

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

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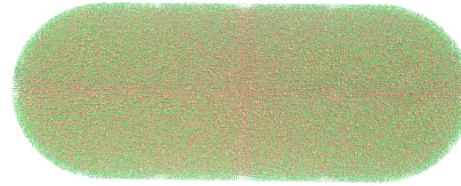
Theoretical and Computational Biophysics Group  
Beckman Institute for Advanced Science and Technology  
University of Illinois at Urbana-Champaign  
<http://www.ks.uiuc.edu/>

High Performance Data Analysis and Visualization Workshop  
IEEE International Symposium on Parallel and Distributed Processing  
Chicago, IL, May 23, 2016

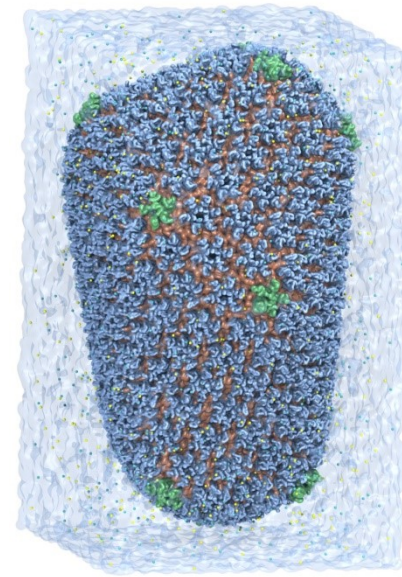


# VMD – “Visual Molecular Dynamics”

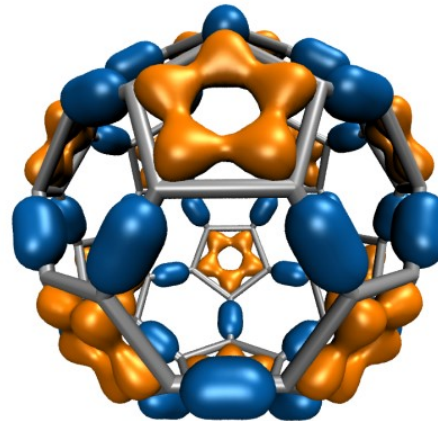
- Visualization and analysis of:
  - molecular dynamics simulations
  - particle systems and whole cells
  - cryoEM densities, volumetric data
  - quantum chemistry calculations
  - sequence information
- User extensible w/ scripting, plugins
- <http://www.ks.uiuc.edu/Research/vmd/>



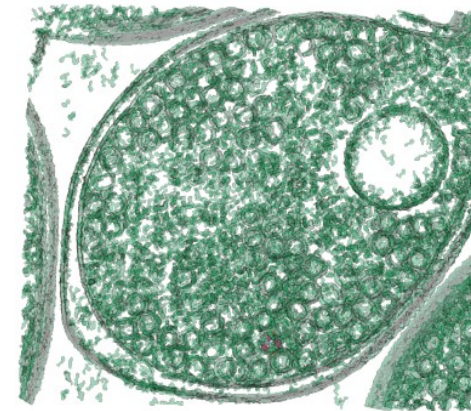
Whole Cell Simulation



MD Simulations

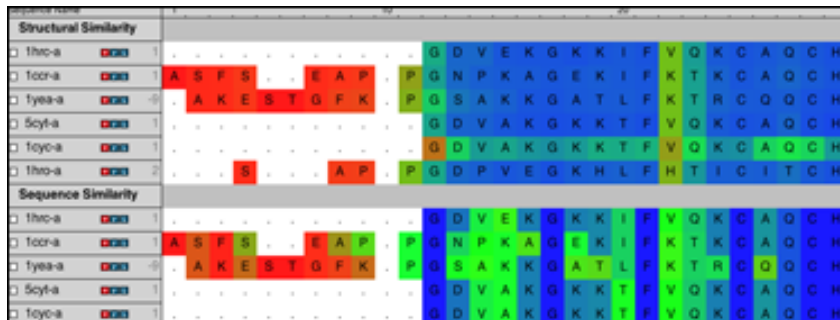


Quantum Chemistry



CryoEM, Cellular Tomography

Structural Similarity	
1lhc-a	1
1ocn-a	1
1yea-a	1
1scyl-a	1
1toy-a	1
1lhc-a	1
Sequence Similarity	
1lhc-a	1
1ocn-a	1
1yea-a	1
1scyl-a	1
1toy-a	1



