

# S8665—VMD: Biomolecular Visualization from Atoms to Cells Using Ray Tracing, Rasterization, and VR

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

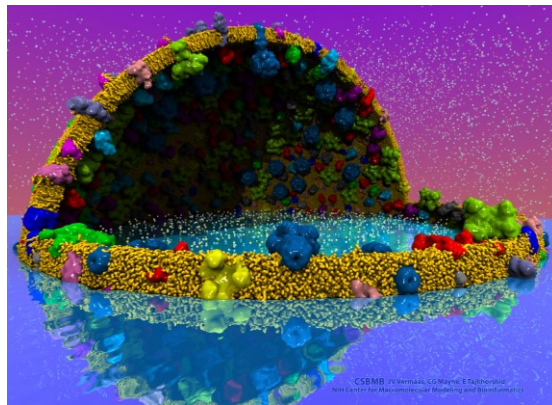
S8665, GPU Technology Conference

11:00-11:50, Hilton Almaden 2,

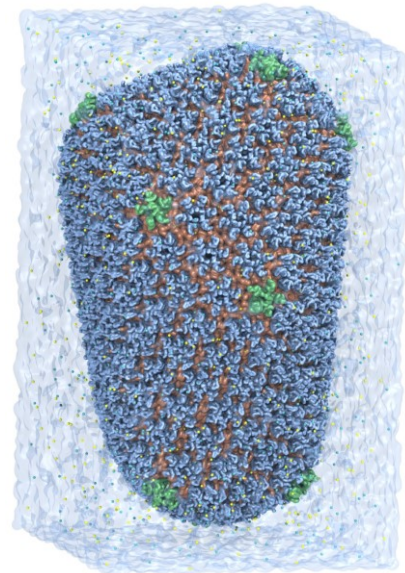
San Jose, CA, Thursday March 29<sup>th</sup>, 2018

# VMD – “Visual Molecular Dynamics”

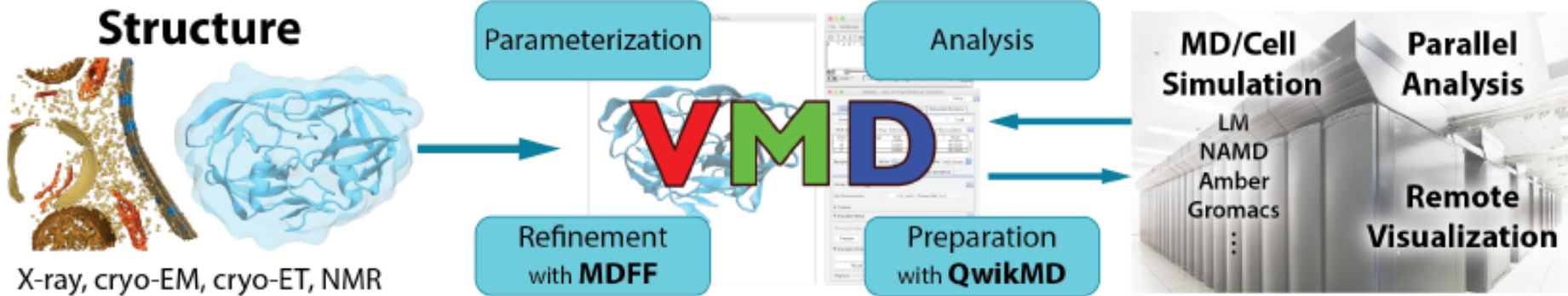
- Visualization and analysis of:
  - Molecular dynamics simulations
  - Lattice cell simulations
  - Quantum chemistry calculations
  - Cryo-EM densities, volumetric data
  - Sequence information
- User extensible scripting and plugins
- <http://www.ks.uiuc.edu/Research/vmd/>



Cell-Scale Modeling



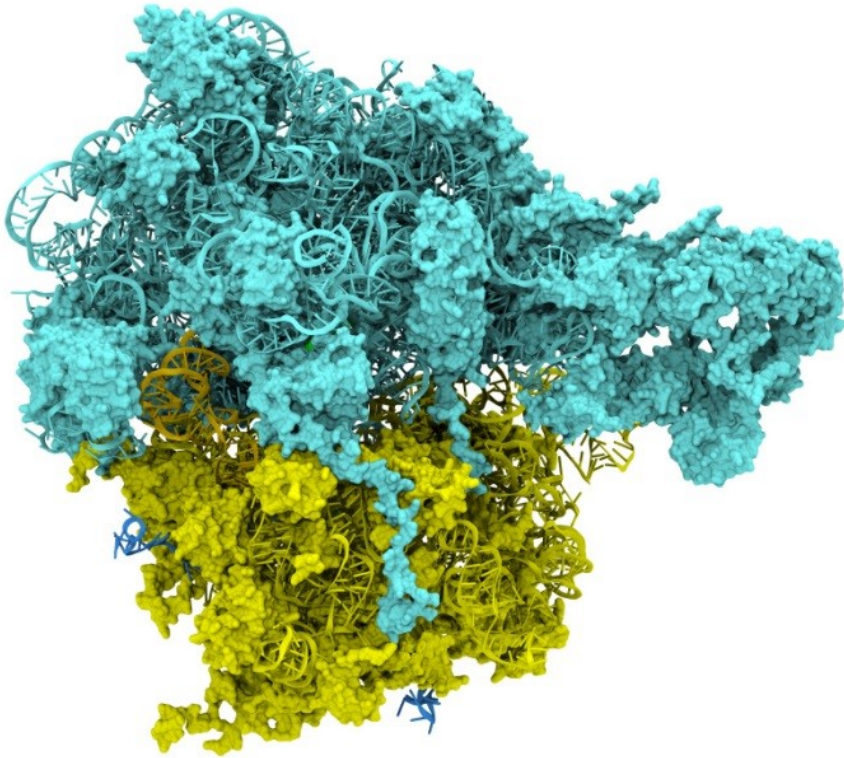
MD Simulation



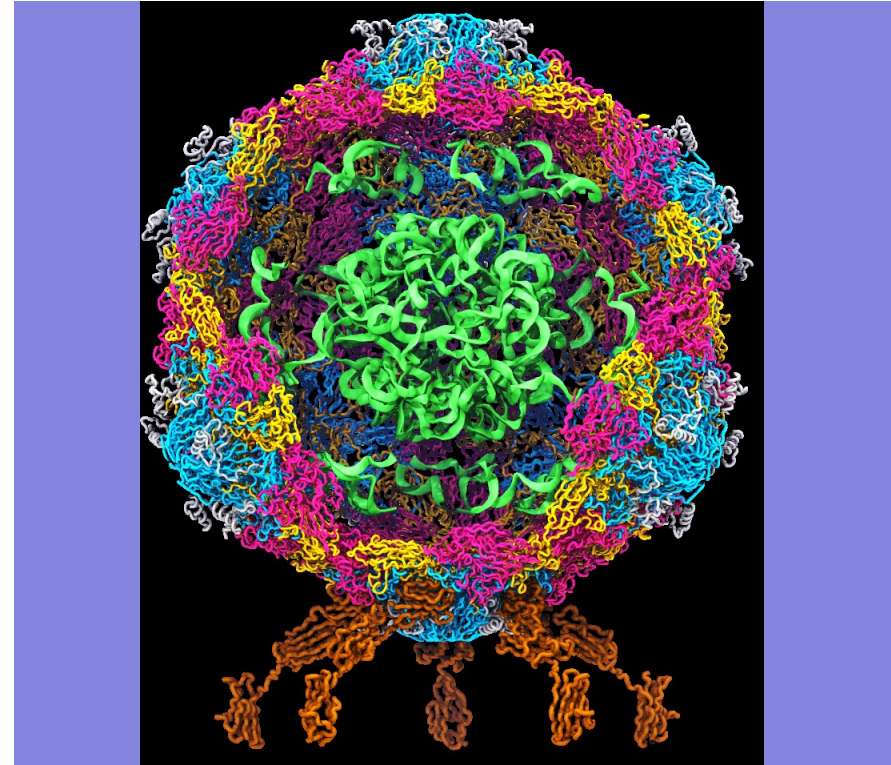
# Goal: A Computational Microscope

Study the molecular machines in living cells

Ribosome: target for antibiotics



Poliovirus

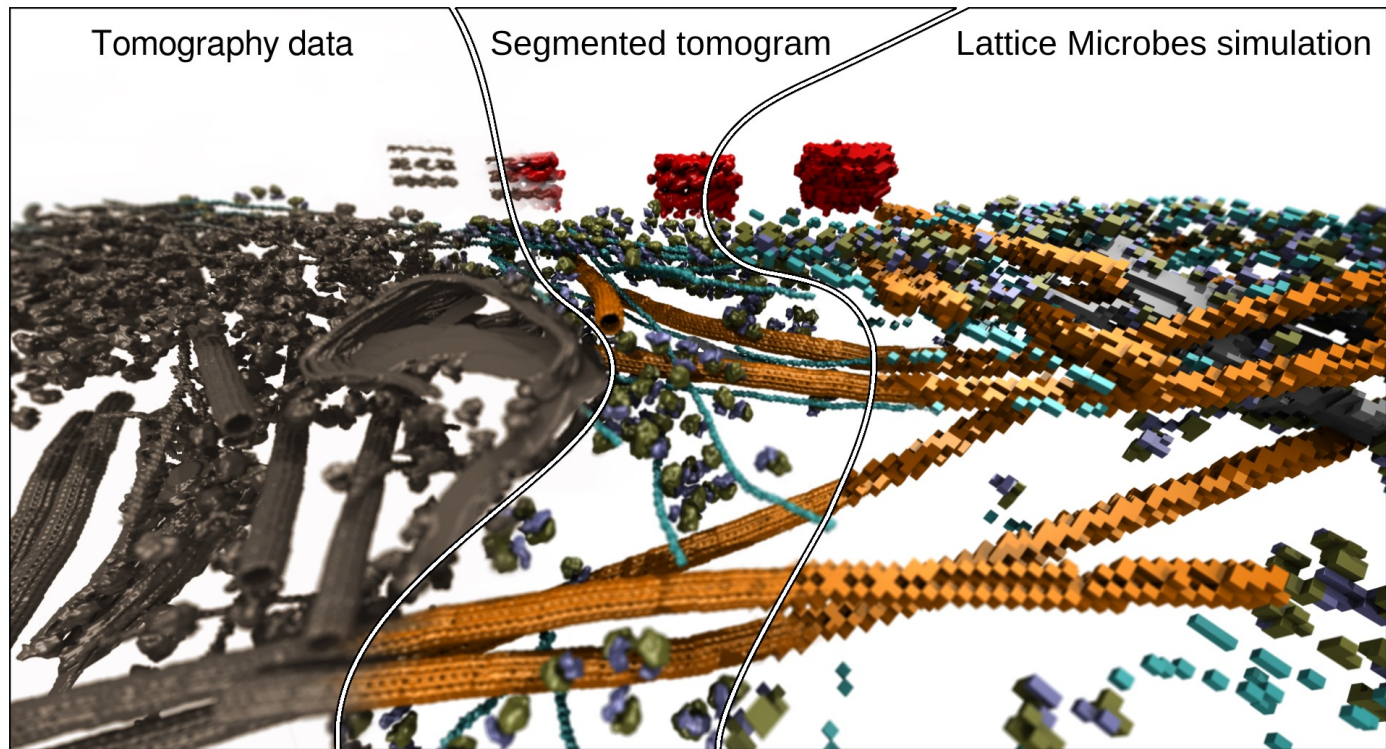




# Cryo-EM / Cryo-ET Image Segmentation

**Evaluate 3-D volumetric electron density maps and segment them, to identify key structural components**

**Index/label components so they can be referred to, colored, analyzed, and simulated...**





# Cryo-EM Density Map Segmentation

## Approach, goals

### Goals:

- **Reach interactive performance rates (under 1 second)** for common density map sizes between  $128^3$  to  $256^3$  voxels
- Handle **next-generation problem sizes ( $768^3$  to  $2048^3$ )** smoothly with only a brief wait

