to OpenGL (2014)

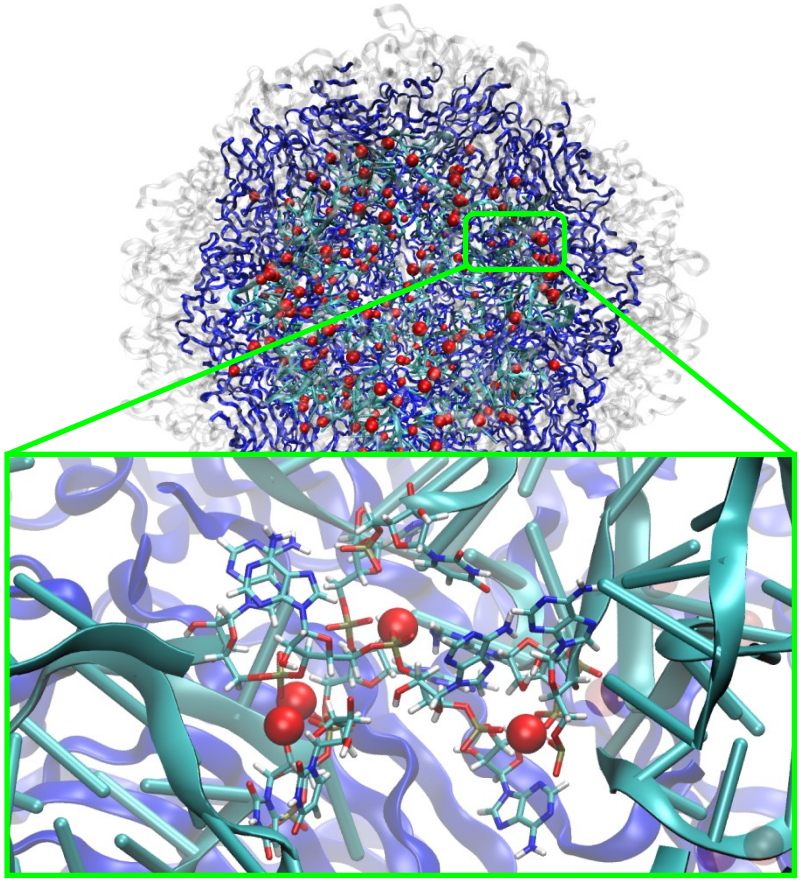


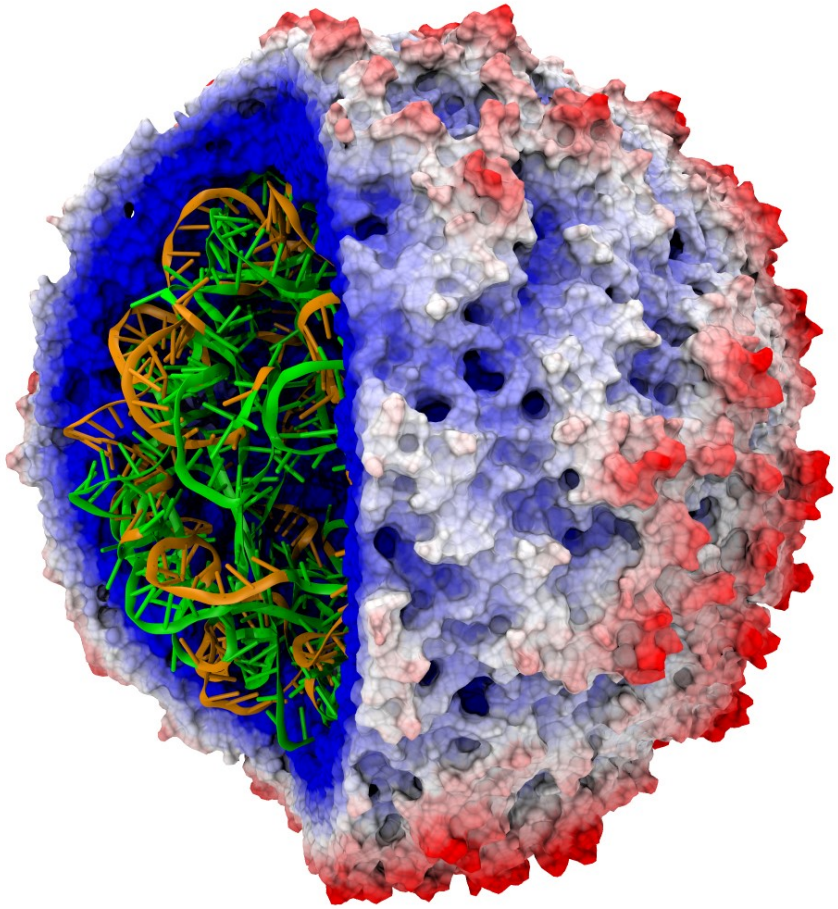
Geometrically Complex Scenes

Ray tracing techniques well matched to molecular viz. needs:

- Curved geometry, e.g. spheres, cylinders, toroidal patches, easily supported
- Greatly reduced memory footprint vs. polygonalization
- Runtime scales only moderately with increasing geometric complexity
- Occlusion culling is “free”, RT acceleration algorithms do this and much more