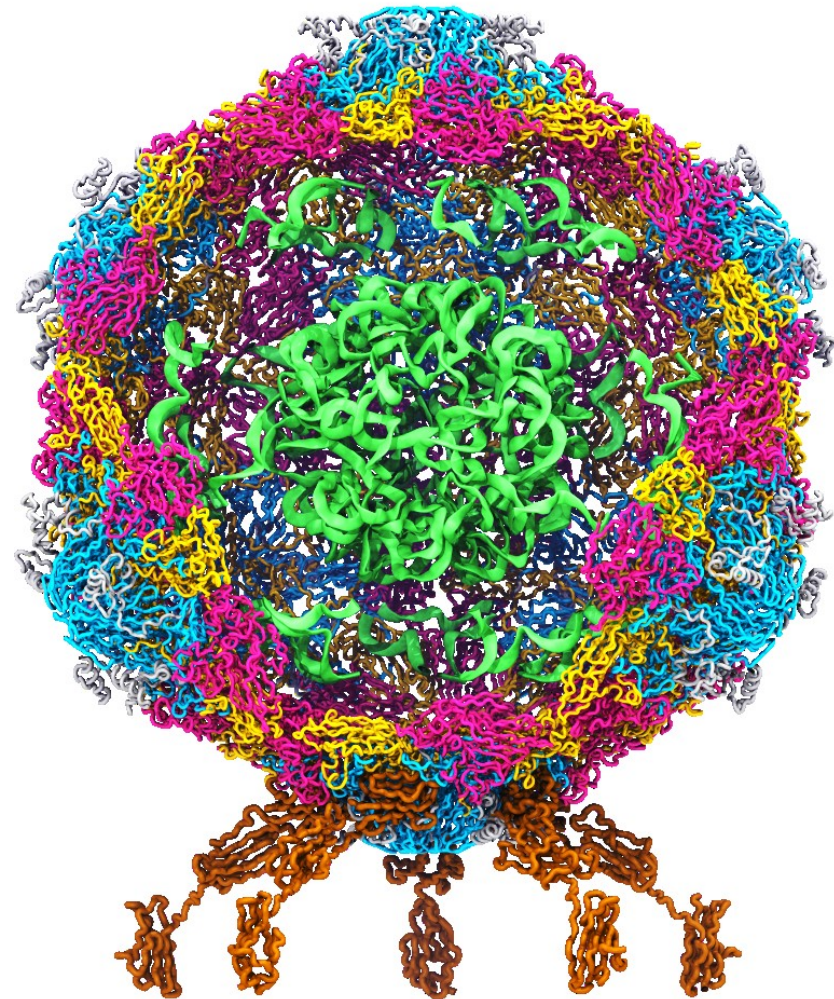
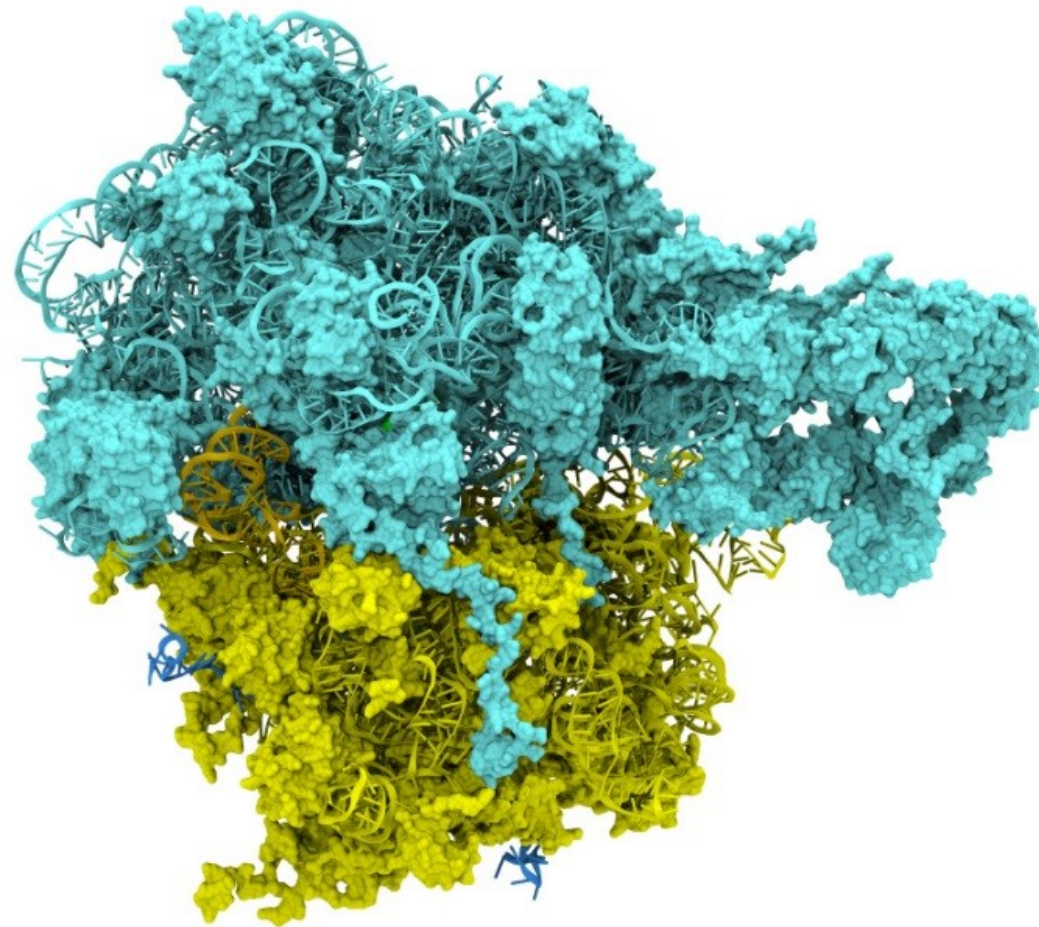
Sequence Data

# Goal: A Computational Microscope

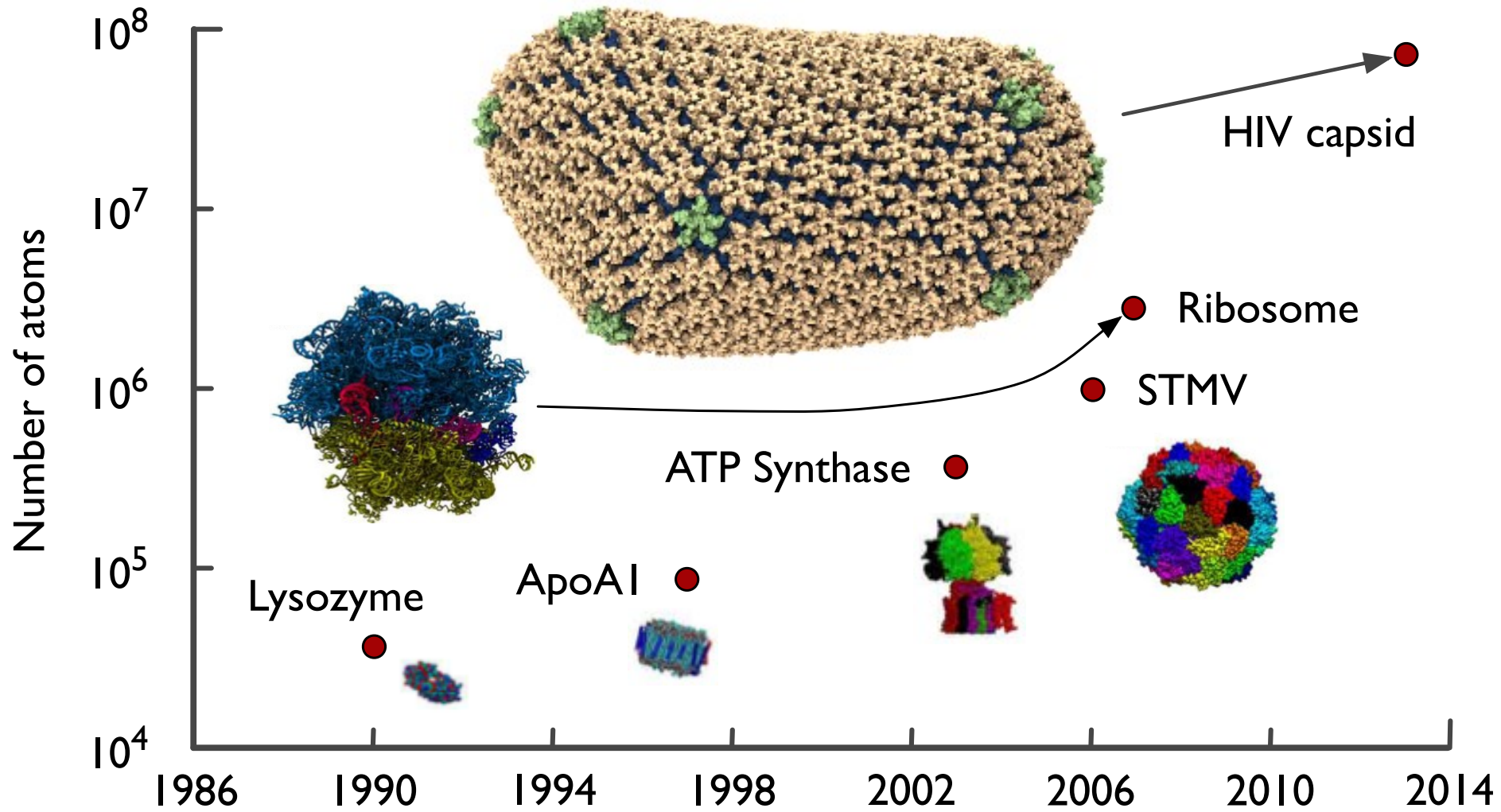
Study the molecular machines in living cells