### Key methods:

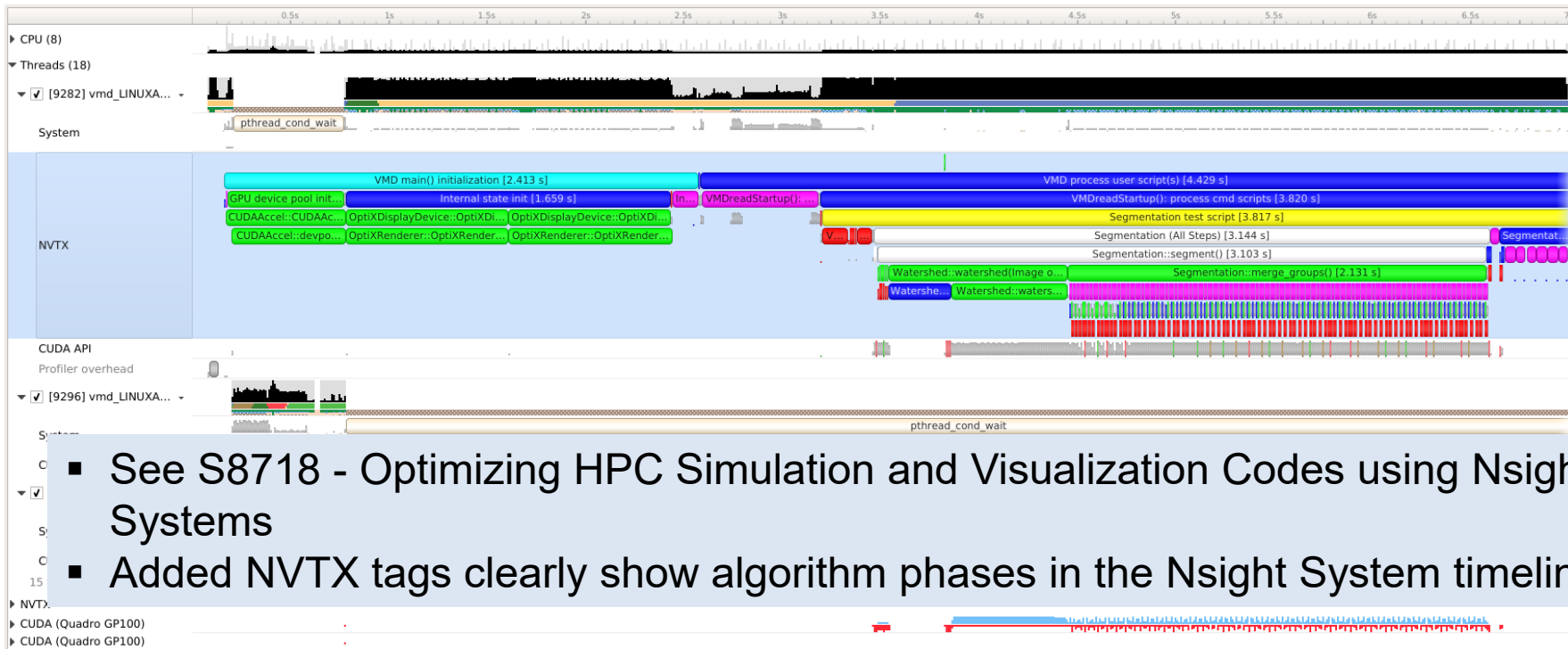
- **Tile-based early-exit schemes** pervasively used for all iterative segmentation update/merge kernels
- **Privatization, shared memory atomic counters** for segmentation group index kernels
- **Significantly faster than published algorithm designs we are aware of**

### Watershed segmentation:

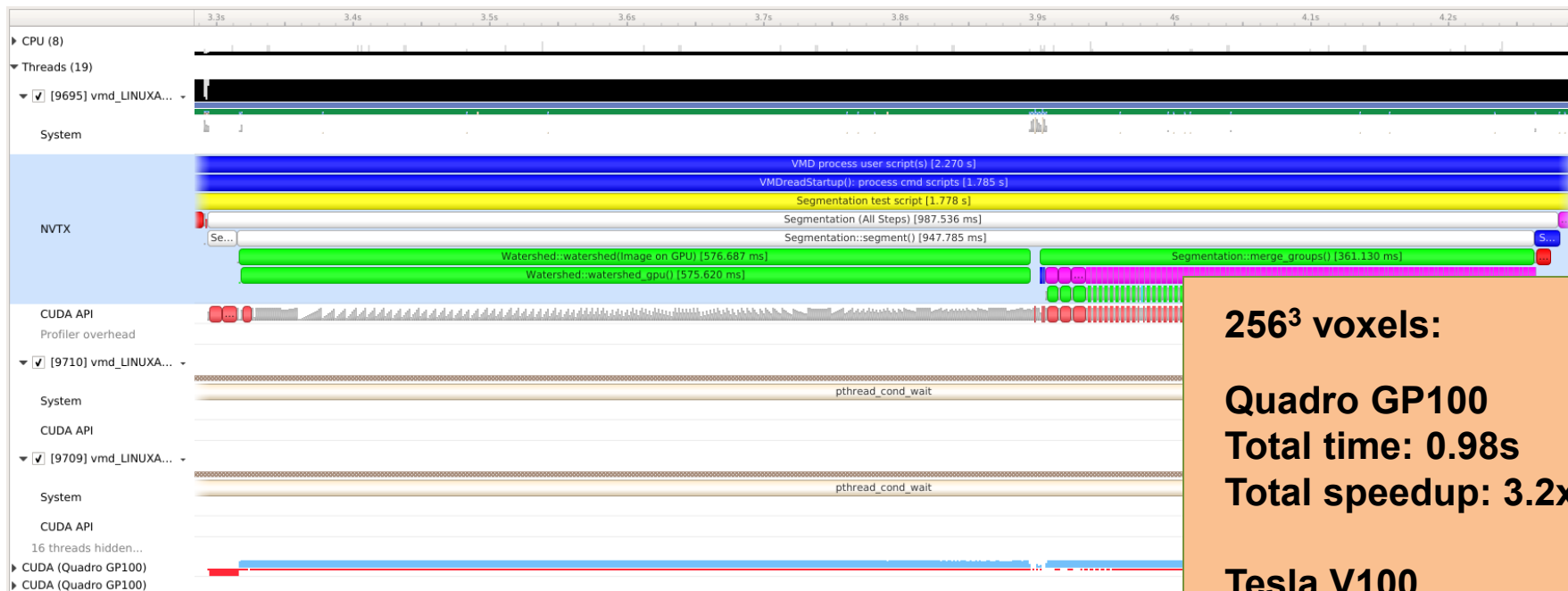
- Smooth/denoise image (e.g. blur)
- Find local minima of image/gradients
- Connect minimum voxels with neighbors of similar intensity, marking them with the same “group” number
- “Grow” each group (merging groups where rules allow) until no more updates occur

Scale-space segmentation variant does further blurring and group merging to reach a user-specified target segment count

# Profiled VMD Segmentation w/ NVIDIA Nsight Systems



# VMD Optimized GPU Segmentation Pipeline



256<sup>3</sup> voxels:

Quadro GP100  
Total time: 0.98s  
Total speedup: 3.2x

Tesla V100  
Total time: 0.67s  
Total speedup: 4.1x

■ VMD GPU Segmentation now over 12x faster than competing tools



# Volta-Specific Segmentation Optimization Opportunities

- Optimized precision for 3-D density maps:
  - Improved memory bandwidth, lower arithmetic cost
  - FP16: half-precision EM density map representation
  - INT8: byte density map representation **for EM tomograms**
- Explore Tensor Core for iterative scale-space segmentation merge/blur convolutions, and initial noise filtering steps:
  - Difficult to prevent TC from becoming mem bandwidth-bound
  - Challenge: CUDA 9.x APIs for TC limit the range of data movement patterns that perform well
  - Some dimensionalities and matrix-based problem decompositions perform much better than others – this is an area of ongoing exploration

# 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:**

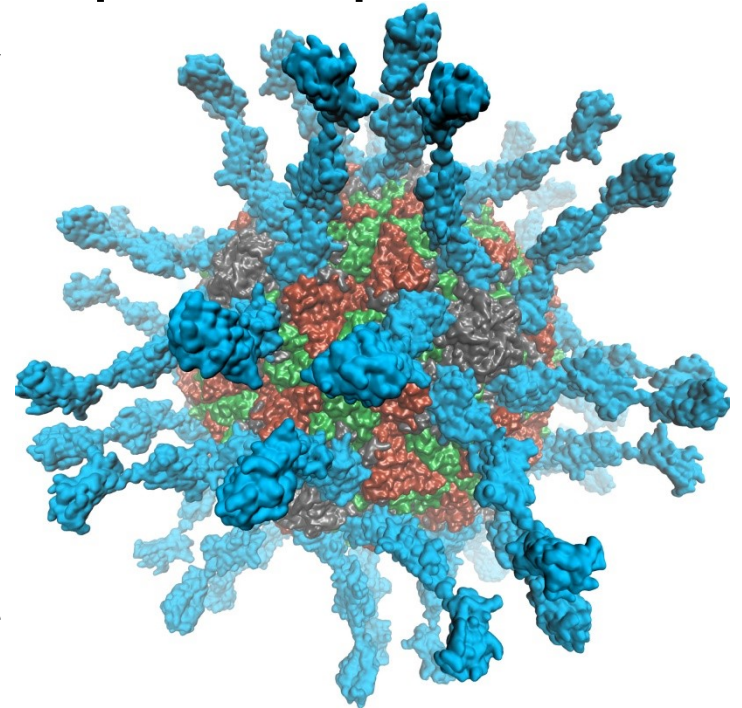
**ORNL Titan, NCSA Blue Waters, Indiana Big Red II,  
CSCS Piz Daint, and similar systems**