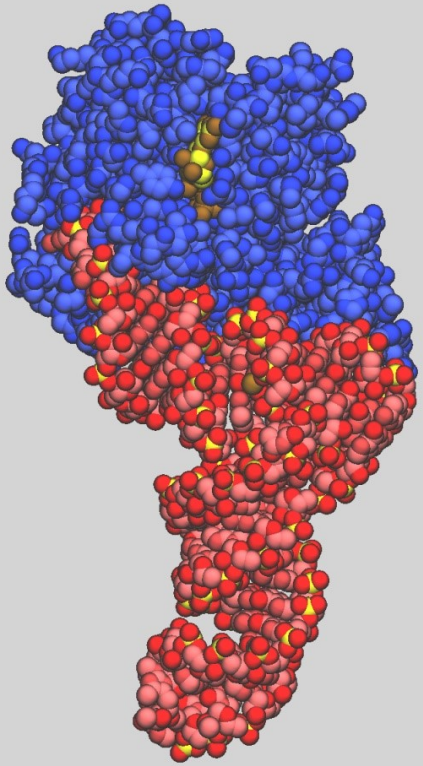




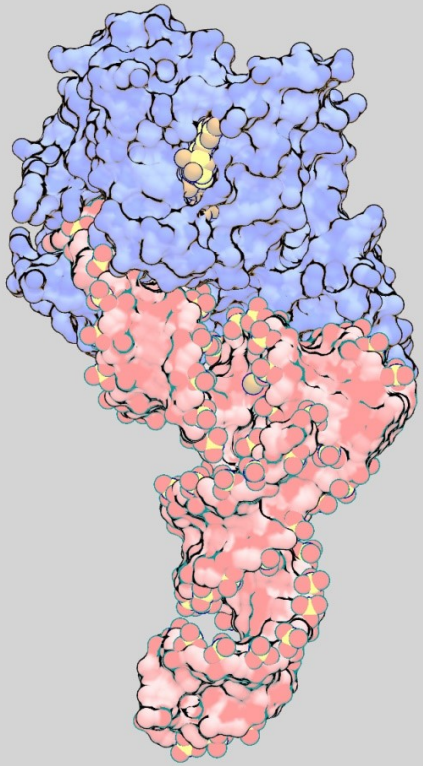
Satellite Tobacco Mosaic Virus

VMD Shading Comparison: EF-Tu

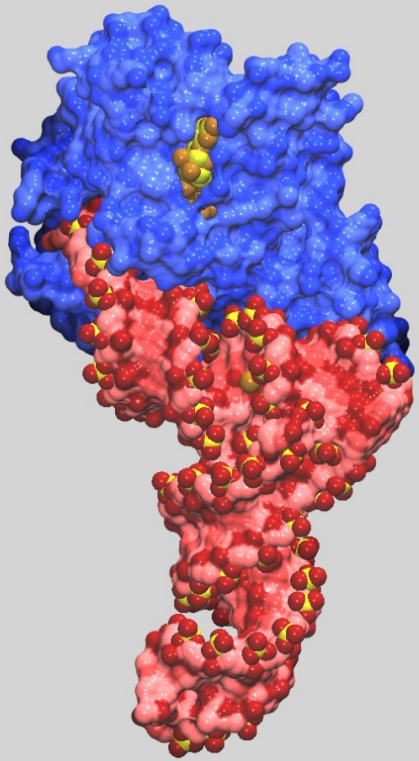
Outline Shader



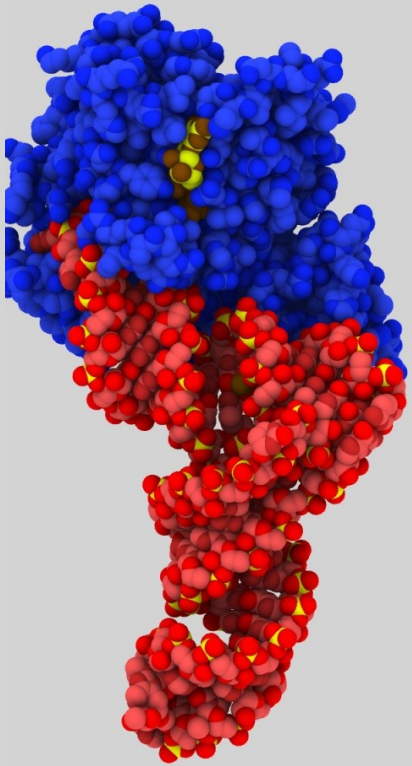
“Goodsell” Shader

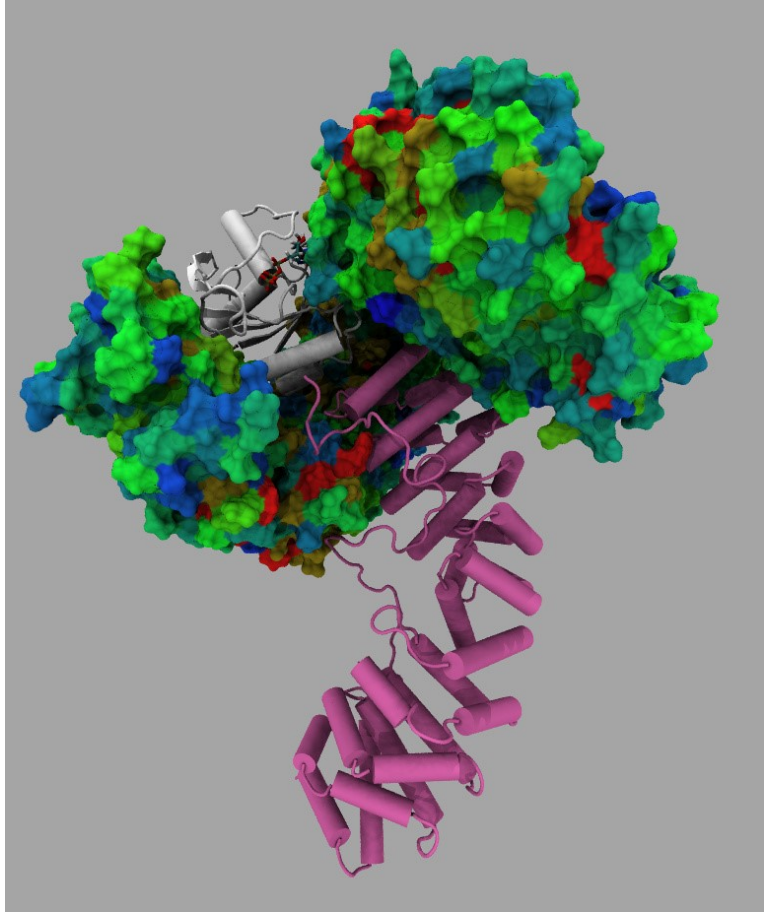


Glossy Shader

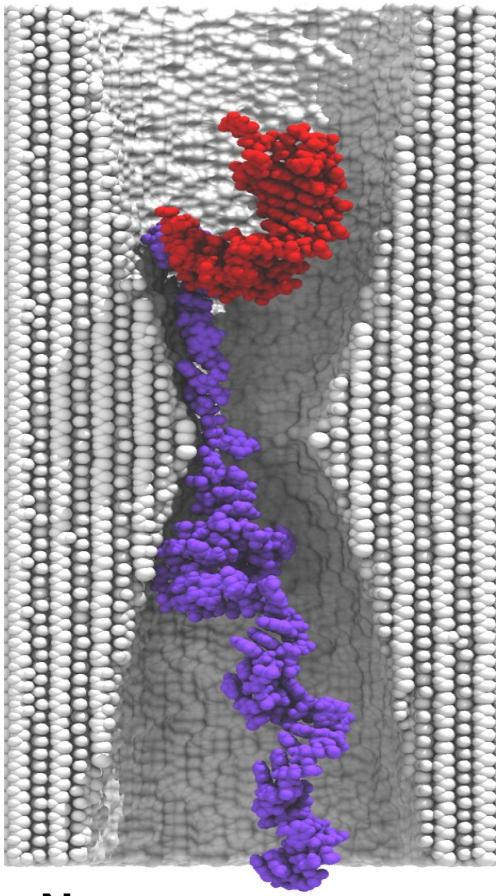


Ambient Occlusion, Shadowing





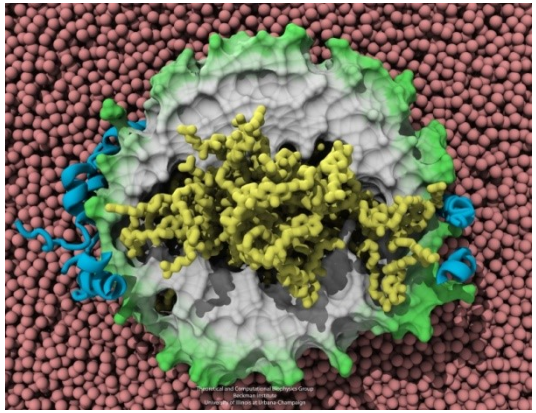
Exportin Cse1p

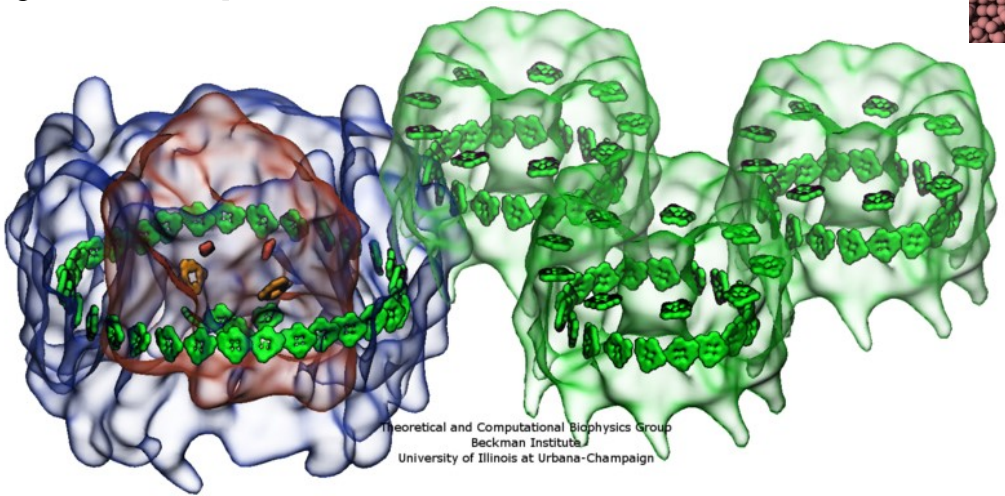


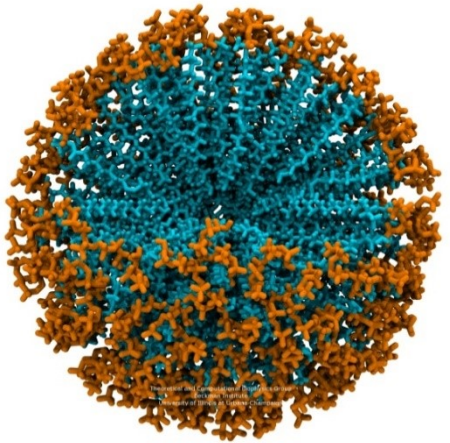
Nanopore

Benefits of Advanced Lighting and Shading Techniques

- Exploit visual intuition
- Spend computer time in exchange for scientists' time, make images that are more easily interpreted