Ribosome: target for antibiotics

Poliovirus

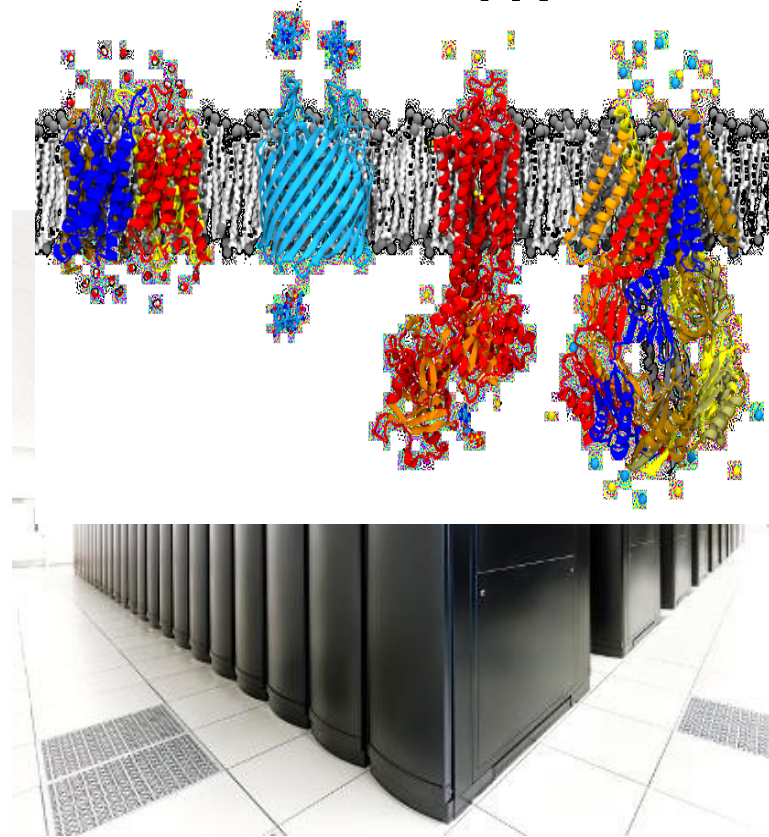


# Computational Biology's Insatiable Demand for Processing Power



# VMD Supports Petascale Biology

- Where to analyze the data?
  - Trajectories too large to download
  - **Analyze 231 TB trajectory set in 15 min, parallel I/O @ 275 GB/sec** on 8,192 nodes
- **Use petascale system compute nodes for all simulation, visualization, and analysis tasks**
- GLX requirement for a running windowing system has been an impediment for use of OpenGL rasterization on large supercomputers
- Few petascale systems support windowing systems on compute nodes, **not supported by system vendors**, so sites must implement themselves
- Blue Waters has mix of node types, what about viz and analysis jobs that span node types?
- **EGL helps solve these problems**



NCSA Blue Waters  
Cray XE6 / XK7 Supercomputer  
22,640 XE6 CPU nodes  
**4,224 XK7 nodes w/ GPUs**

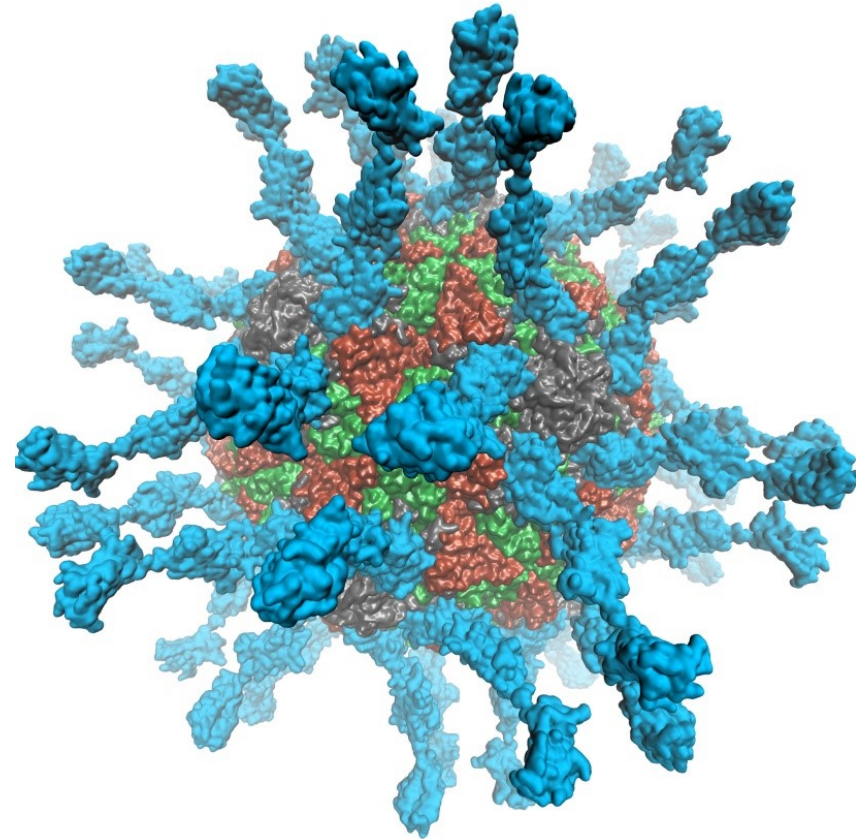
**Unlocking the Full Potential of the Cray XK7 Accelerator.** M. D. Klein  
and J. E. Stone. Cray Users Group, Lugano Switzerland, May 2014.