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

# VMD supports EGL for in-situ and parallel rendering on clouds, clusters, and supercomputers

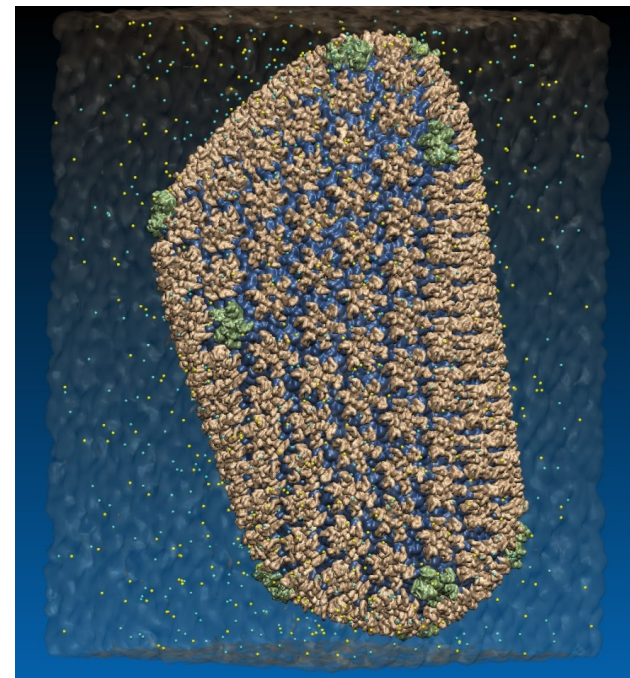
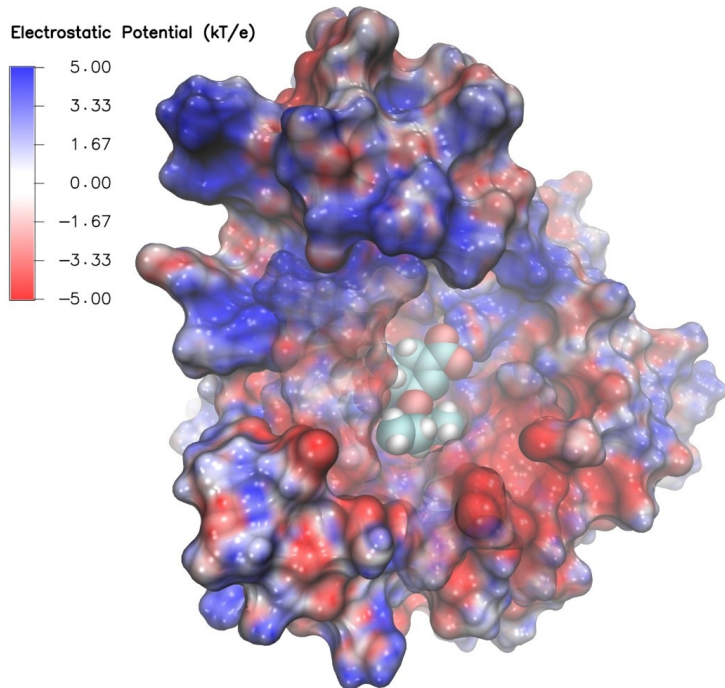
- **No windowing system dependency**
- Easily deploy parallel VMD builds supporting off-screen rendering
- Maintains 100% of VMD OpenGL shaders and rendering features
- Support high-quality vendor-supported commercial OpenGL implementations in HPC systems that were previously limited to Mesa



**Poliovirus**



# VMD EGL Rendering: Supports full VMD GLSL shading features, multisample antialiasing, ray cast spheres, 3-D tex mapping, ...



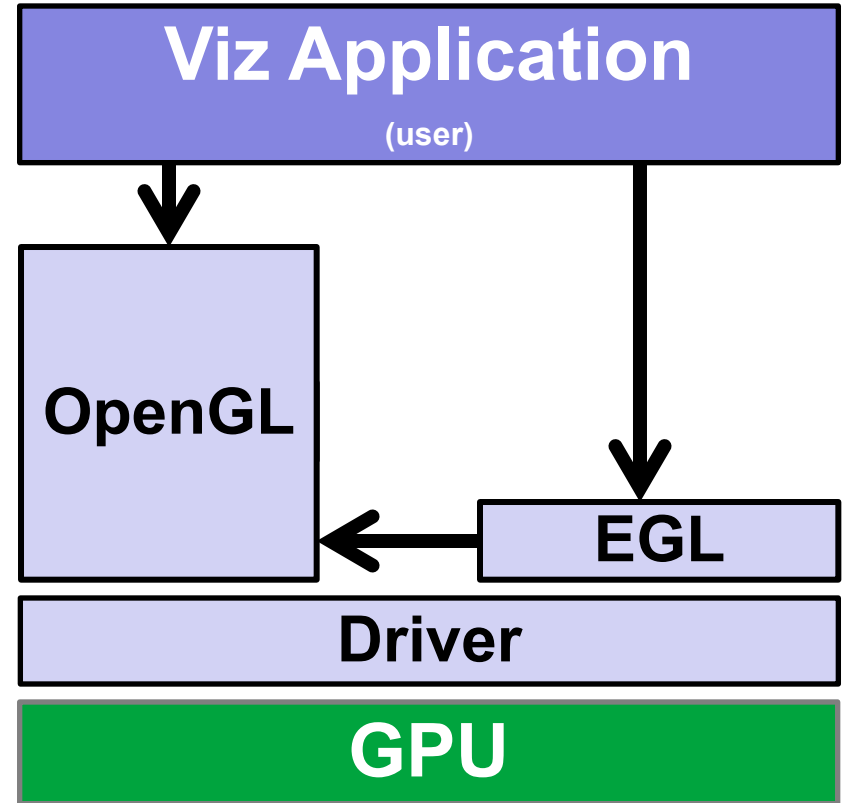
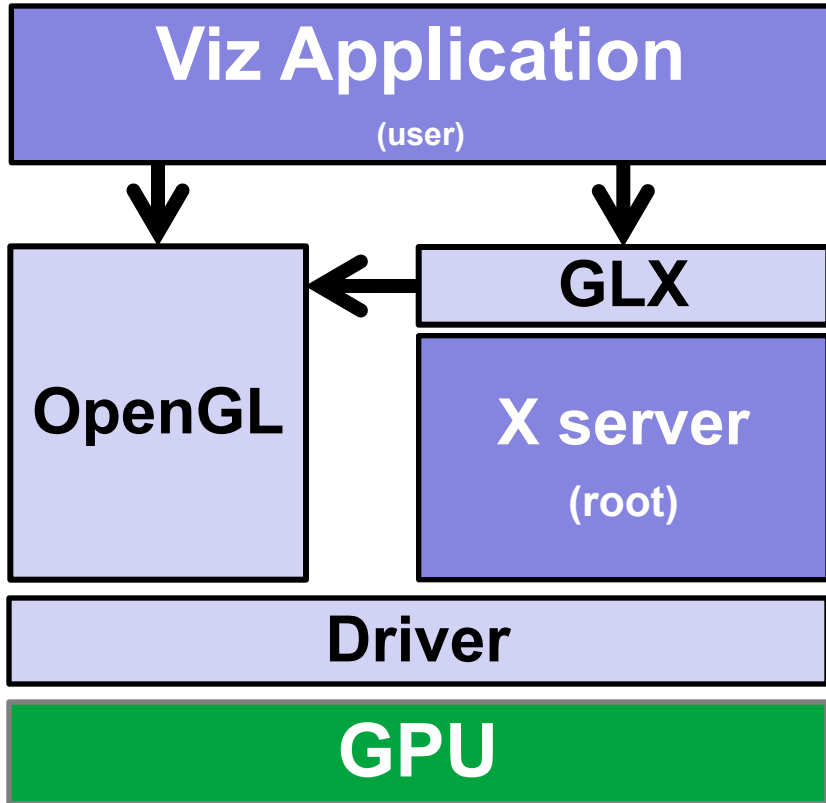
**Swine Flu A/H1N1 neuraminidase bound to Tamiflu**

**64M atom HIV-1 capsid simulation**

**High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL.**

J. E. Stone, P. Messmer, R. Sisneros, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE IPDPSW, pp. 1014-1023, 2016.

# OpenGL: GLX vs. EGL



# 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





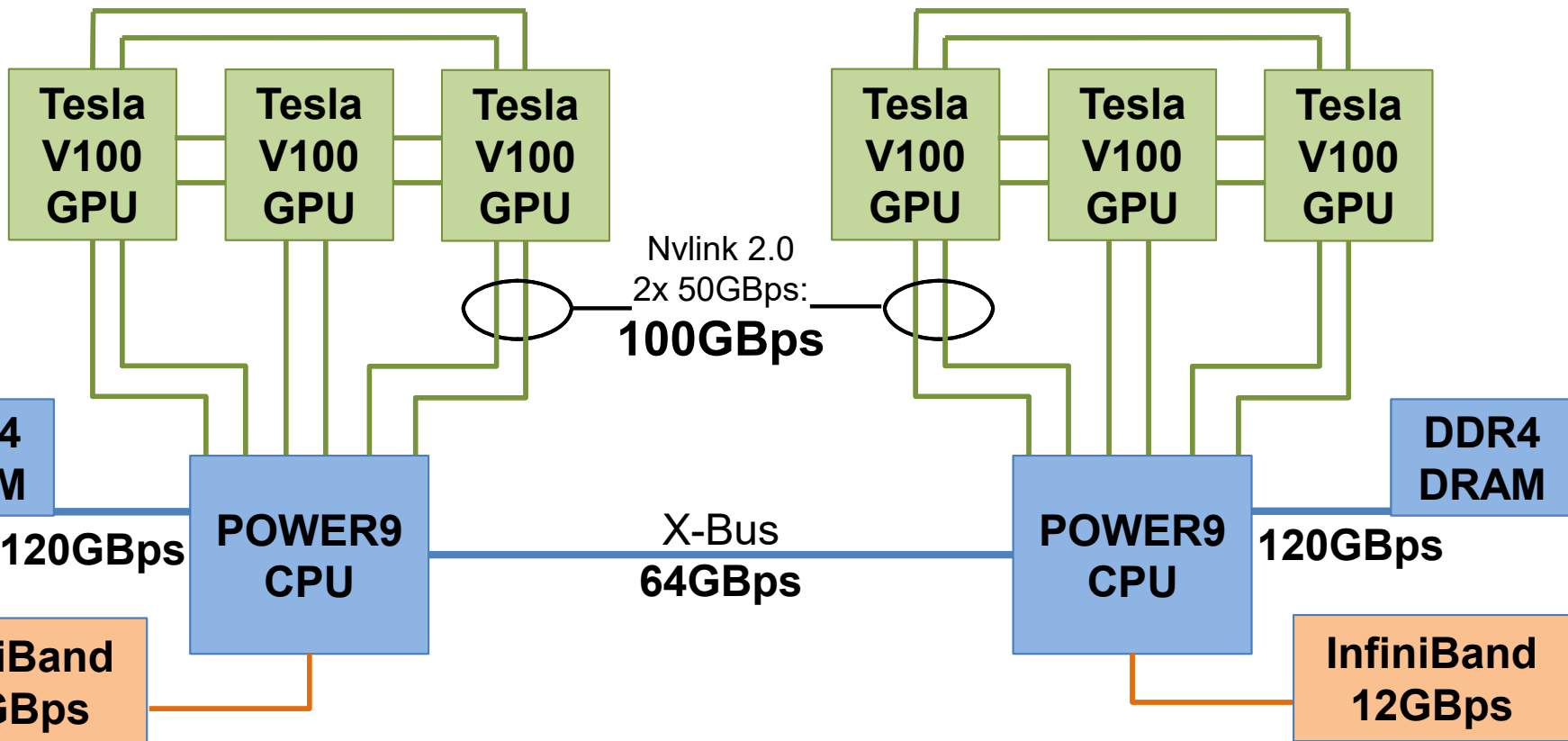
# Benefits of EGL Platform Interfaces

- **EGL interfaces make it EASY to bind a GPU to a thread with optimal CPU affinity with respect to NUMA topology, NVLink GPU topology**
  - High-perf. multi-GPU image compositing, video streaming
  - EGL plays nicely with MPI, CUDA/OpenCL, OptiX, NVENC, etc
  - NVIDIA EGL supports multiple GPU indexing schemes, e.g. **PCIe ordering**
  - **Exploit NVLink interconnect topology on IBM OpenPOWER platforms, DOE/ORNL “Summit” system**