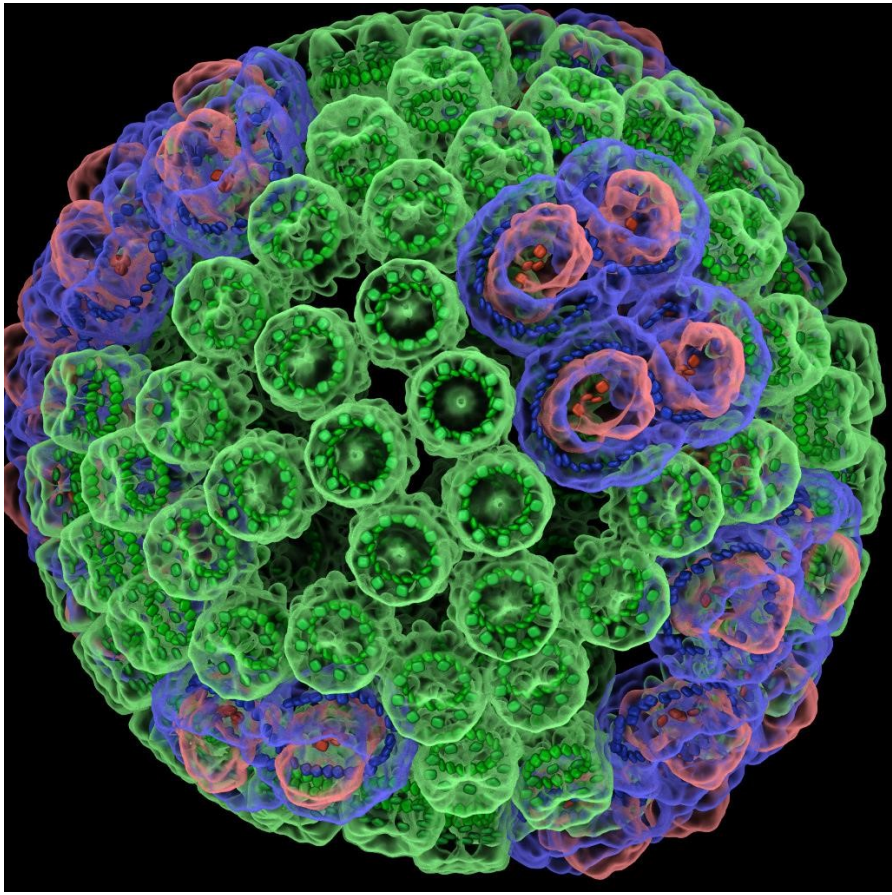


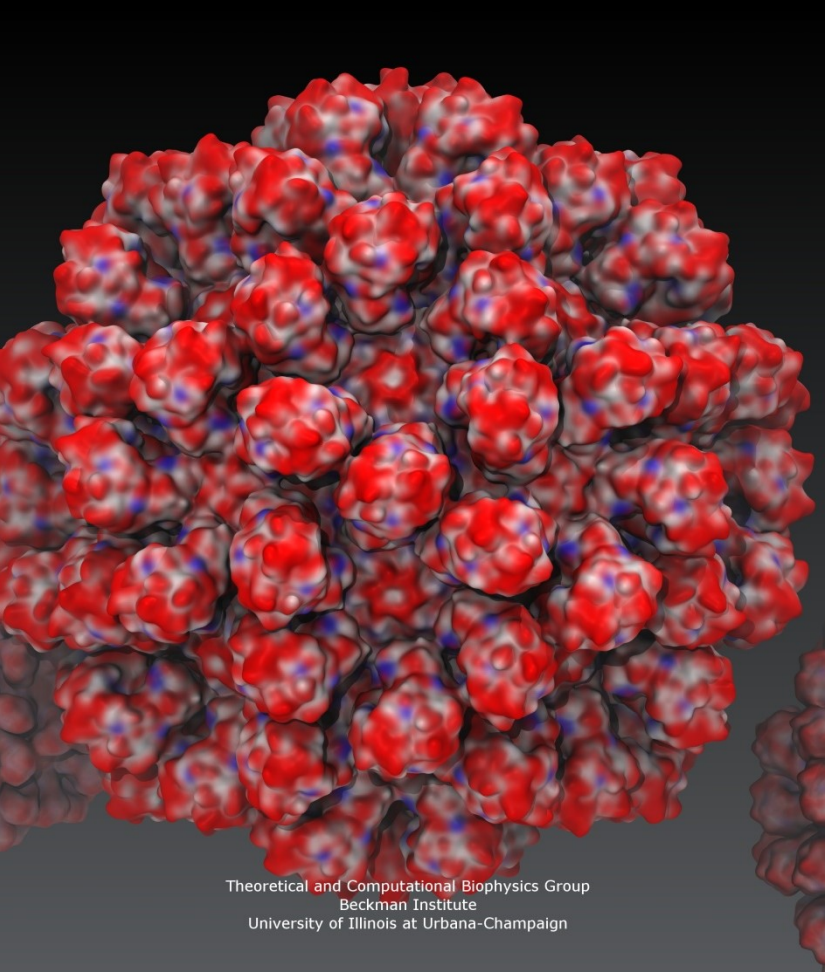


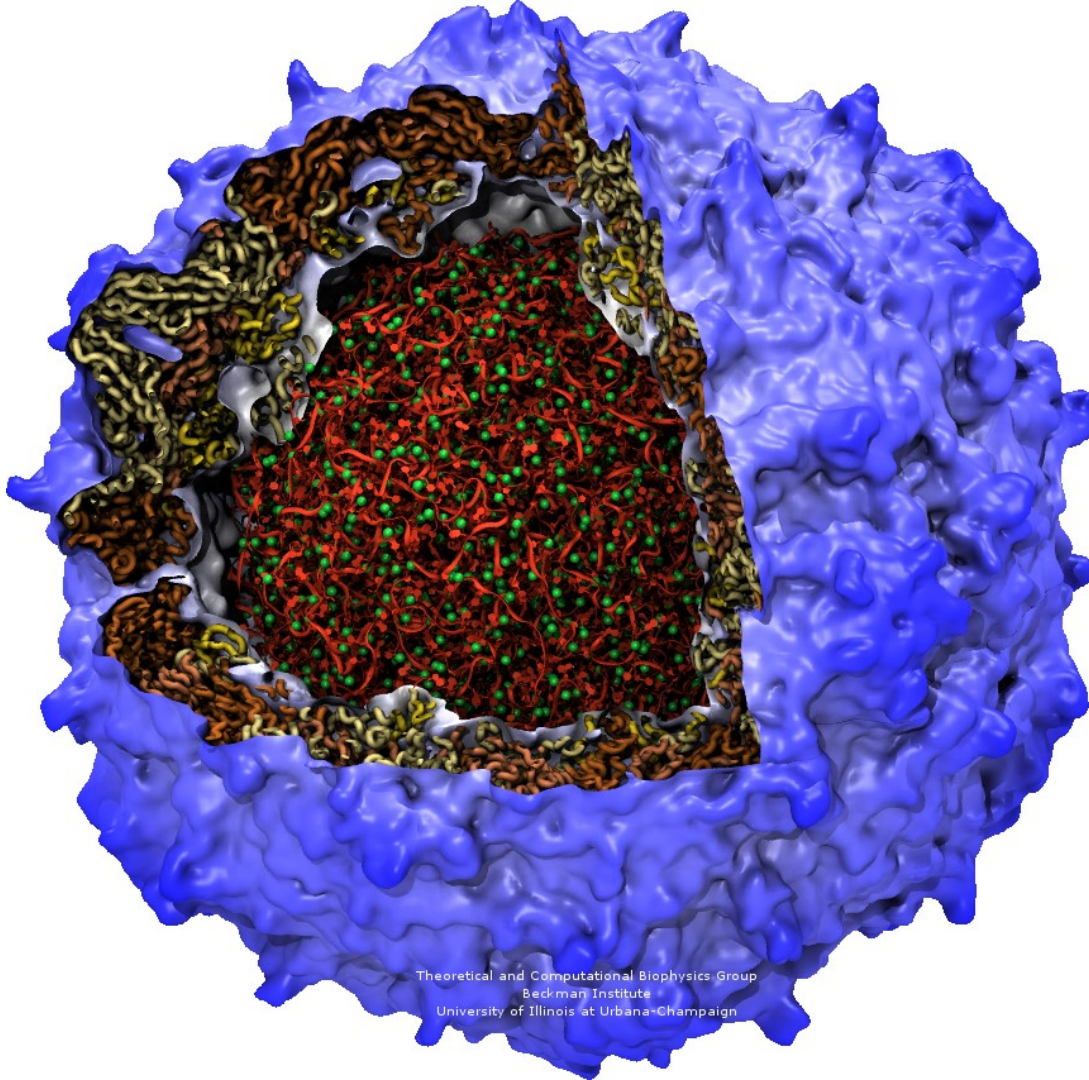


High Fidelity Interactive Visualization

- VMD interactive ray tracing
  - Interactive ray tracing on GPUs with progressive refinement of image and lighting quality
  - Fully interactive rendering of large structures with advanced lighting features, and WYSIWYG “What you see is what you get” final image output