# Weaknesses of GLX for HPC

- Requires a windowing system
- Cedes all hardware-specific interactions to window sys., leaving apps with no information about physical devices
- No real support for NUMA or multi-GPU:
  - GLX and OpenGL predate NUMA hw
  - No easy way to observe proper NUMA CPU thread affinity due to excessive abstraction
  - Difficult to exploit multiple GPUs in parallel

# Adaptation of VMD to EGL for in-situ and parallel rendering on clouds, clusters, and supercomputers

- Eliminate dependency on windowing systems
  - Avoid complex failure modes, e.g. X server dies but app continues
  - Eliminate job launch overhead associated with window sys
  - Use fewer system resources
- Simplified deployment of parallel VMD builds supporting off-screen rendering on both GPUs and software rasterization
- Maintains 100% of VMD OpenGL shaders and rendering features



**Poliovirus**

# Déjà Vu

- Sun Microsystems proposed “gIP” extension to solve these problems
- When Sun exited high performance graphics relatively soon thereafter, gIP died too...
- Aside from projects at TACC (a large Sun site at the time), gIP didn't get very far
- Concepts good, still largely relevant, but we had to wait (**12 years!!\*\***) for a new multi-vendor API to arise that could support this usage cleanly:  
**Enter EGL**

**\*\* I have been pestering vendors for this for most of the 12 years!**



Presentation to OpenGL ARB,  
Sep. 21-22, 2004

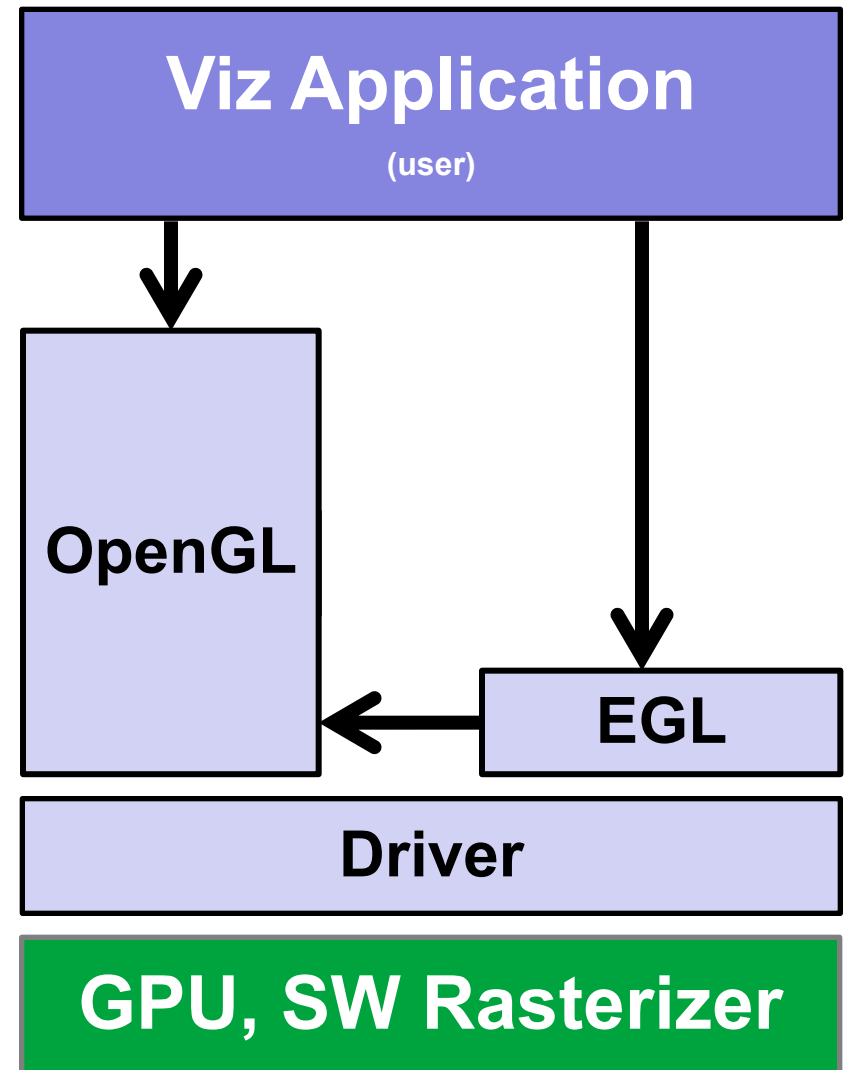
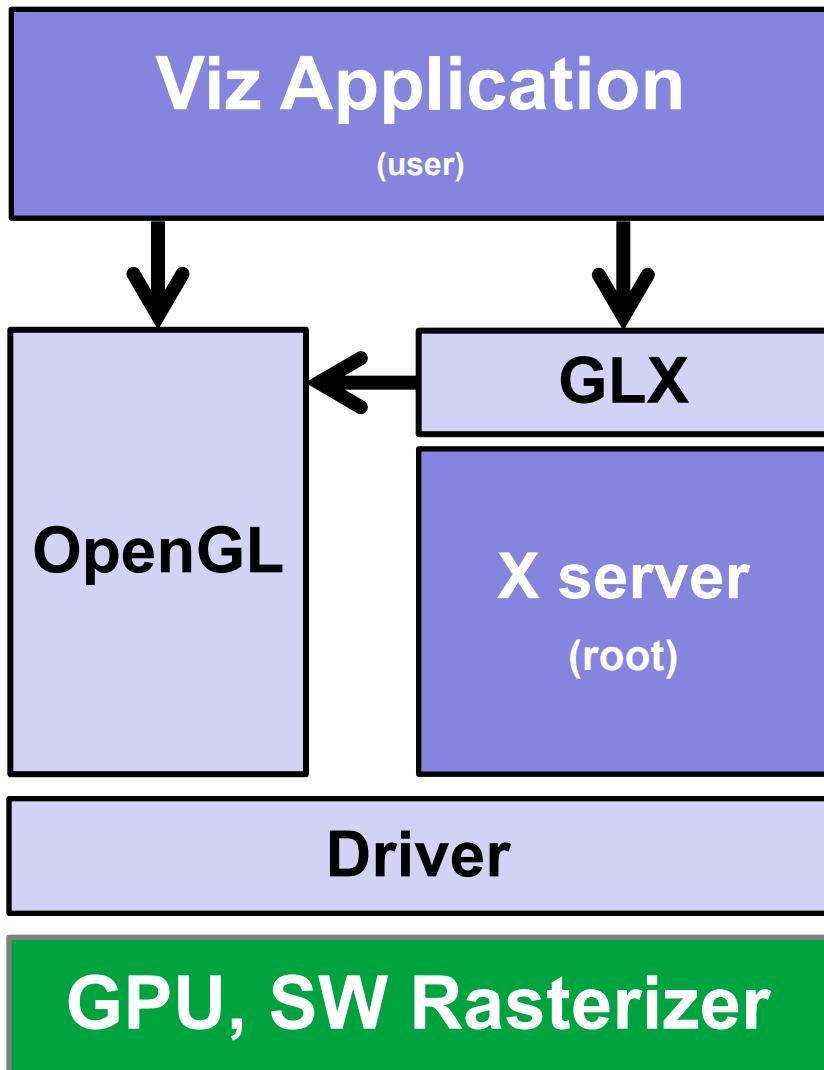