# IBM AC922 Summit Node

3 GPUs Per CPU Socket





<https://www.khronos.org/vulkan/>

- **High performance, low-overhead, reduced abstraction, rasterization API:**
  - Modern API, benefits from past experiences with OpenGL, DX, etc
  - Core features essentially start w/ OpenGL 4.x function, and continue from there
  - Fewer extensions required for modern functionality
  - Significantly reduced API overheads relative to OpenGL, **some apps have seen up to ~3x performance gains vs. traditional OpenGL**
- Shaders (e.g. GLSL) compiled to SPIR-V intermediate code at **app compile time**
- **Compile-time validation** of shaders, rendering pipelines (lower runtime overhead)
- Core Vulkan doesn't deal with on-screen display, only rendering
  - Integration with windowing system is handled by Vulkan "WSI" extensions
- **Multi-GPU rendering included in the new Vulkan 1.1 spec!**

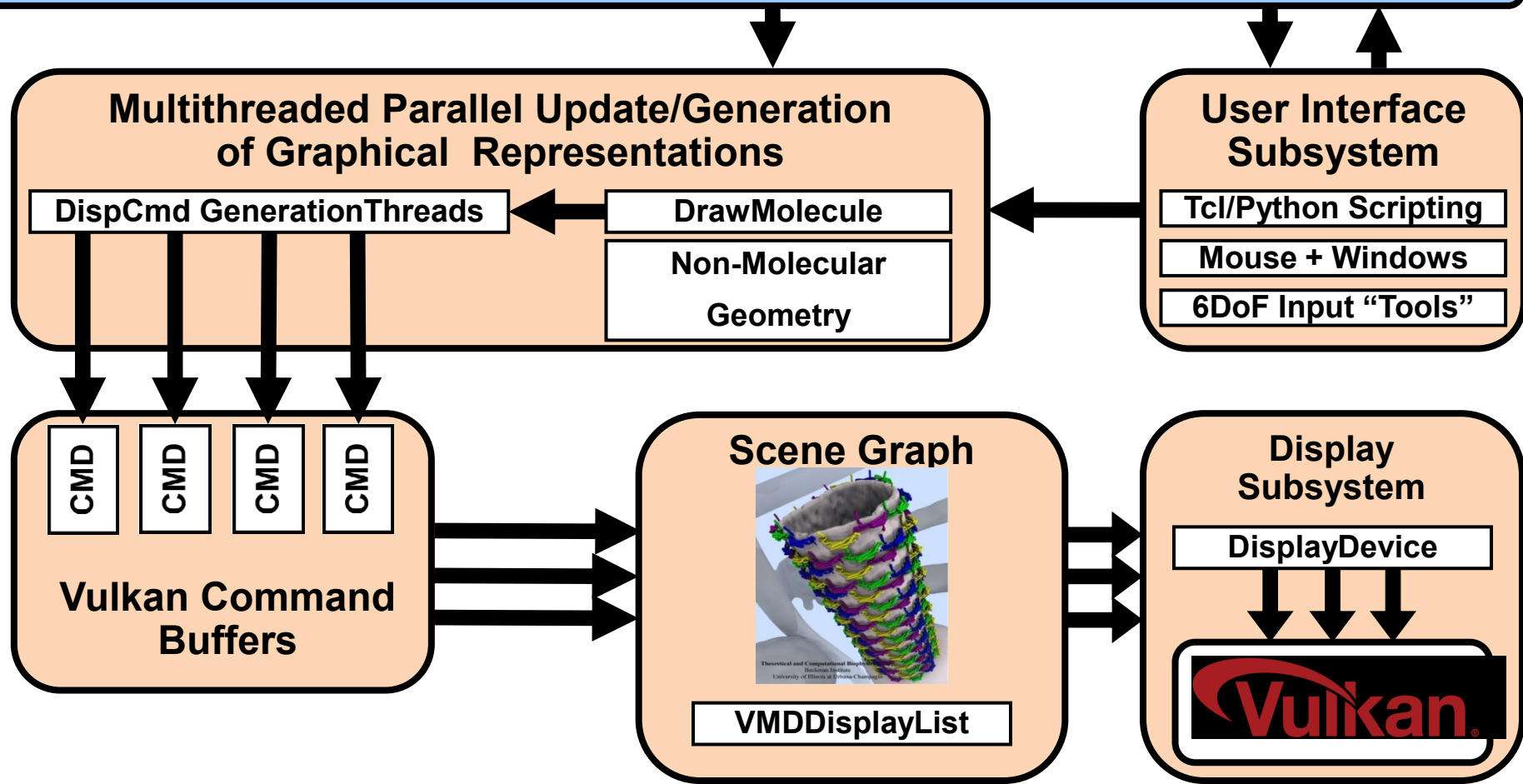
# VMD on



- ***In-progress: Vulkan-based rasterization path for VMD***
- **Vulkan opportunities for VMD:**
  - **Vulkan ideally suited** as the API for **high-end GPUs**
  - Maintain existing OpenGL renderer to support integrated/legacy GPUs
  - **Parallel Vulkan command buffer generation** will allow deep multithreading of time-varying VMD graphical representation updates
  - VMD Vulkan rendering path will be able to go all-in on techniques that are only viable on high-end GPUs
  - **Headless operation supported**, akin to EGL and GLX Pbuffer APIs



# Molecular Structure Data and Global VMD State



# Vulkan<sup>®</sup> on Cloud/HPC Systems

- Straightforward use within Amazon EC2 AMIs
- Containers: requires just a few additional steps beyond those for OpenGL, placement of **Vulkan-specific JSON files**, etc.
- **Early tests have demonstrated viability of off-screen Vulkan rendering on Cray XC50 supercomputers:**
  - **Headless Vulkan works on CSCS Piz Daint test and development system**
- Vulkan SDK open source, eases debug/testing/deployment on new or specialized systems such as HPC platforms:
  - Compilation of Vulkan SDK on IBM POWER9 pretty close to “out-of-box”
  - A few small missing pieces (assembly language in Vulkan loader) for POWER9 might be relatively easy to address
  - **Support OpenPOWER, ORNL Summit, with SDK updates, future drivers?**
  - **I will find out. Watch this space! 😊**

# 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).

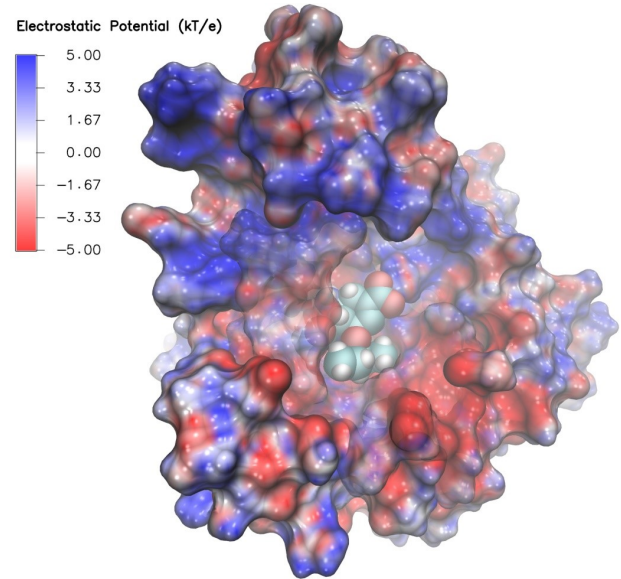
**QwikMD-integrative molecular dynamics toolkit for novices and experts.** Joao V. Ribeiro, Rafael C. Bernardi, Till Rudack, John E. Stone, James C. Phillips, Peter L. Freddolino, and Klaus Schulten. *Scientific Reports*, 6:26536, 2016.

**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 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 / NAMD / LM, NGC Containers

## Registry

[Get API Key](#)



### Documentation

How to use NGC containers on supported platforms >

### Repositories

**nvidia** ^

**hpc** v

- candle
- gamess
- gromacs
- lammps
- lattice-microbes
- namd
- relion
- vmd

**nvidia-hpcvis** v

- index
- paraview-holodeck
- paraview-index
- paraview-optim

### hpc/vmd

```
docker pull nvcr.io/hpc/vmd:cuda9-ubuntu1604-egl-1.9.4a17
```

## VMD

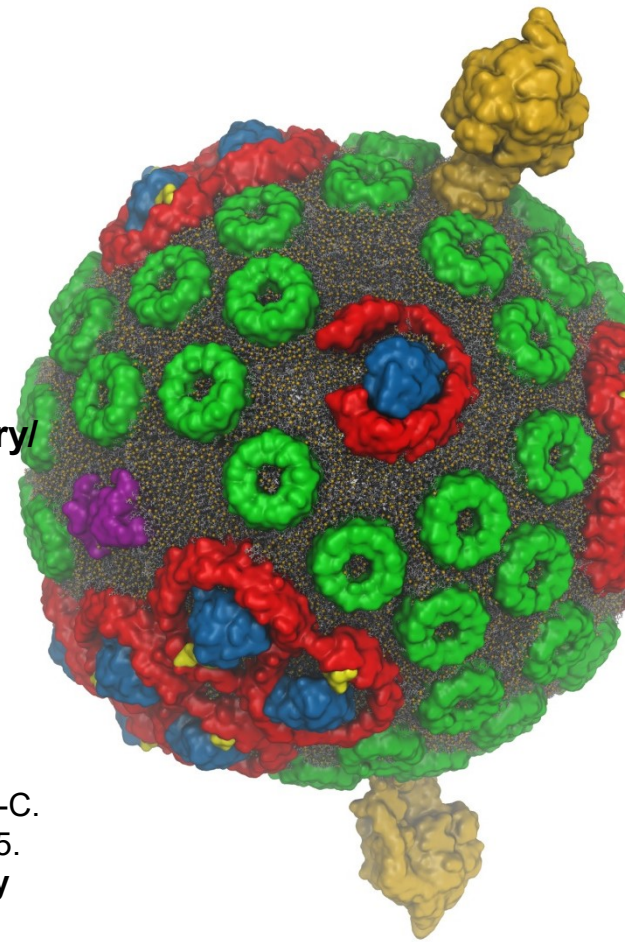
VMD is designed for modeling, visualization, and analysis of biomolecular systems such as proteins, nucleic acids, lipid membranes, carbohydrate structures, etc. VMD provides a wide variety of graphical representations for visualizing and coloring molecular structures: molecular surfaces, space-filling CPK spheres and cylinders, licorice bonds, backbone tubes and ribbons, secondary structure cartoons, and others.