Theoretical and Computational Biophysics Group
Beckman Institute
University of Illinois at Urbana-Champaign


Theoretical and Computational Biophysics Group
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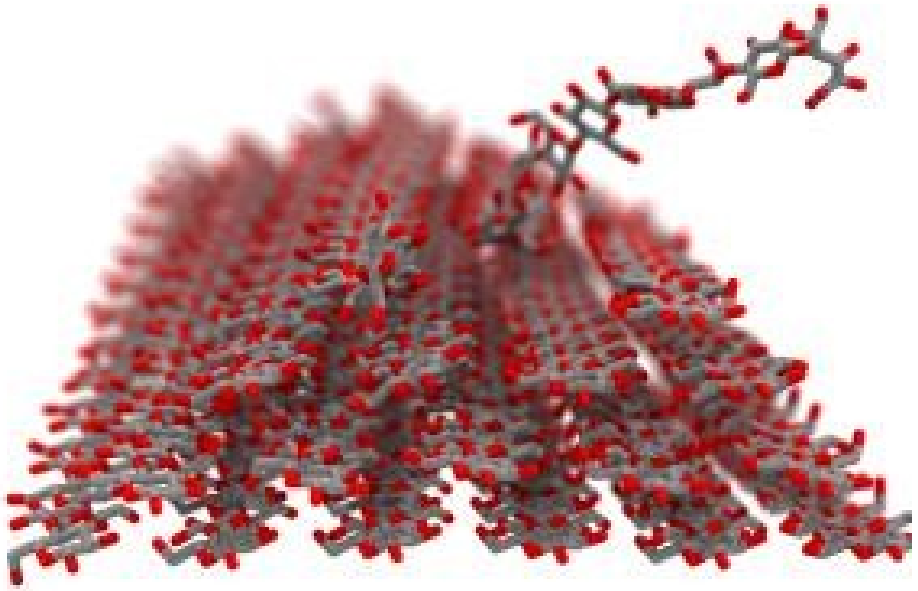
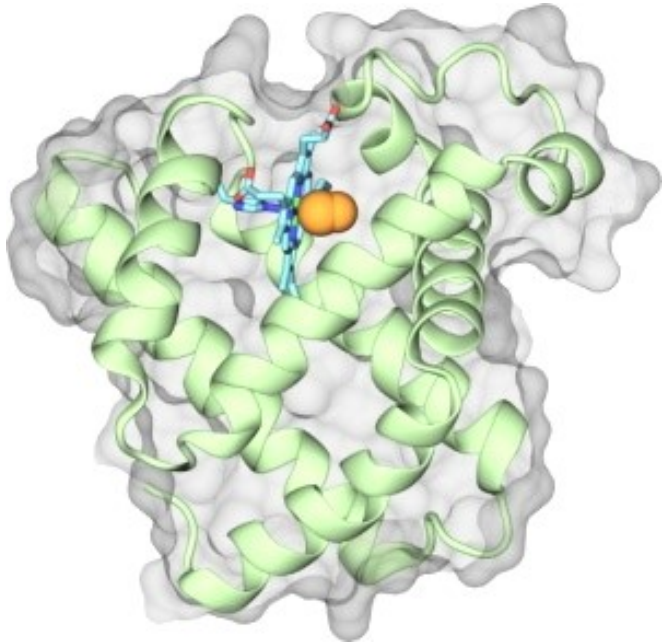
Diverse Shading and Lighting Approaches