# What is EGL?

- Interface between OpenGL rasterization APIs and underlying platform
- Manages GL context, sw/hw resources, interacts with window sys. or underlying hardware
- Originated with OpenGL for embedded sys., phones
- EGL supports OpenGL ES, full OpenGL, and other Khronos APIs, e.g. OpenVG
- To make use of EGL with full OpenGL, apps are linked against **libOpenGL.so**, EGL is used for context creation, and extensions are found via **eglGetProcAddress()**
- Current GL drivers from leading hardware vendors support EGL with full OpenGL



# OpenGL: GLX vs. EGL



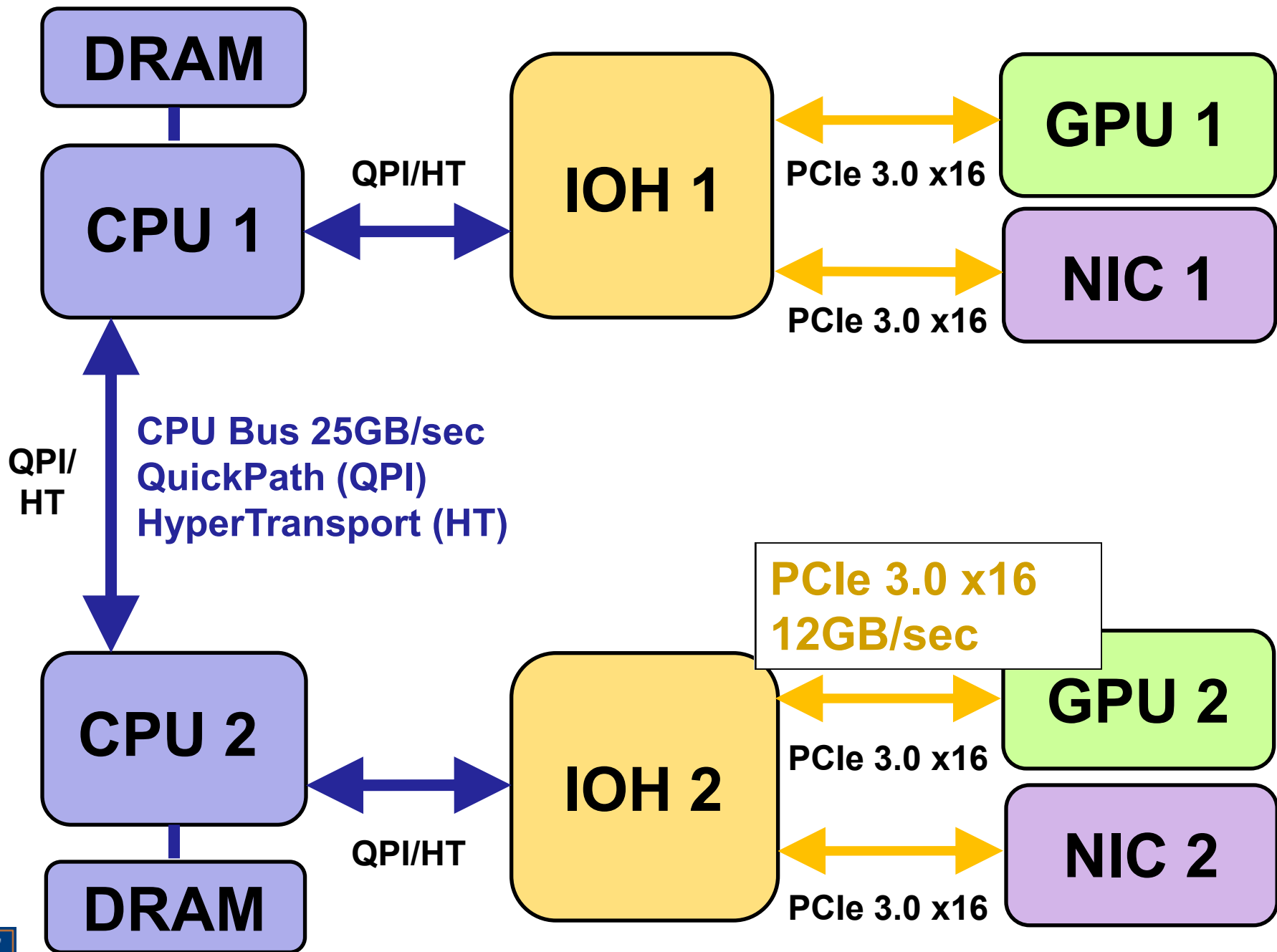
# Eliminating the Windowing System

- Improves parallel job startup, simplicity
- Reduce OS threads, ctx switches, resource usage
- Gotchas:
  - All library dependencies have to be window-system-free, or “tricked” with the use of stub functions
  - App must find alternate sources for fonts and other resources typically provided by the window sys.

# Benefits of EGL Platform Interfaces

- **Eliminate the need for brittle HACKS** to support both GPU rasterization and sw rasterization in the same binary!
- Enumerate and select among available implementations, **potentially supports multiple vendors in the same node**
- Allows **specific target implementation** to be bound, e.g., GPU, CPU-integrated GPU, software rasterizer
- EGL interfaces make it **EASY** to bind a CPU thread to a particular GPU or sw rasterizer context:
  - **Bind CPU threads to NUMA-optimal GPUs, MPI ranks**
  - **High-perf. multi-GPU image compositing**
- Minor similarity to OpenCL platform interfaces





# EGL Loose Ends

- The order of GPU or sw renderer “device” indices is determined by the vendor’s EGL implementation
- EGL can interoperate with MPI, CUDA, OpenCL, OptiX, NVENC, etc.
- Potential issue for device index order with interop APIs:
  - Proprietary APIs for graphics, compute, and video encode/decode may use arbitrary device indexing schemes
  - NVIDIA EGL implementation supports multiple indexing schemes, e.g. **PCIe-based index ordering**, which can be used to help tame the entropy among multiple APIs
- Interop APIs may support zero-copy for only certain types of EGL objects, e.g. FBOs vs. Pbuffer
- Use of FBOs vs. Pbuffers may require new shaders for features like MSAA that are “free” with a Pbuffer