VMD can be used to animate and analyze the trajectory of a molecular dynamics (MD) simulation. In particular, VMD can act as a graphical front end for an external MD program by



# 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**



**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.

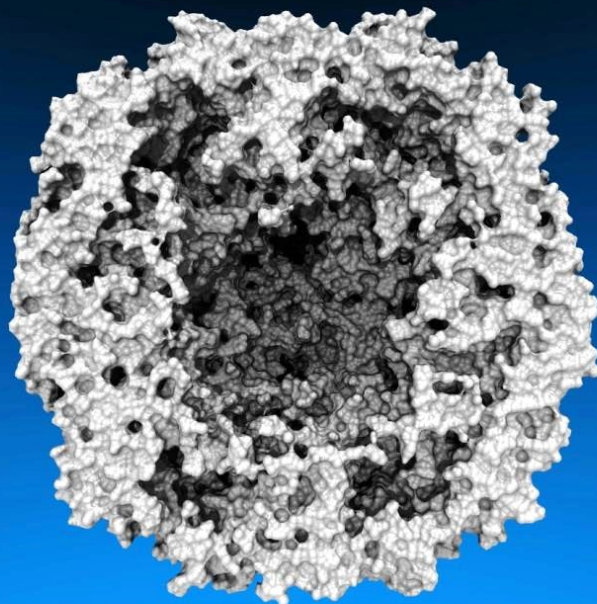
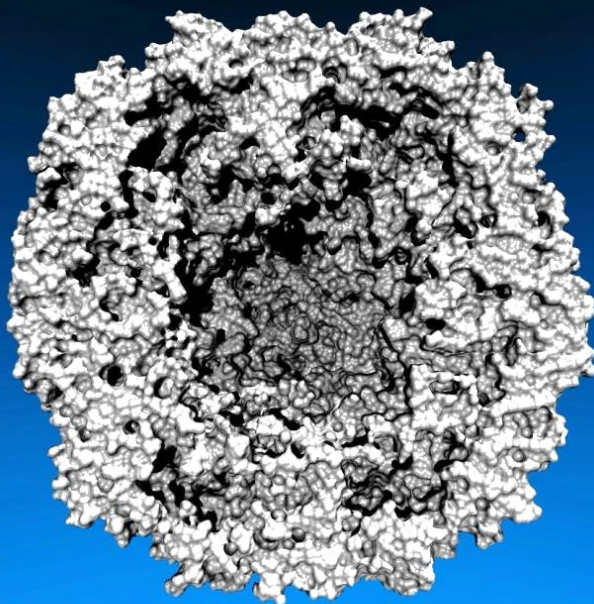
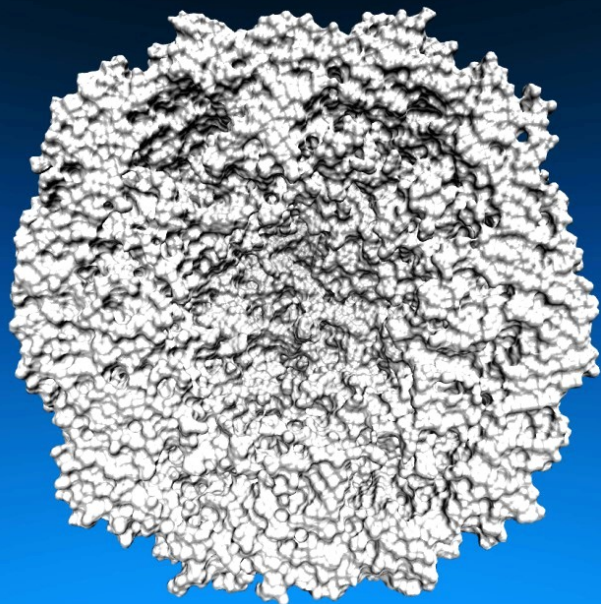
**VMD/OptiX GPU Ray Tracing of all-atom Chromatophore w/ lipids.**

# Lighting Comparison, STMV Capsid

**Two lights, no shadows**

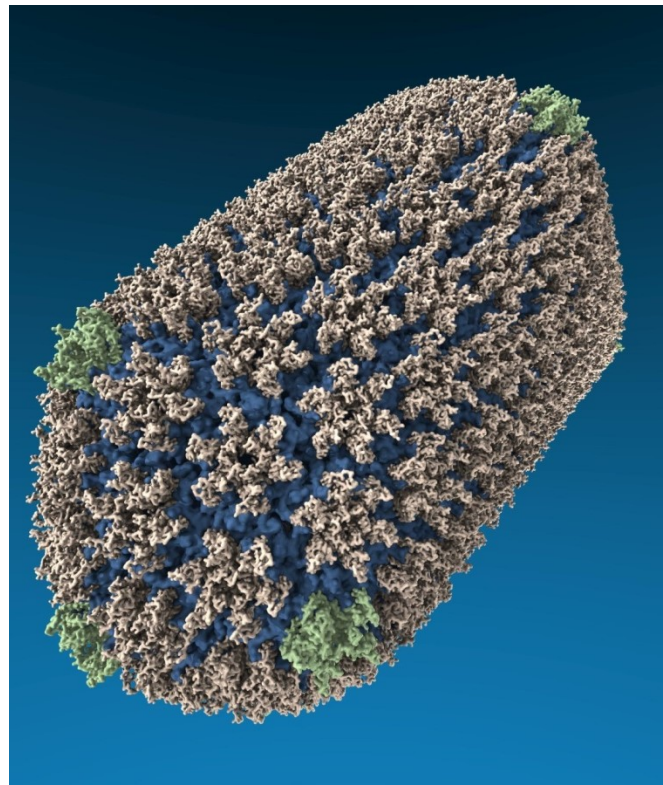
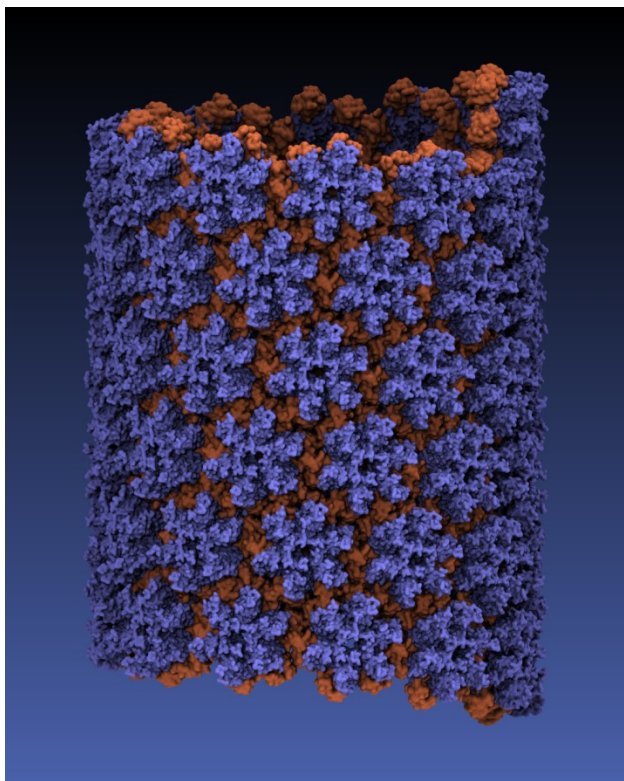
**Two lights, hard shadows, 1 shadow ray per light**

**Ambient occlusion + two lights, 144 AO rays/hit**



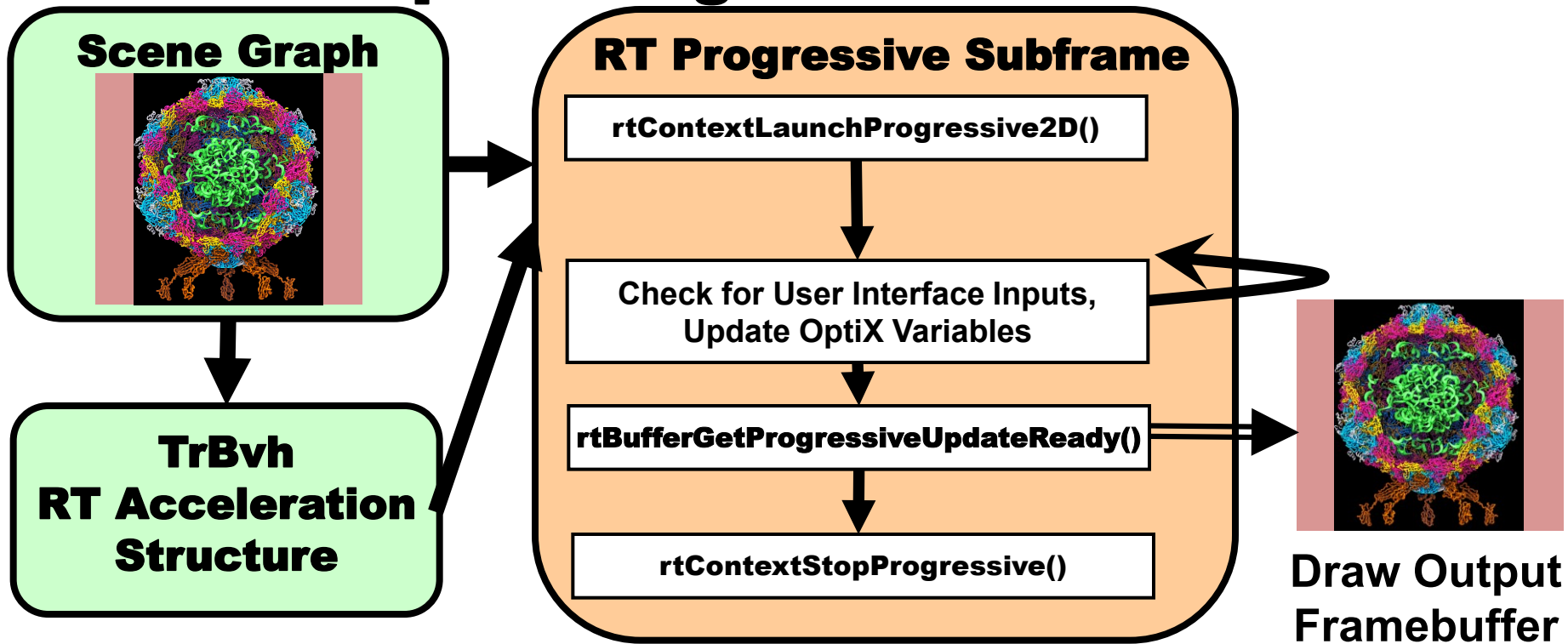


# VMD “QuickSurf” Representation, Ray Tracing



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

# VMD TachyonL-OptiX Interactive RT w/ OptiX Progressive RT API

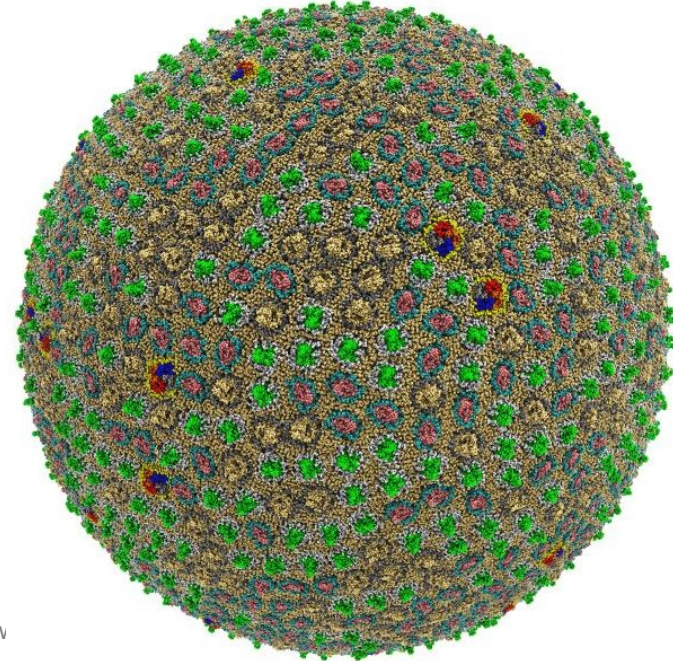


# Preparation, Visualization, Analysis of All-Atom Cell-Scale Simulations

- Interactive rasterization w/ OpenGL/EGL now, **Vulkan** in future releases of VMD
  - **Interactive ray tracing on CPUs and GPUs**
  - Support for large host memory (TB), up to **2 billion atoms per “molecule” now**
  - Parallel analysis, visualization w/ MPI
- 200 nm spherical envelope
  - Membrane with ~50% occupancy by proteins
  - 63M atoms in envelope model