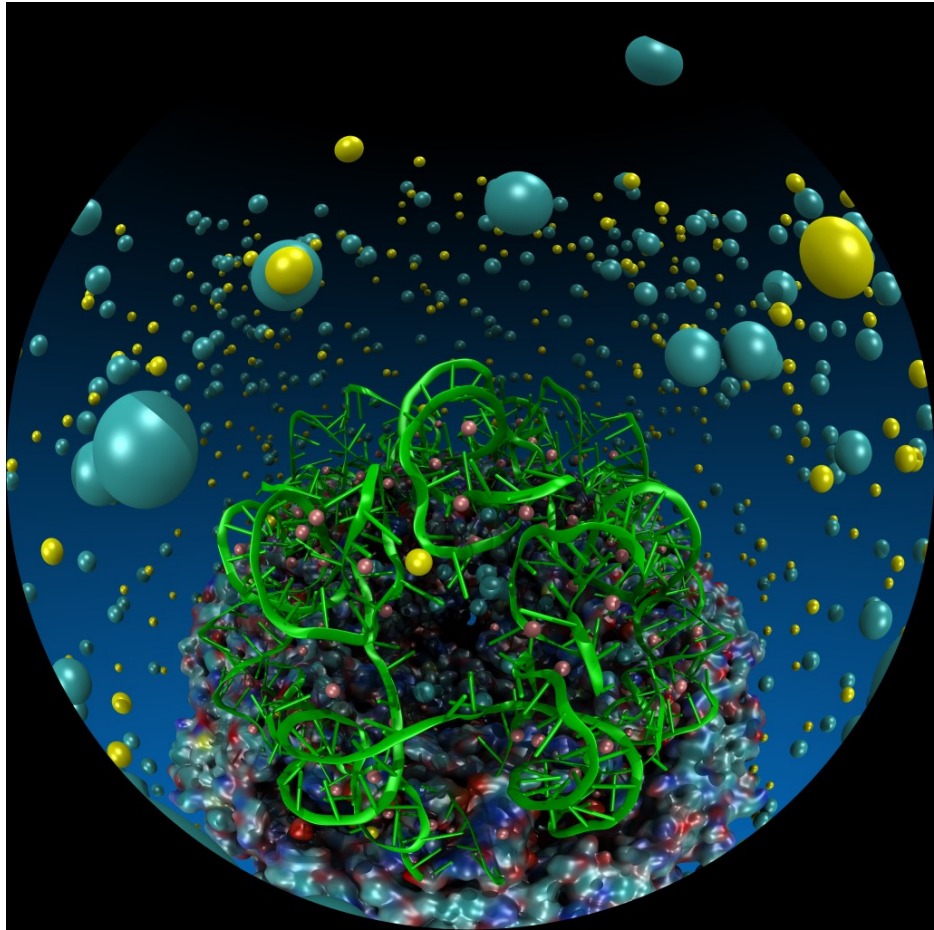
Decrystallization: Interactive Ray Tracing w/ Ambient Occlusion Lighting, Depth of Field Focal Blur



Myoglobin

VMD Planetarium Dome Master Camera

- RT-based dome projection -- rasterization poorly suited to non-planar projections
- Fully interactive RT with ambient occlusion, shadows, depth of field, reflections, and so on
- Both mono and stereoscopic
- No further post-processing required

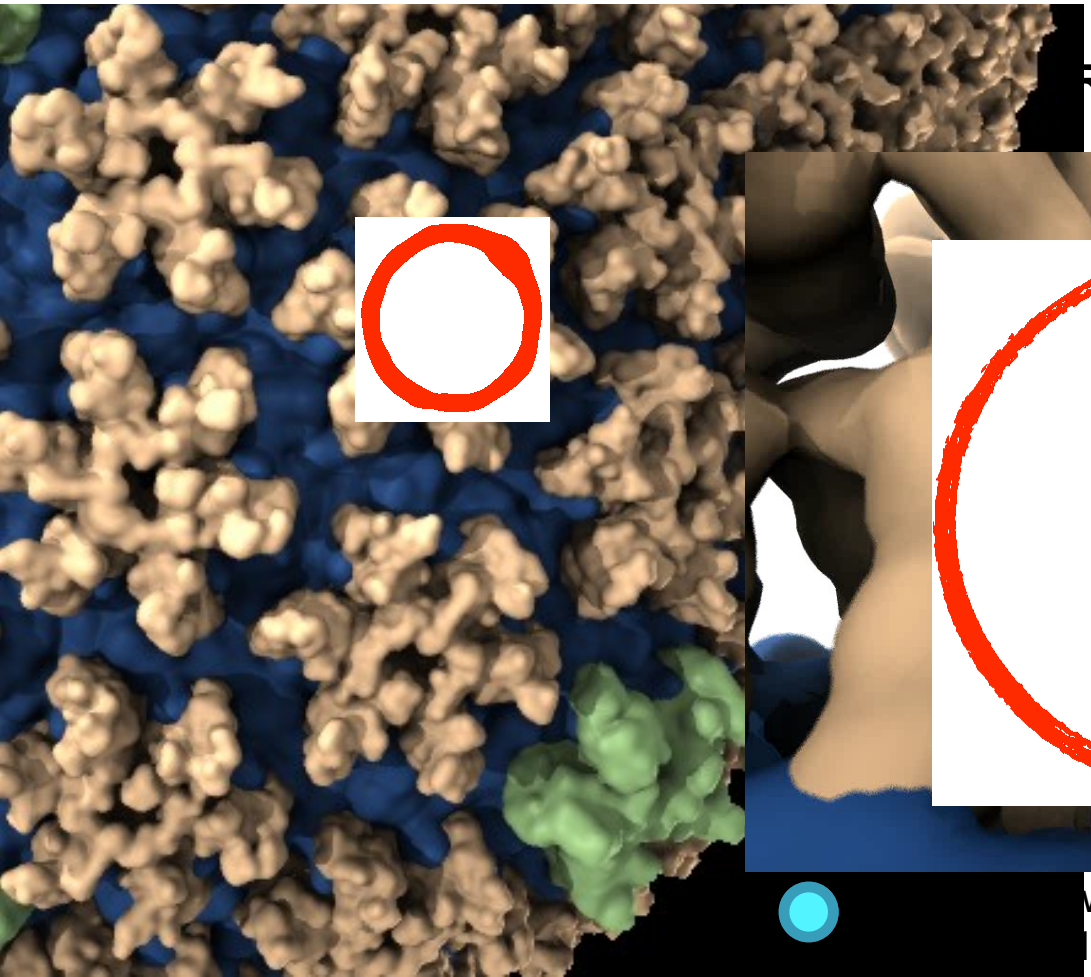


Immersive Viz. w/ VMD

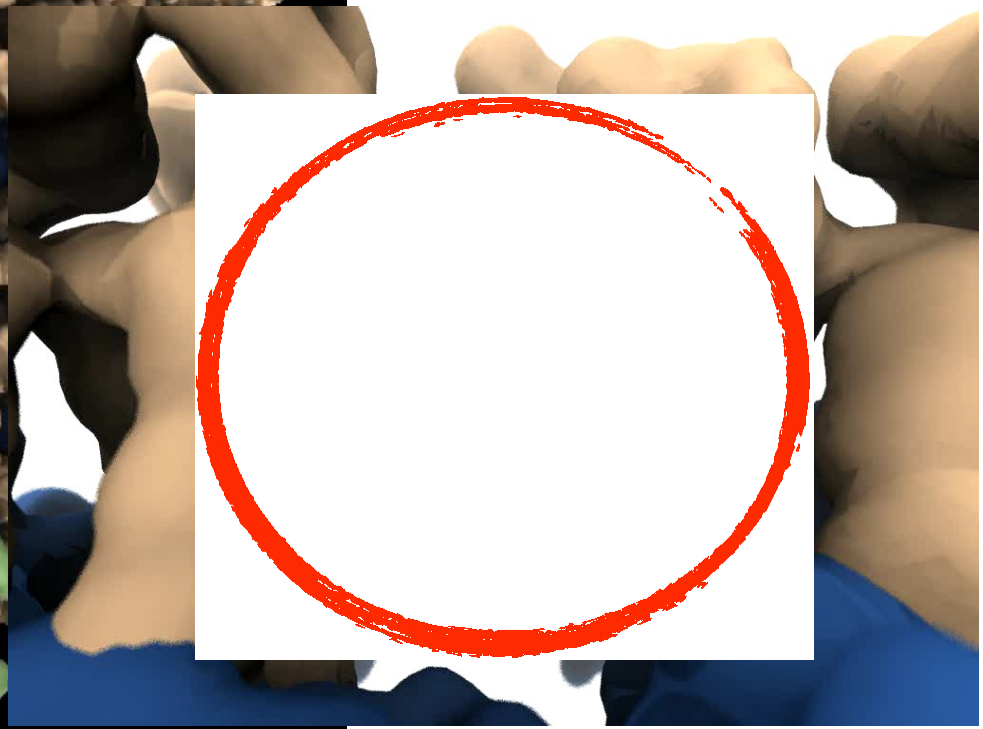
- VMD began as a CAVE app (1993)
- Use of immersive viz by molecular scientists limited due to cost, complexity, lack of local availability, convenience
- Commoditization of HMDs excellent opportunity to overcome cost/availability
- This leaves many challenges still to solve:
  - Incorporate support for **remote visualization**
  - UIs, **multi-user collaboration**/interaction
  - **Rendering perf for large molecular systems**
  - Accomodate limitations idiosyncracies of commercial HMDs