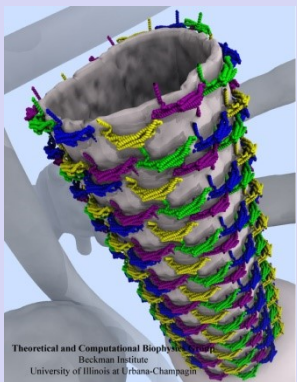
# Modifying VMD for EGL

- New DisplayDevice subclass implementation for EGL
- Updates to GL extension enumeration to use EGL APIs when appropriate
- Use compiled-in Hershey font libs
- Eliminated last use of libGLU
- Provide stubs for X11 fctns referenced by other libs, e.g. old revs of OptiX



# Molecular Structure Data and Global VMD State

## Scene Graph



## Graphical Representations

DrawMolecule

Non-Molecular  
Geometry

## User Interface Subsystem

Tcl/Python Scripting

Mouse + Windows

6DoF Input "Tools"

## Display Subsystem

VMDDisplayList

DisplayDevice

OpenGLRenderer

GLX+X11+Drv

OpenGL Pbuffer/FBO

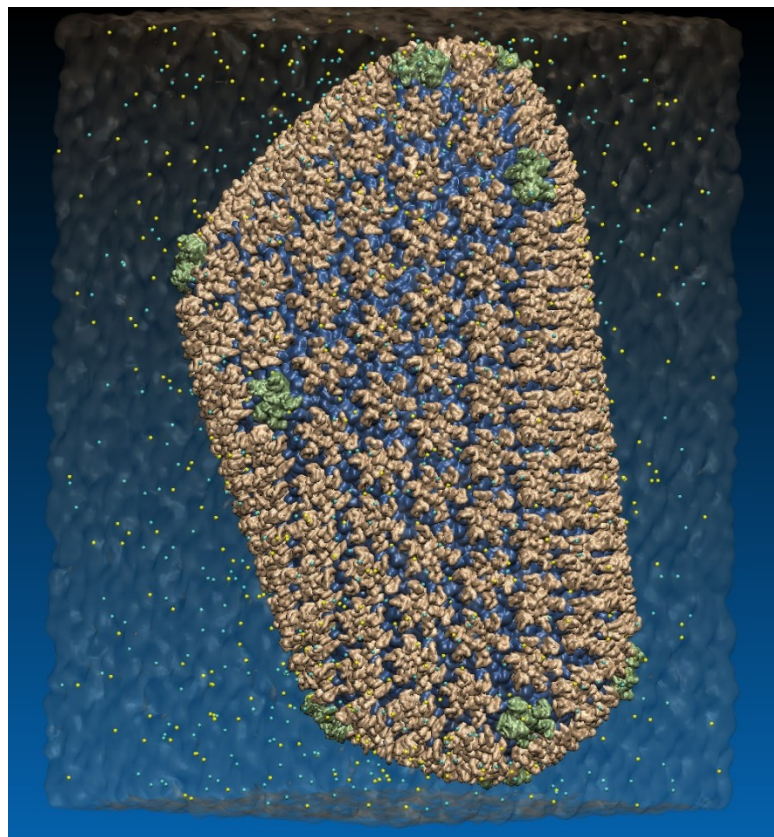
Windowed OpenGL

EGL+Drv

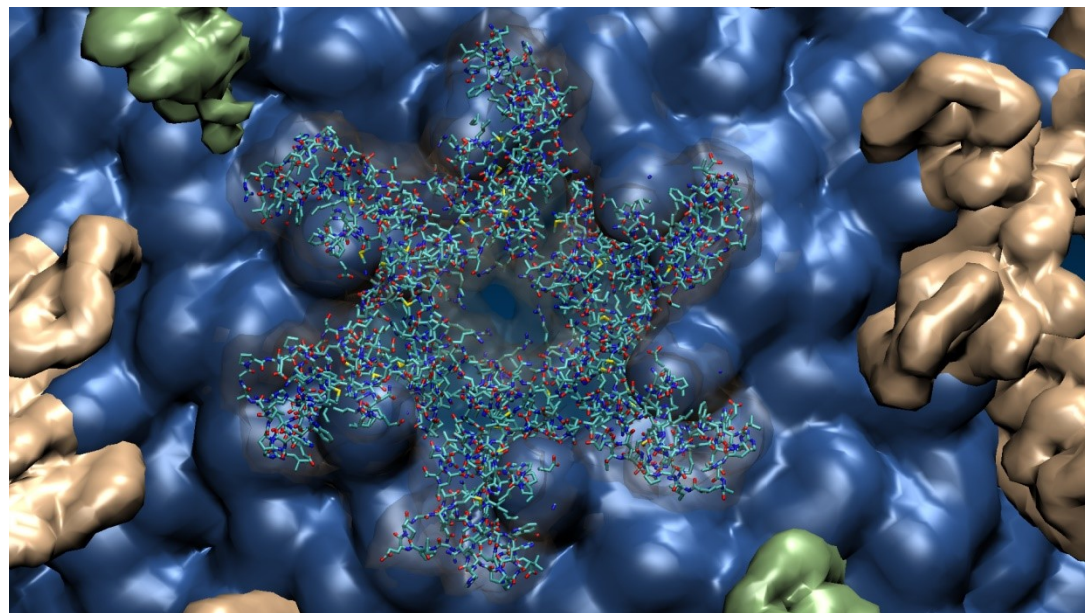
OpenGL Pbuffer/FBO



# VMD EGL Rendering of HIV-1 Movie on Amazon AWS EC2 g2.8xlarge

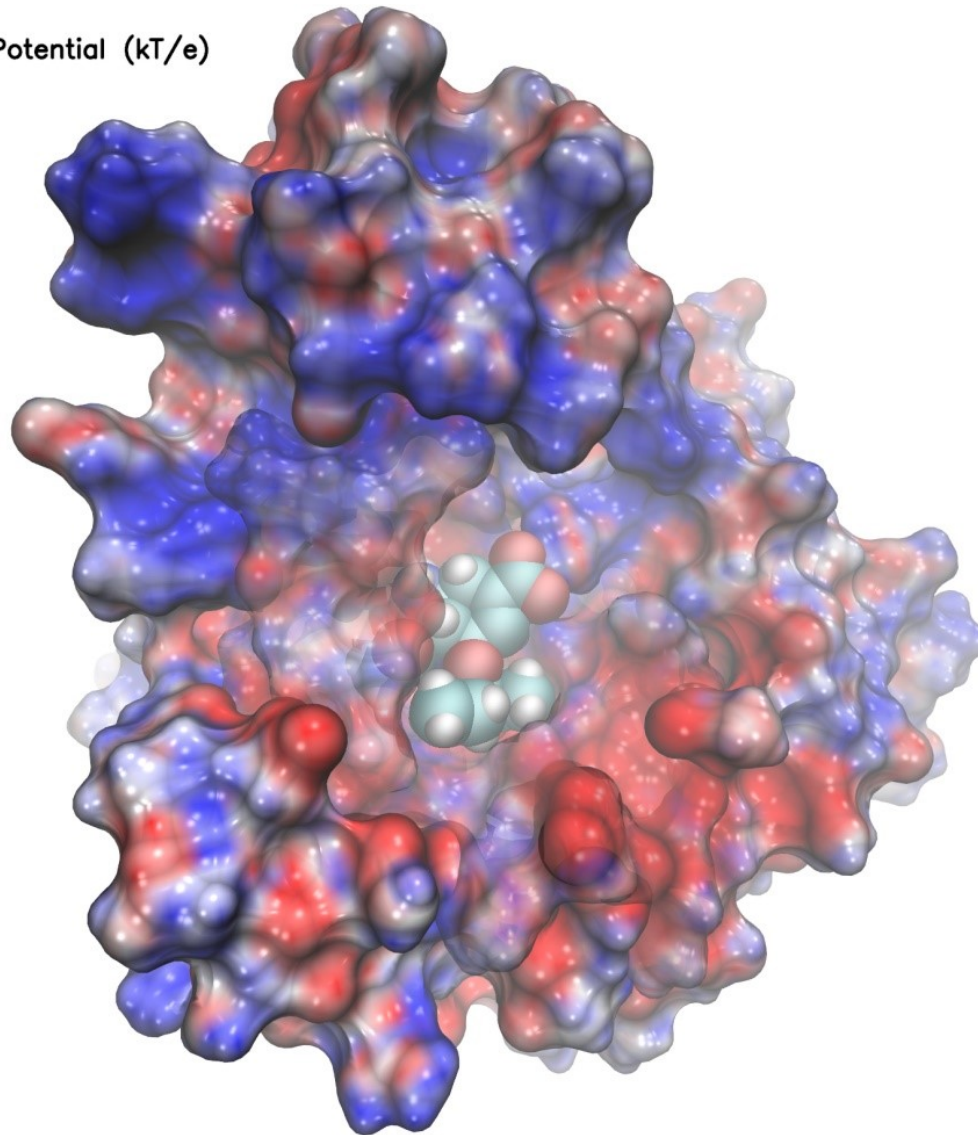
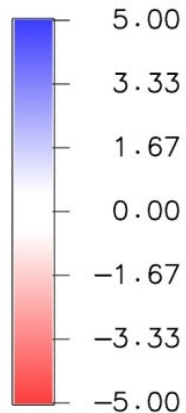


**64M atom HIV-1 capsid  
simulation rendered via EGL**



**Close-up view of HIV-1 hexamer  
rendered via EGL**

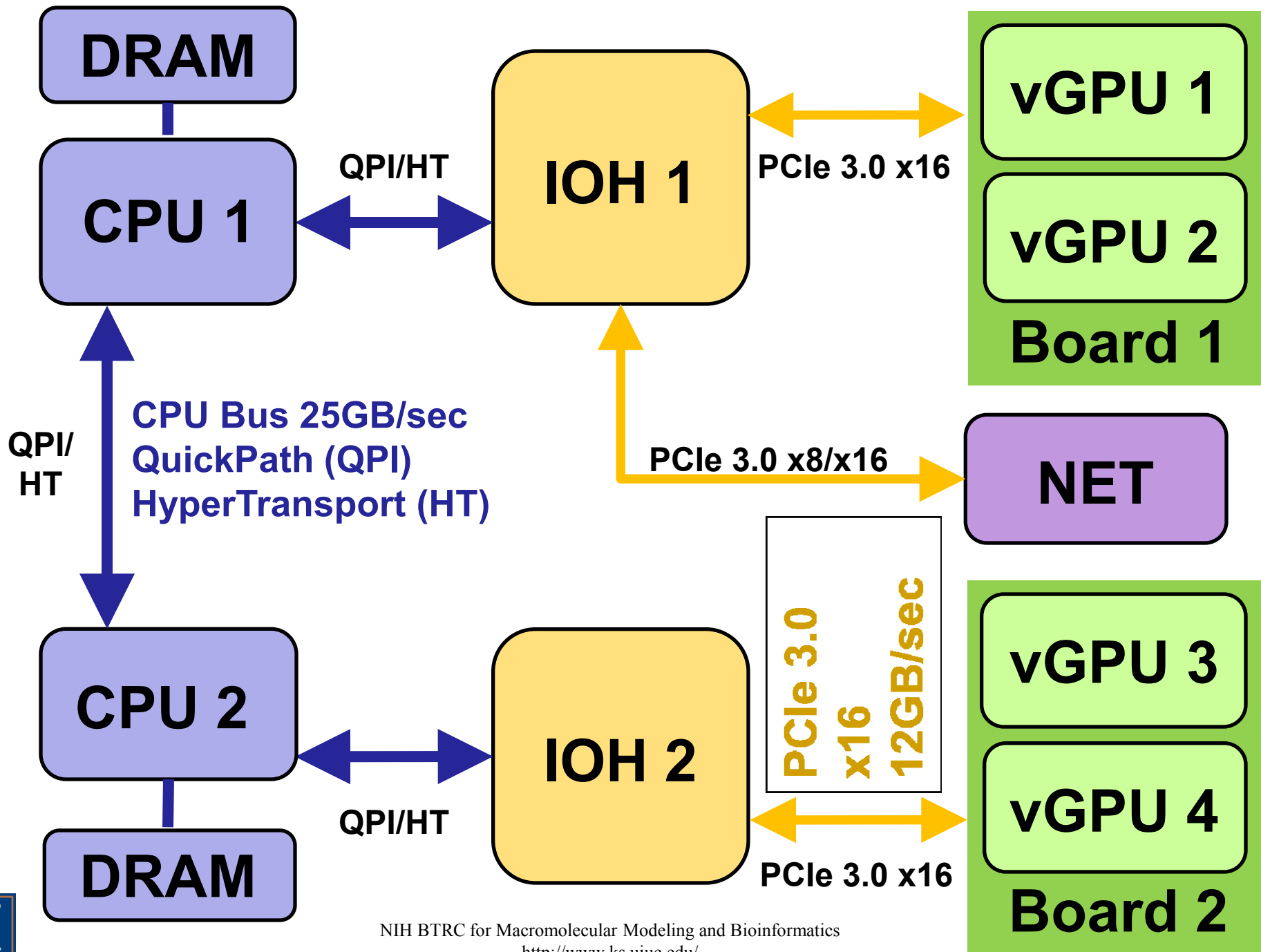
Electrostatic Potential (kT/e)