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

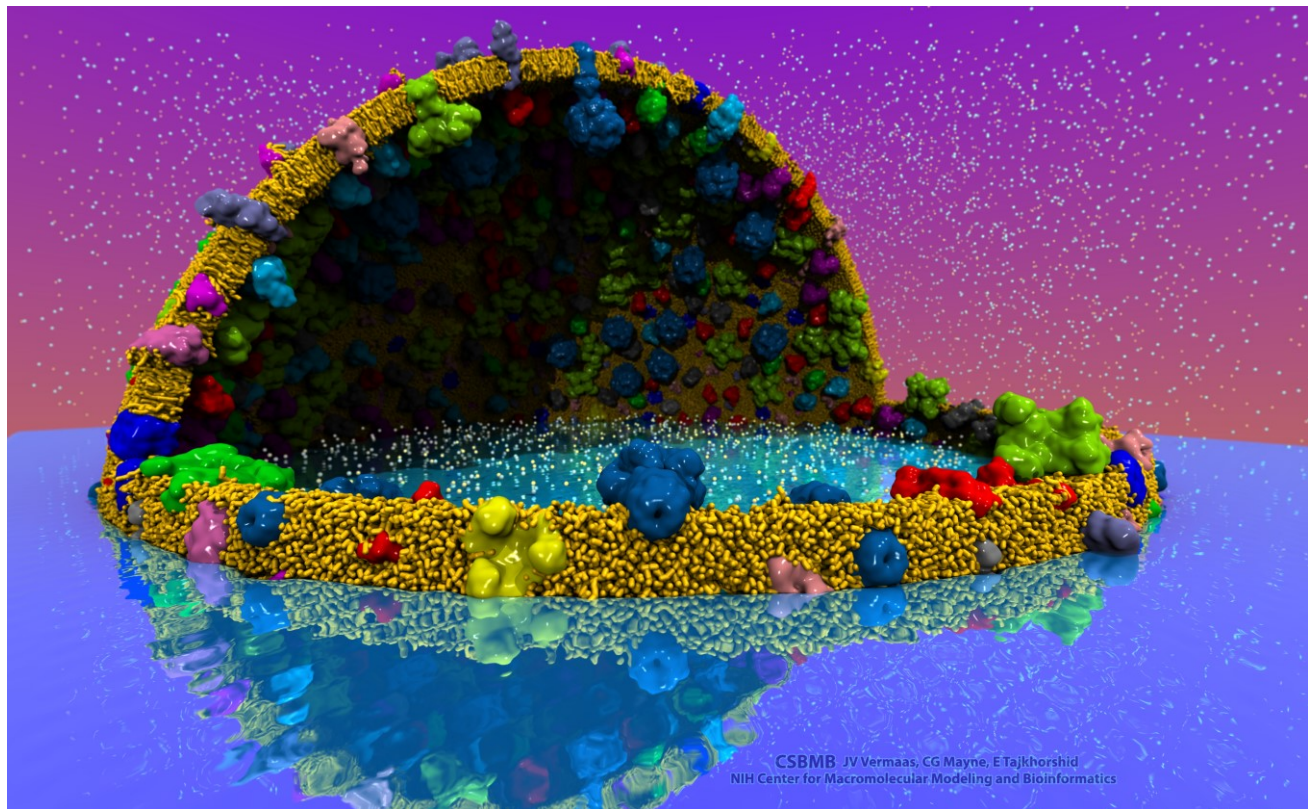
**High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL.** J.E. Stone, ..., K. Schulten. IEEE High Performance Data Analysis and Visualization, IPDPSW, pp. 1014-1023, 2016.





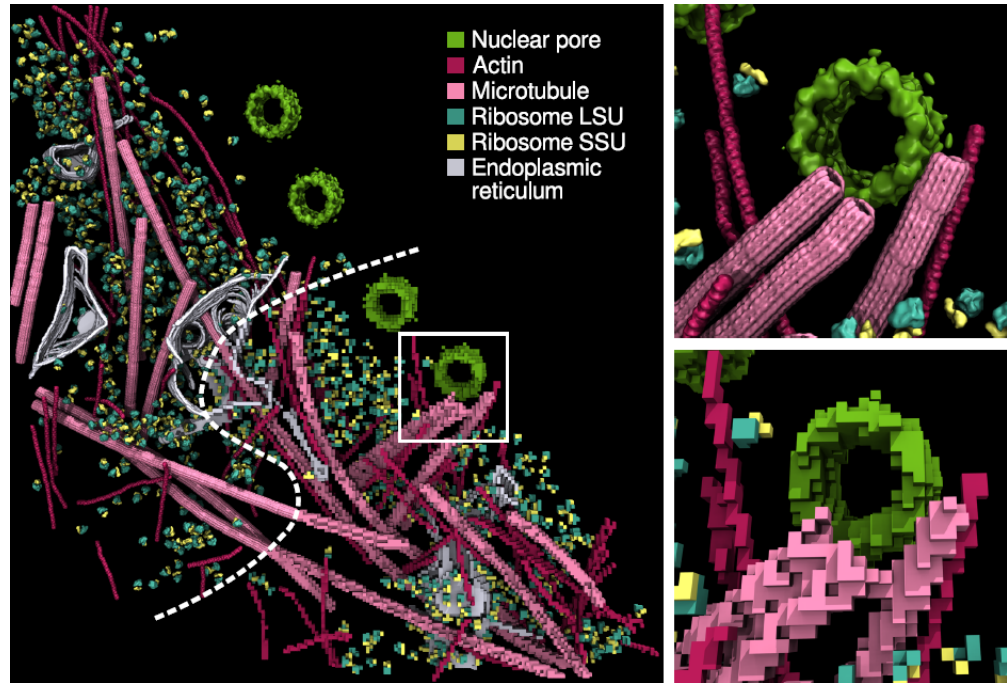
# Proto-Cell Rendered with VMD+OptiX

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



# 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.

# 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





# Immersive Viz. w/ VMD

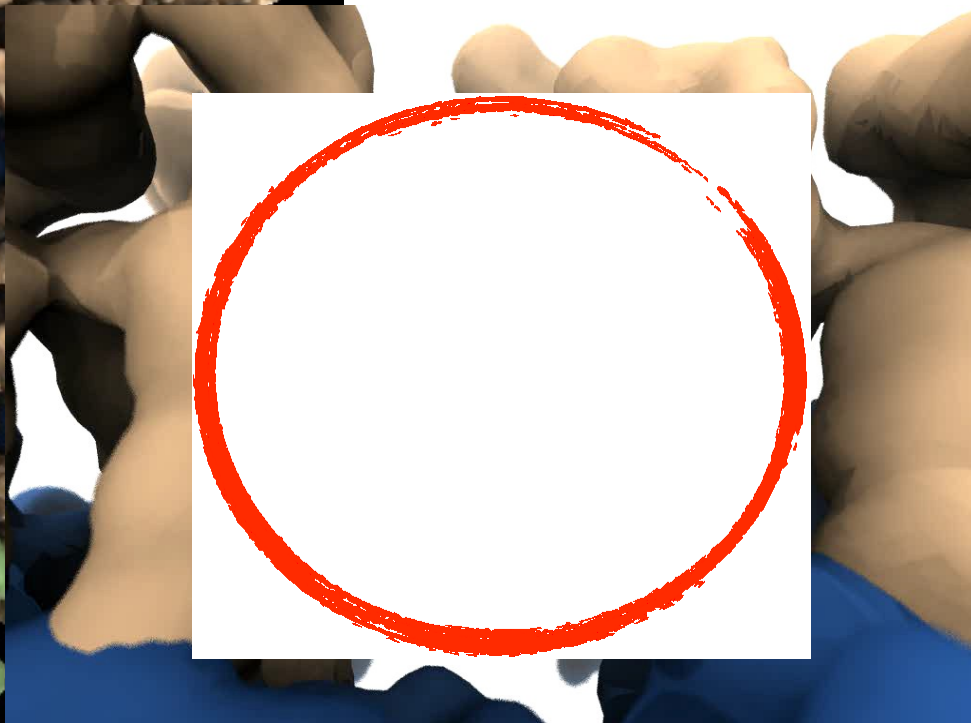
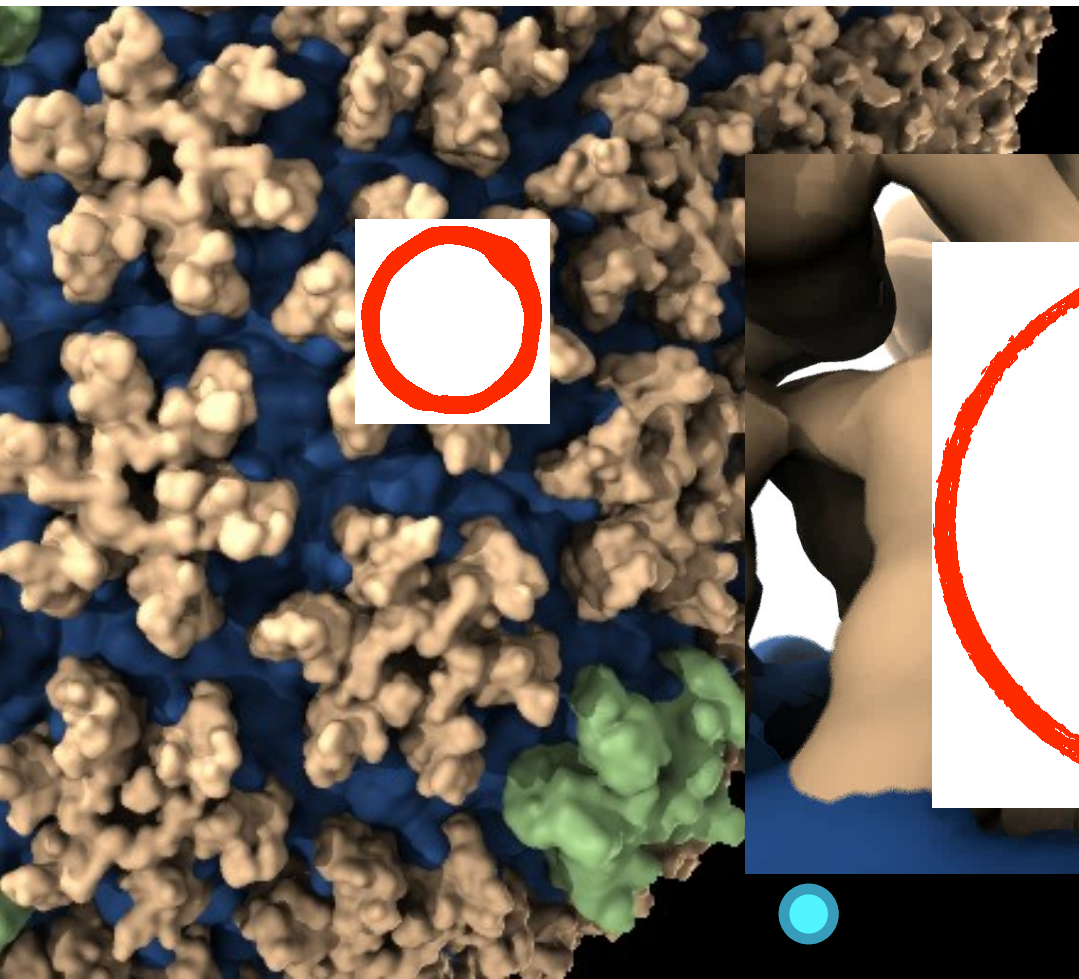
- VMD began as a CAVE app (1993)
- Use of immersive viz by molecular scientists limited due to cost, complexity, lack of local availability, convenience
- Commoditization of HMDs excellent opportunity to overcome cost/availability
- This leaves many challenges still to solve:
  - Incorporate support 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  $\mu$ s sim!