VMD running in a CAVE w/ VR Juggler

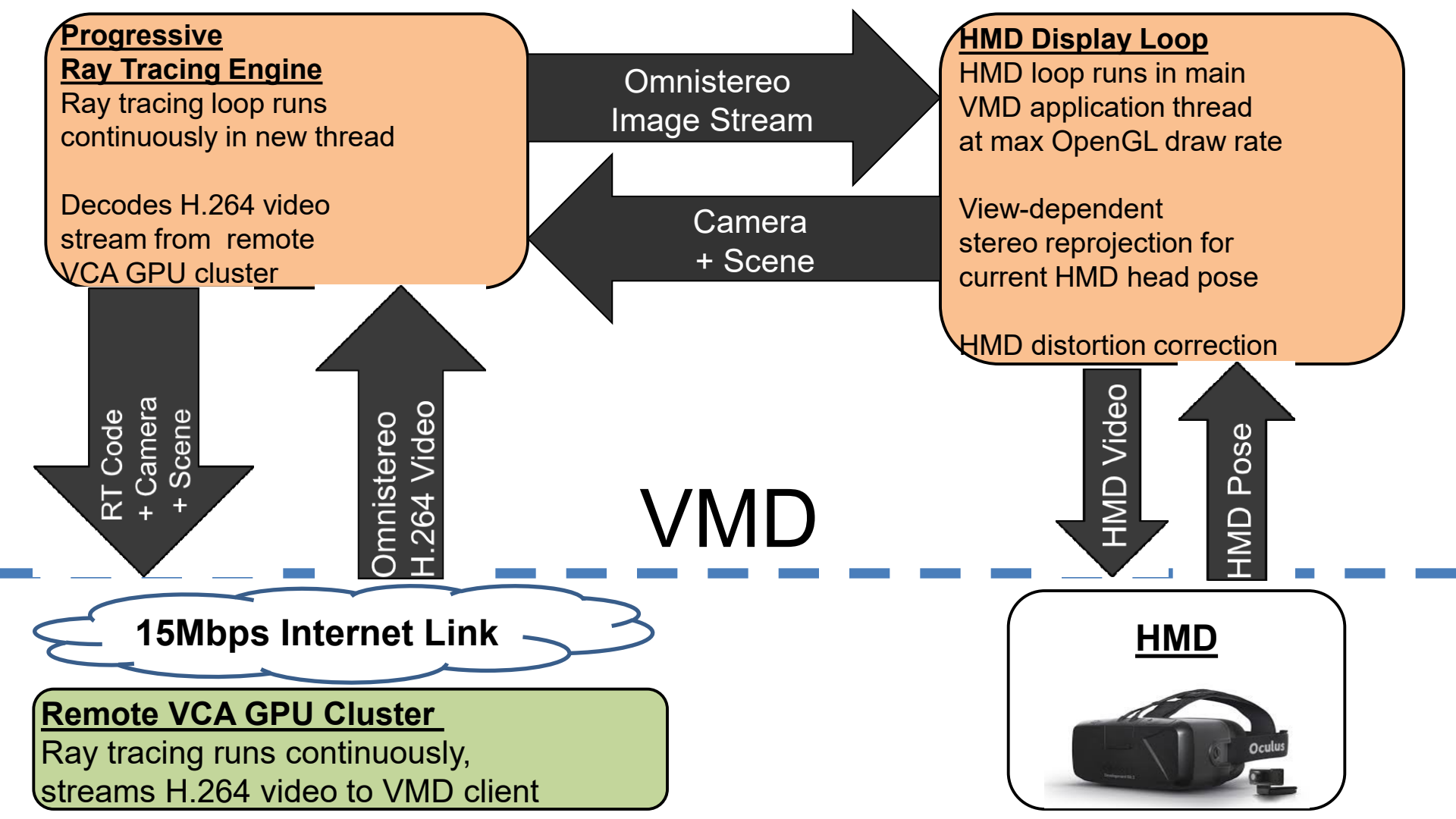
Goal: Intuitive interactive viz. in crowded molecular complexes



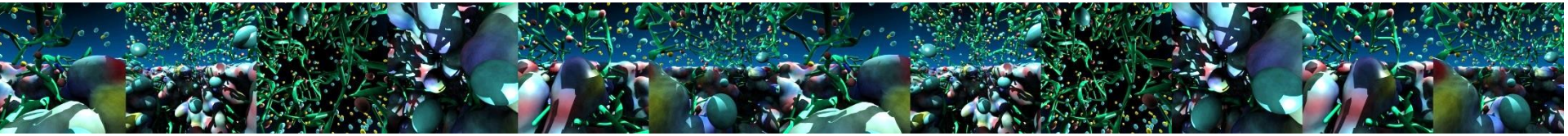
Results from 64 M atom, 1 μs sim!



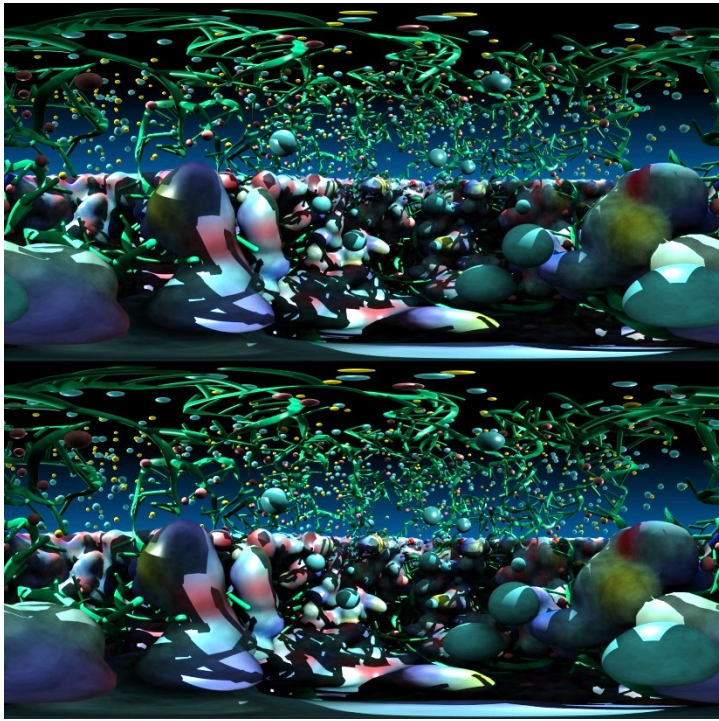
v of chloride ions permeating
capsid hexameric centers

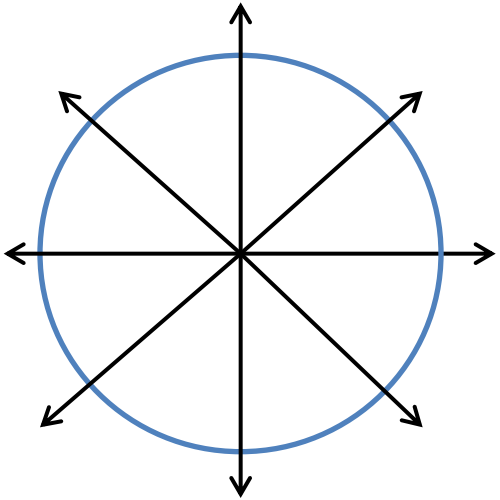

Progressive
Ray Tracing Engine
Ray tracing loop runs continuously in new thread
Decodes H.264 video stream from remote VCA GPU cluster
Omnistereo Image Stream
Camera + Scene
HMD Display Loop
HMD loop runs in main VMD application thread at max OpenGL draw rate
View-dependent stereo reprojection for current HMD head pose
HMD distortion correction
RT Code + Camera + Scene
Omnistereo H.264 Video
HMD Video
HMD Pose
VMD
15Mbps Internet Link
Remote VCA GPU Cluster
Ray tracing runs continuously, streams H.264 video to VMD client
HMD
Oculus