Number of chloride ions permeating  
capsid hexameric centers



# In-Progress VMD VR Development, Demos

VMD VR ray tracing:  
Google Cardboard [1]  
Demo w/ Indiana U., SC'15 [2]

Prototype of VR user  
interaction with VMD  
models in **room-scale VR**  
with NVIDIA @ SC'16



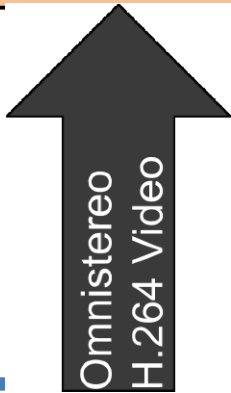
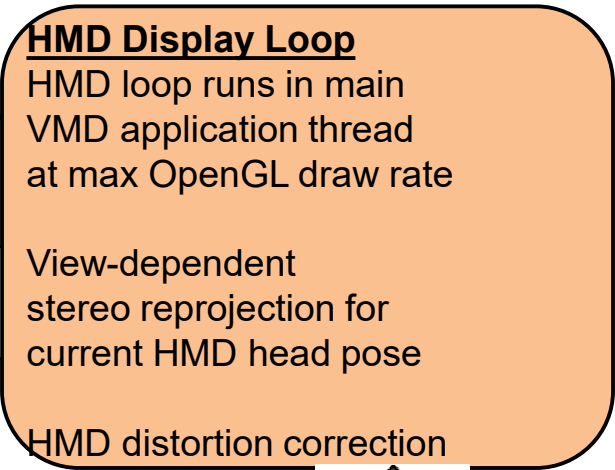
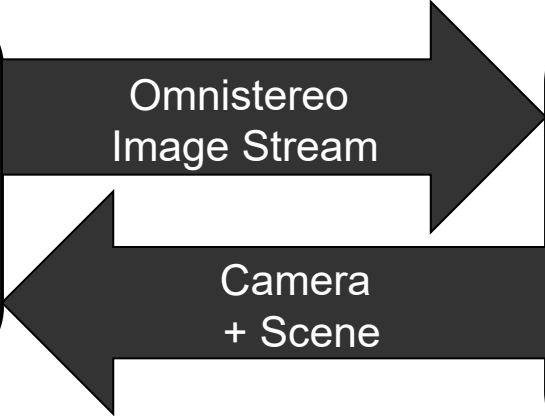
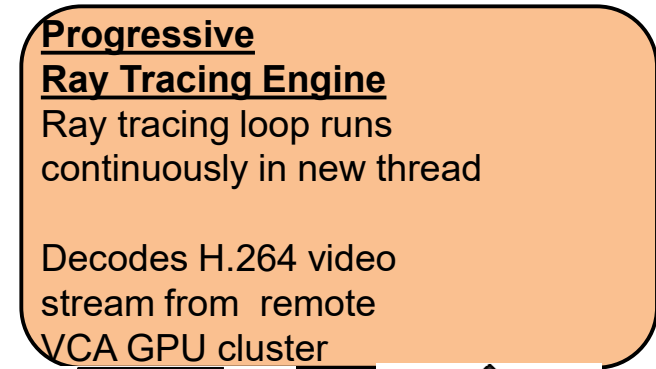
[1] **Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing.** Stone et al., J. Parallel Computing, 55:17-27, 2016.

[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.

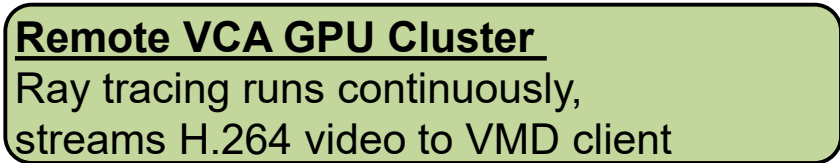
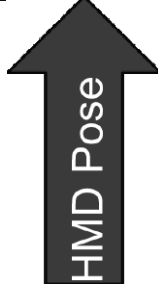
VMD Chromatophore Demo,  
NVIDIA VR Room at SC'16

# HMD Ray Tracing Challenges

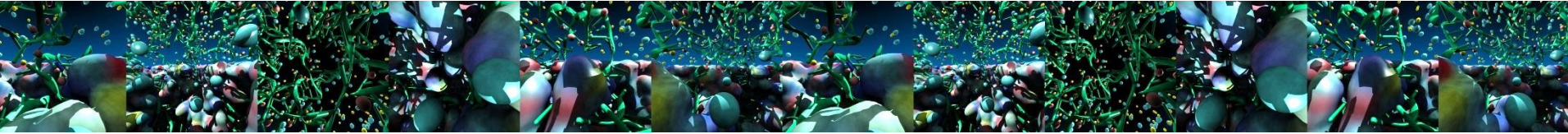
- HMDs require high frame rates (**90Hz or more**) and minimum latency between IMU sensor reads and presentation on the display
- Multi-GPU workstations fast enough to direct-drive HMDs at required frame rates for simple scenes with direct lighting, hard shadows
- Advanced RT effects such as AO lighting, depth of field require much **larger sample counts**, impractical for direct-driving HMDs
- **Remote viz. required** for many HPC problems due to **large data**
- **Remote viz. latencies too high for direct-drive of HMD**
- **Our two-phase approach: moderate-FPS remote RT combined with local high-FPS view-dependent HMD reprojection w/ OpenGL**



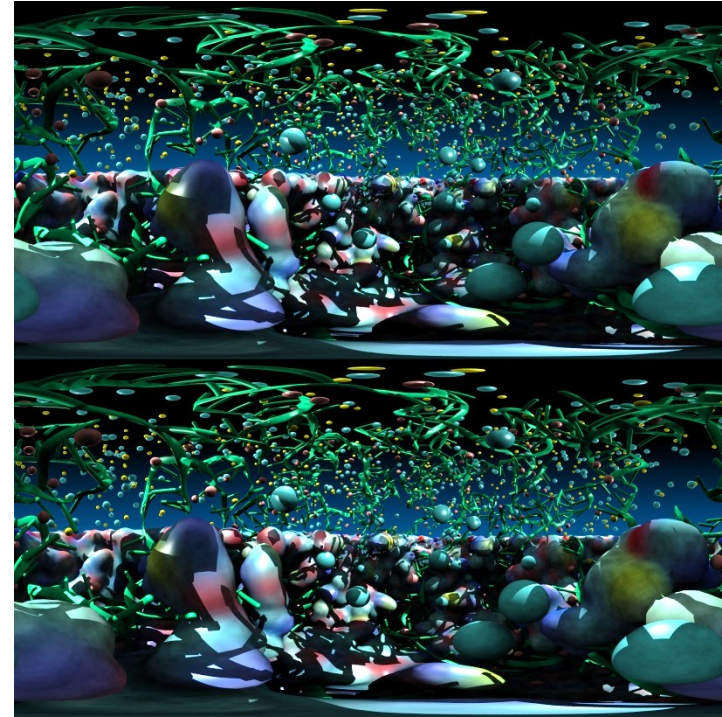
VMD

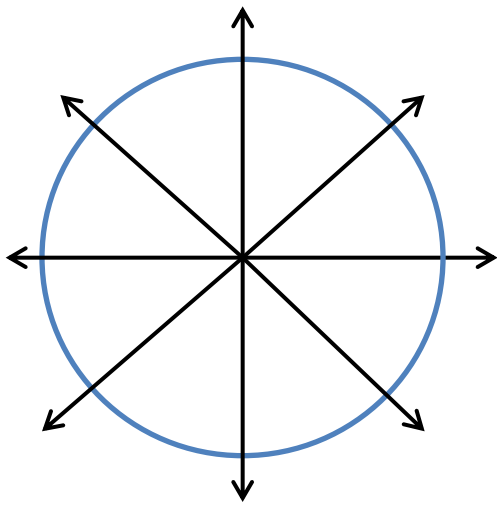


# Stereoscopic Panorama Ray Tracing w/ OptiX

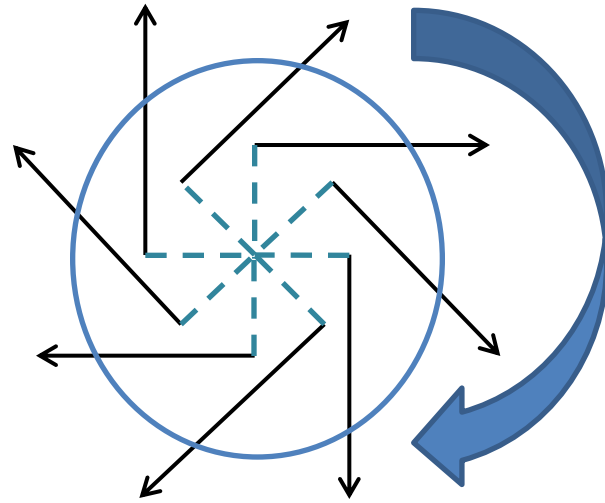


- **Render 360° images and movies for VR headsets such as Oculus Rift, Google Cardboard**
- Ray trace panoramic stereo spheremaps or cubemaps for very high-frame-rate display via OpenGL texturing onto simple geometry
- Stereo requires spherical camera projections **poorly suited to rasterization**
-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