Stereoscopic Panorama Ray Tracing w/ OptiX

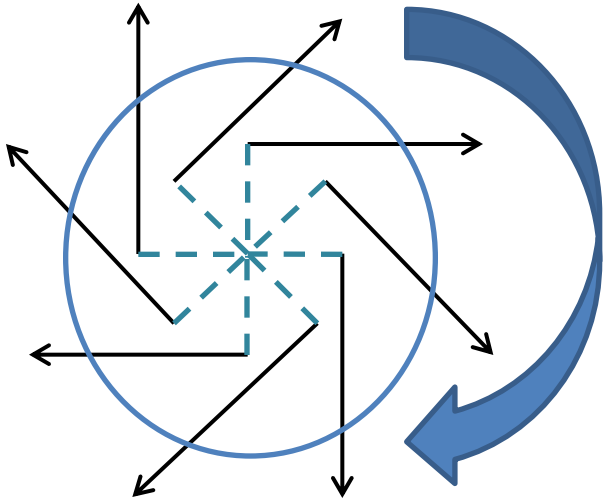


- **Render 360° images and movies for VR headsets such as Oculus Rift, Google Cardboard**
- Ray trace panoramic stereo spheremaps or cubemaps for very high-frame-rate display via OpenGL texturing onto simple geometry
- Stereo requires spherical camera projections **poorly suited to rasterization**
- Benefits from OptiX multi-GPU rendering and load balancing, **remote visualization**



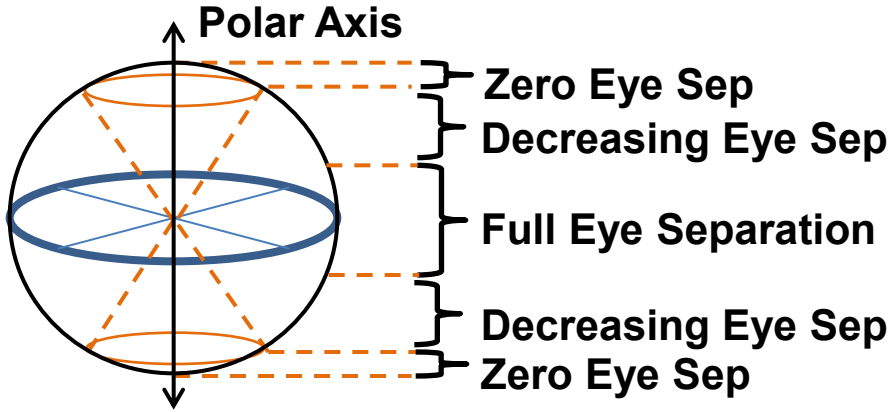


A) Monoscopic circular projection.
Eye at center of projection (COP).

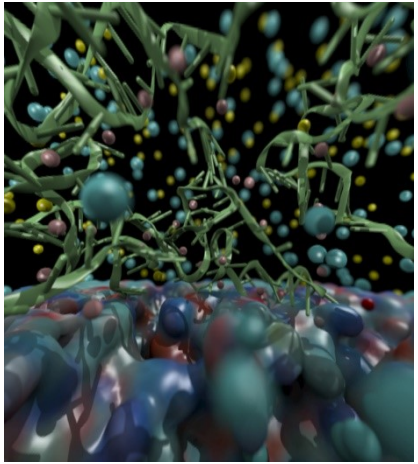
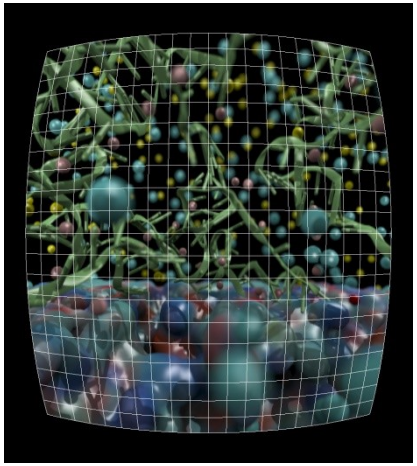
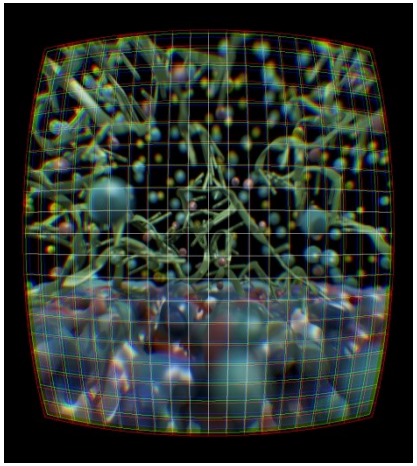
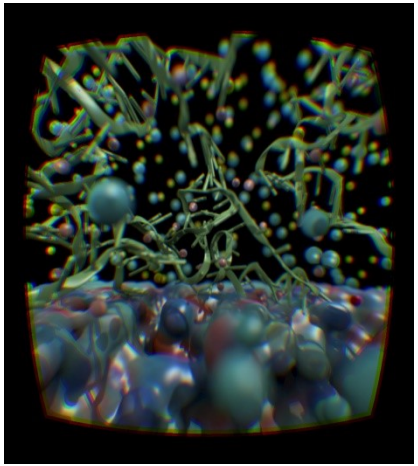
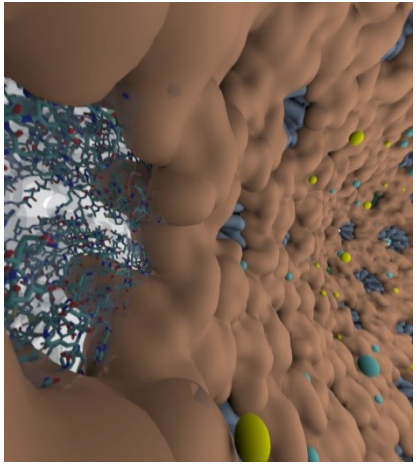
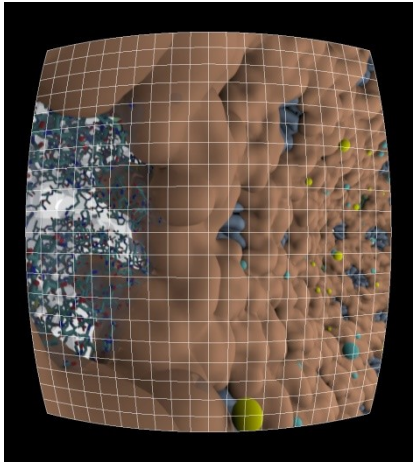
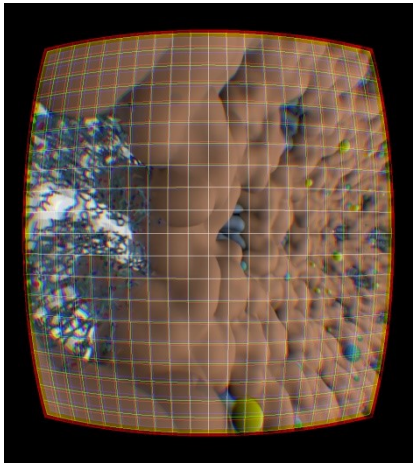
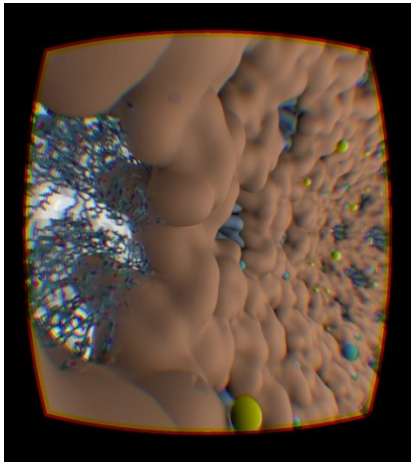


B) Left eye stereo circular projection.
Eye offset from COP by half of interocular distance.