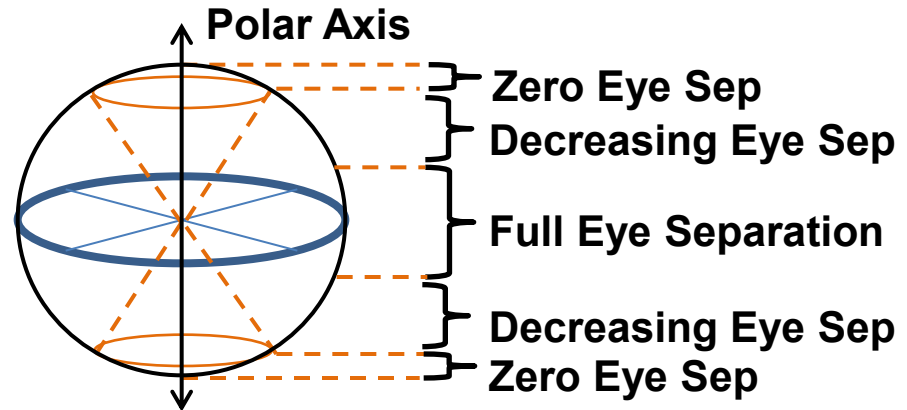


**A) Monoscopic circular projection.  
Eye at center of projection (COP).**



**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.**

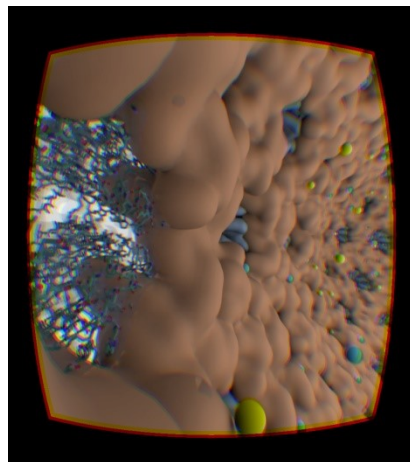
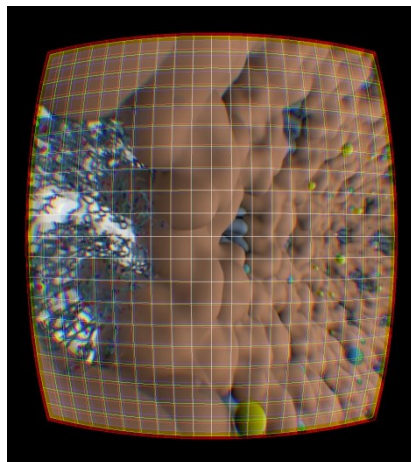
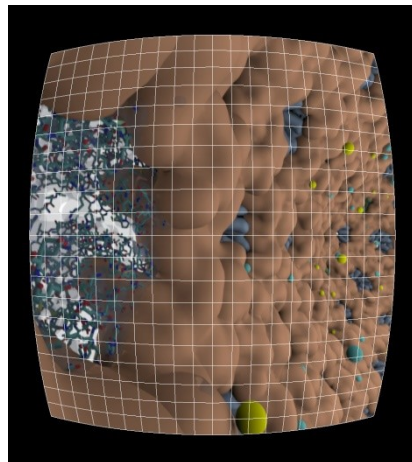
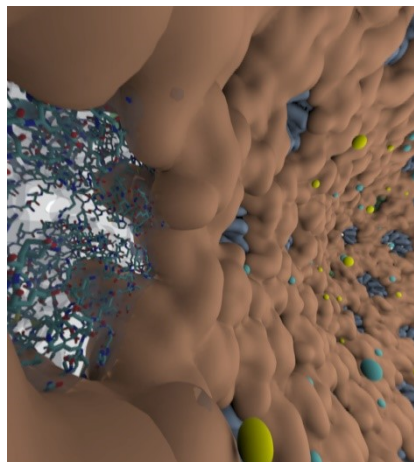
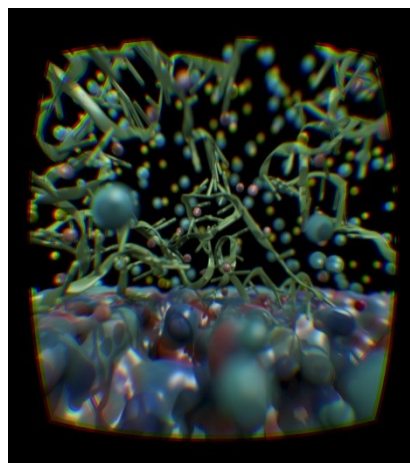
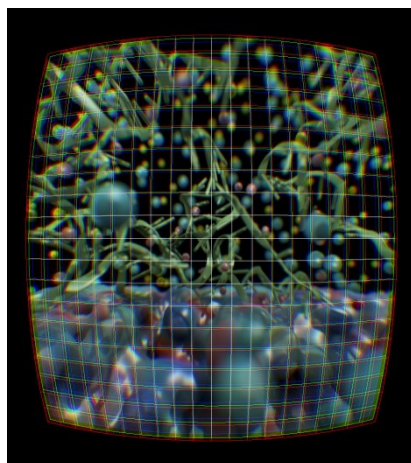
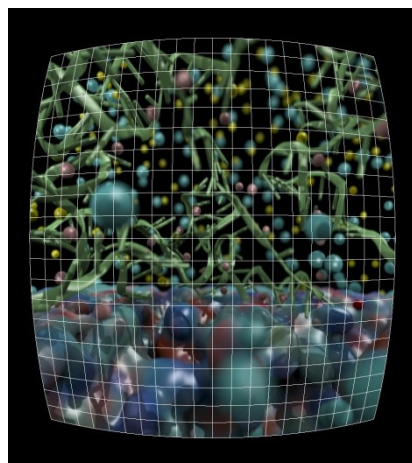
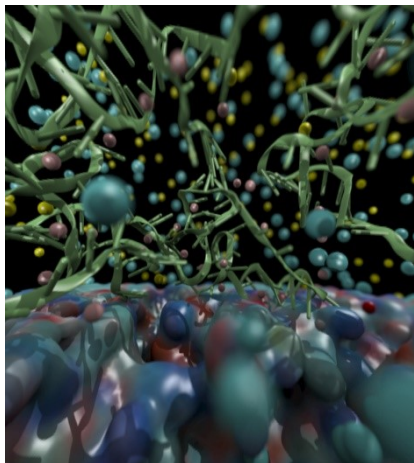






**Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering.** J. E. Stone, W. R. Sherman, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshops (IPDPSW), pp. 1048-1057,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





# Ongoing VR Work

- OpenXR – cross platform multi-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, ...

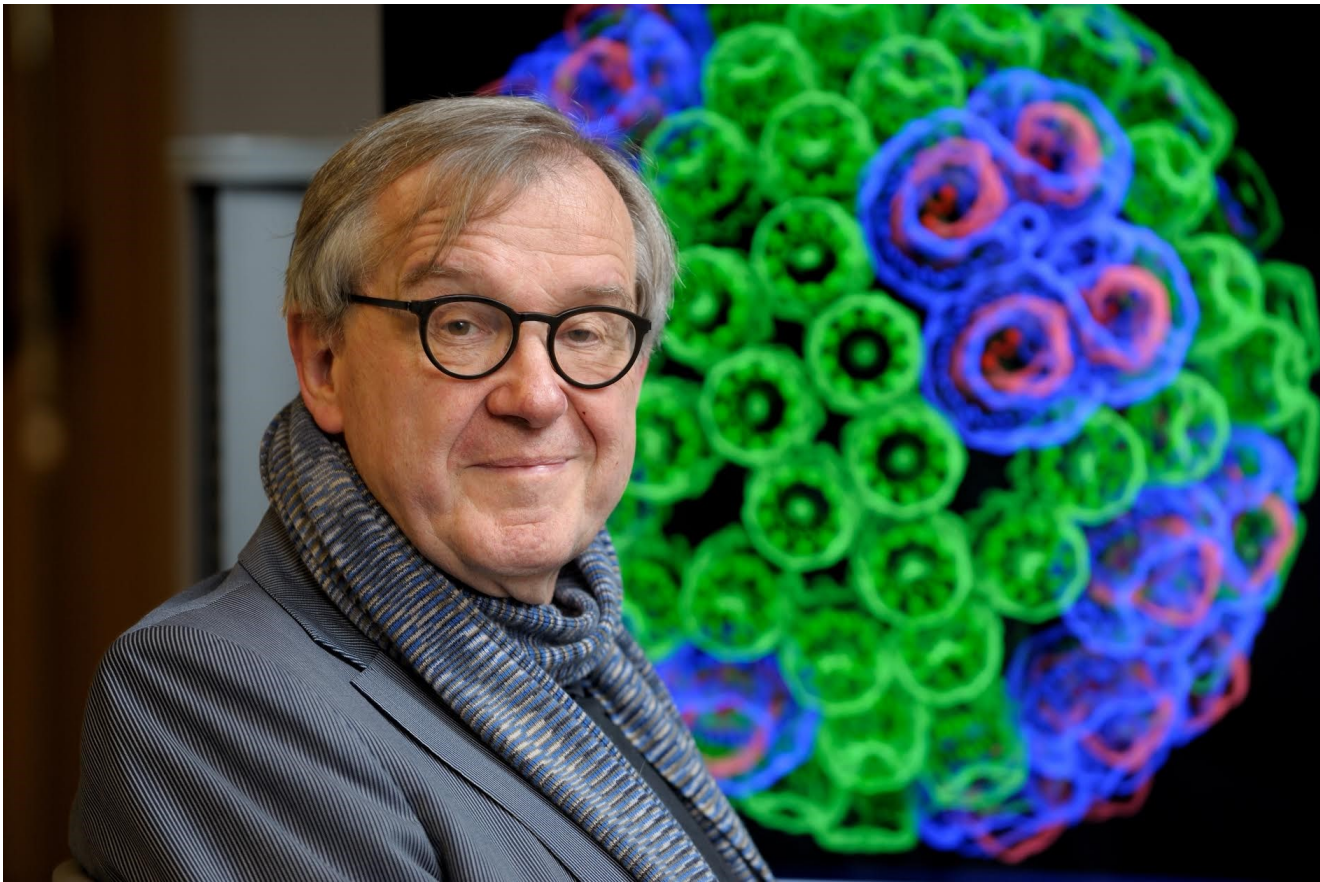
# Please See These Other Talks:

- S8727 - Improving NAMD Performance on Volta GPUs
- S8718 - Optimizing HPC Simulation and Visualization Codes using Nsight Systems
- S8747 - ORNL Summit: Petascale Molecular Dynamics Simulations on the Summit POWER9/Volta Supercomputer
- SE150572 - OpenACC User Group Meeting
- S8665: VMD: Biomolecular Visualization from Atoms to Cells Using Ray Tracing, Rasterization, and VR

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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)
- **Challenges of Integrating Stochastic Dynamics and Cryo-electron Tomograms in Whole-cell Simulations.** T. M. Earnest, R. Watanabe, J. E. Stone, J. Mahamid, W. Baumeister, E. Villa, and Z. Luthey-Schulten. J. Physical Chemistry B, 121(15): 3871-3881, 2017.
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- **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.
- **High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL.** J. E. Stone, P. Messmer, R. Sisneros, and K. Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), pp. 1014-1023, 2016.
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- **Atomic Detail Visualization of Photosynthetic Membranes with GPU-Accelerated Ray Tracing.** J. E. Stone, M. Sener, K. L. Vandivort, A. Barragan, A. Singharoy, I. Teo, J. V. Ribeiro, B. Isralewitz, B. Liu, B.-C. Goh, J. C. Phillips, C. MacGregor-Chatwin, M. P. Johnson, L. F. Kourkoutis, C. Neil Hunter, and K. Schulten. *J. Parallel Computing*, 55:17-27, 2016.
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\*\*\*Winner of the **SC'14 Visualization and Data Analytics Showcase**
- **Runtime and Architecture Support for Efficient Data Exchange in Multi-Accelerator Applications.** J. Cabezas, I. Gelado, J. E. Stone, N. Navarro, D. B. Kirk, and W. Hwu. *IEEE Transactions on Parallel and Distributed Systems*, 26(5):1405-1418, 2015.
- **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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- **Simulation of reaction diffusion processes over biologically relevant size and time scales using multi-GPU workstations.** M. J. Hallock, J. E. Stone, E. Roberts, C. Fry, and Z. Luthey-Schulten. *Journal of Parallel Computing*, 40:86-99, 2014.

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- **Fast Visualization of Gaussian Density Surfaces for Molecular Dynamics and Particle System Trajectories.** M. Krone, J. Stone, T. Ertl, and K. Schulten. *EuroVis Short Papers*, pp. 67-71, 2012.
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- **OpenCL: A Parallel Programming Standard for Heterogeneous Computing.** J. Stone, D. Gohara, G. Shi. *Computing in Science and Engineering*, 12(3):66-73, 2010.
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- **GPU Clusters for High Performance Computing.** V. Kindratenko, J. Enos, G. Shi, M. Showerman, G. Arnold, J. Stone, J. Phillips, W. Hwu. *Workshop on Parallel Programming on Accelerator Clusters (PPAC)*, In Proceedings IEEE Cluster 2009, pp. 1-8, Aug. 2009.
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- **Probing Biomolecular Machines with Graphics Processors.** J. Phillips, J. Stone. *Communications of the ACM*, 52(10):34-41, 2009.
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J. Phillips, J. Stone, K. Schulten. *Proceedings of the 2008 ACM/IEEE Conference on Supercomputing*, IEEE Press, 2008.
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- **Accelerating molecular modeling applications with graphics processors.** J. Stone, J. Phillips, P. Freddolino, D. Hardy, L. Trabuco, K. Schulten. *J. Comp. Chem.*, 28:2618-2640, 2007.
- **Continuous fluorescence microphotolysis and correlation spectroscopy.** A. Arkhipov, J. Hüve, M. Kahms, R. Peters, K. Schulten. *Biophysical Journal*, 93:4006-4017, 2007.

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