C) Stereo eye separation smoothly decreased to zero at zenith and nadir points on the polar axis to prevent incorrect stereo when HMD sees the poles.



Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering. J. E. Stone, W. R. Sherman, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshops (IPDPSW), pp. 1048-1057, 2016.

Ongoing VR Work

- OpenXR – cross platform muti-vendor HMD support
- Ray tracing engine and optimizations:
  - **AI denoising for better average quality**
  - Interactive RT stochastic sampling strategies to improve interactivity
  - Improved omnidirectional cubemap/spheremap sampling approaches
  - **AI multi-view warping to allow rapid in-between view generation amid multiple HMD head locations**
  - **H.265 for high-res omnidirectional video streaming**
  - **Multi-node parallel RT and remote viz. on general clusters and supercomputers, e.g. NCSA Blue Waters, ORNL Titan**
- Tons of work to do on VR user interfaces, multi-user collaborative visualization, …

Acknowledgements

- Theoretical and Computational Biophysics Group, University of Illinois at Urbana-Champaign
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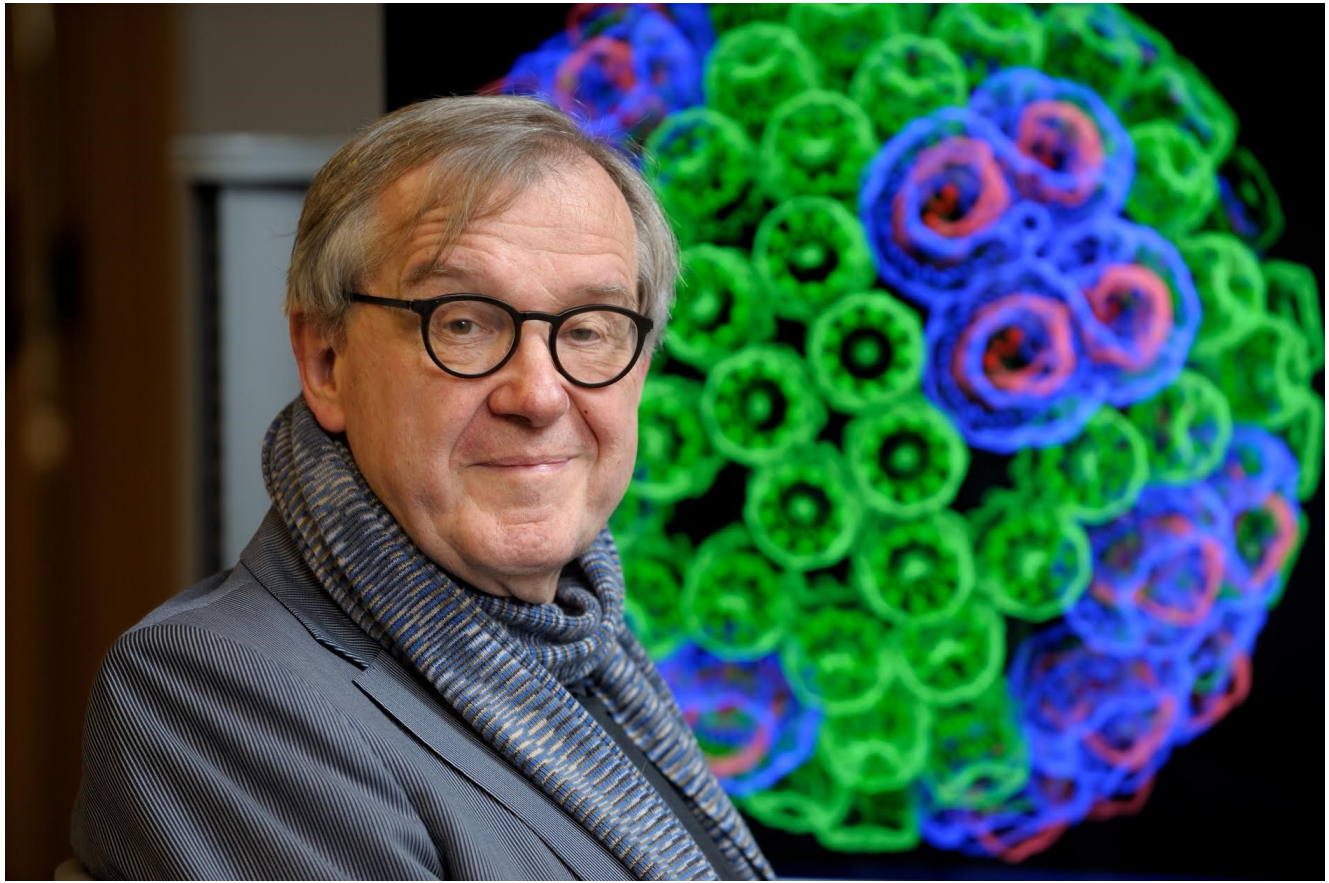
  - NSF Blue Waters:
    NSF OCI 07-25070, PRAC “The Computational Microscope”,
    ACI-1238993, ACI-1440026



“When I was a young man, my goal was to look with mathematical and computational means at the inside of cells, one atom at a time, to decipher how living systems work. That is what I strived for and I never deflected from this goal.” – Klaus Schulten

Related Publications

http://www.ks.uiuc.edu/Research/gpu/

- **NAMD goes quantum: An integrative suite for hybrid simulations.** Melo, M. C. R.; Bernardi, R. C.; Rudack T.; Scheurer, M.; Riplinger, C.; Phillips, J. C.; Maia, J. D. C.; Rocha, G. D.; Ribeiro, J. V.; Stone, J. E.; Neese, F.; Schulten, K.; Luthey-Schulten, Z.; Nature Methods, 2018. (**In press)**
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- **Early Experiences Porting the NAMD and VMD Molecular Simulation and Analysis Software to GPU-Accelerated OpenPOWER Platforms.** J. E. Stone, A.-P. Hynninen, J. C. Phillips, and K. Schulten. International Workshop on OpenPOWER for HPC (IWOPH'16), LNCS 9945, pp. 188-206, 2016.
- **Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering.** J. E. Stone, W. R. Sherman, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), pp. 1048-1057, 2016.
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- **Unlocking the Full Potential of the Cray XK7 Accelerator.** M. D. Klein and J. E. Stone. Cray Users Group, Lugano Switzerland, May 2014.
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- **Immersive Out-of-Core Visualization of Large-Size and Long-Timescale Molecular Dynamics Trajectories.** J. Stone, K. L. Vandivort, and K. Schulten. G. Bebis et al. (Eds.): *7th International Symposium on Visual Computing (ISVC 2011)*, LNCS 6939, pp. 1-12, 2011.
- **Fast Analysis of Molecular Dynamics Trajectories with Graphics Processing Units – Radial Distribution Functions.** B. Levine, J. Stone, and A. Kohlmeyer. *J. Comp. Physics*, 230(9):3556-3569, 2011.

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