**Swine Flu A/H1N1 neuraminidase bound to Tamiflu: VMD EGL rendering demonstrating full support for all VMD shaders and OpenGL features, multisample antialiasing, ray cast spheres, 3-D texture mapping, ...**

# VMD EGL Performance Tests

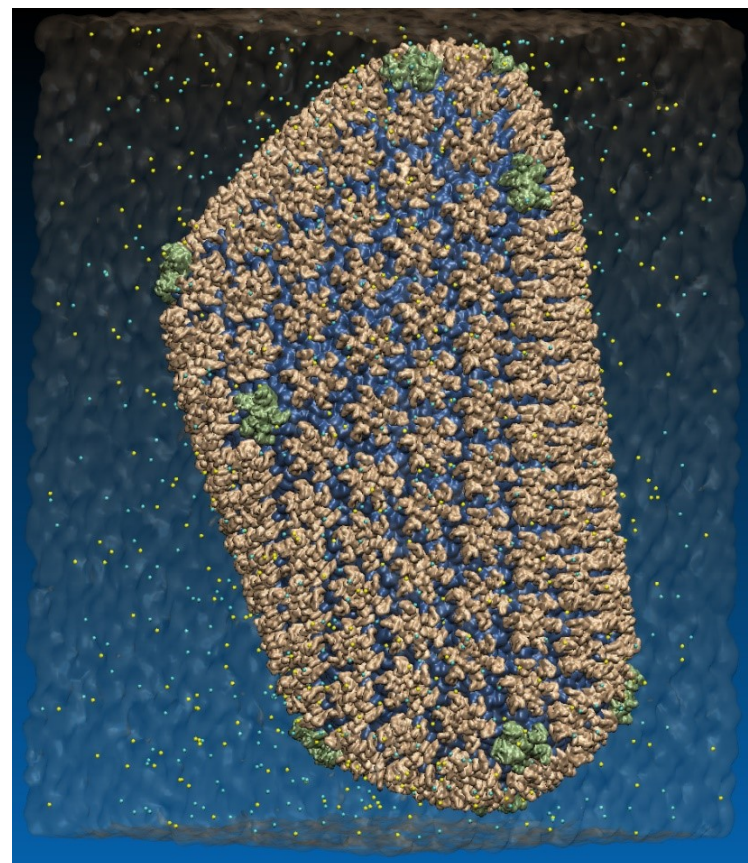
- Initial development performed on workstations
- Parallel MPI tests all performed on Amazon AWS EC2 “g2.8xlarge” instance types:
  - **Easy test deployment, no disruption to production clusters**
  - Installed devel EGL drivers on Amazon G2 GPU instance
  - **Added MPI-rank to EGL index GPU affinity rules for Amazon EC2 G2 instances**
- Performance tests were based on a movie rendering for HIV-1 capsid visualization
  - AWS EBS not comparable to supercomputer storage sys!
  - To mitigate I/O impact, tests used instance-local SSDs for output images, input becomes bottleneck at 32 nodes...



# VMD EGL Performance on Amazon EC2 Cloud

MPI Ranks	EC2 “G2.8xlarge” GPU Instances	HIV-1 movie rendering time (sec), (I/O %) 3840x2160 resolution
1	1	626s (10% I/O)
2	1	347s (19% I/O)
4	1	221s (31% I/O)
8	2	141s (46% I/O)
16	4	107s (64% I/O)
32	8	90s (76% I/O)

**Performance at 32 nodes reaches ~48 FPS**



**64M atom HIV-1 capsid simulation rendered via EGL**

# HPC Viz. Apps Supporting EGL Today

- ParaView
- VMD
- VTK



# Future Work

- VMD support for EGL w/ NVENC and other hardware video encoding APIs for remote visualization
- Production EGL support on CSCS Piz Daint (in test now), NCSA Blue Waters, ORNL Titan, etc.
- EGL-based compositing for multi-GPU node architectures similar to the upcoming ORNL and LLNL “Summit” and “Sierra” systems
- Testing EGL with latest Mesa and OpenSWR, e.g. for ANL “Theta”, “Aurora”

# Acknowledgements

- Theoretical and Computational Biophysics Group, University of Illinois at Urbana-Champaign
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  - NSF Blue Waters:  
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ACI-1238993, ACI-1440026
  - NIH support: 9P41GM104601, 5R01GM098243-02







# NIH BTRC for Macromolecular Modeling and Bioinformatics

1990-2017

**Beckman Institute  
University of Illinois at  
Urbana-Champaign**



# Related Publications

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

- **Immersive Molecular Visualization with Omnidirectional Stereoscopic Ray Tracing and Remote Rendering.** John E. Stone, William R. Sherman, and Klaus Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), 2016. **(In-press)**
- **High Performance Molecular Visualization: In-Situ and Parallel Rendering with EGL.** John E. Stone, Peter Messmer, Robert Sisneros, and Klaus Schulten. High Performance Data Analysis and Visualization Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), 2016. **(In-press)**
- **Evaluation of Emerging Energy-Efficient Heterogeneous Computing Platforms for Biomolecular and Cellular Simulation Workloads.** John E. Stone, Michael J. Hallock, James C. Phillips, Joseph R. Peterson, Zaida Luthey-Schulten, and Klaus Schulten. 25th International Heterogeneity in Computing Workshop, IEEE International Parallel and Distributed Processing Symposium Workshop (IPDPSW), 2016. **(In-press)**
- **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, 2016. **(In-press)**
- **Chemical Visualization of Human Pathogens: the Retroviral Capsids.** Juan R. Perilla, Boon Chong Goh, John E. Stone, and Klaus Schulten. SC'15 Visualization and Data Analytics Showcase, 2015.



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- **Visualization of Energy Conversion Processes in a Light Harvesting Organelle at Atomic Detail.** M. Sener, J. E. Stone, A. Barragan, A. Singharoy, I. Teo, K. L. Vandivort, B. Isralewitz, B. Liu, B. Goh, J. C. Phillips, L. F. Kourkoutis, C. N. Hunter, and K. Schulten. SC'14 Visualization and Data Analytics Showcase, 2014.  
**\*\*\*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, 2014. **(In press)**
- **Unlocking the Full Potential of the Cray XK7 Accelerator.** M. D. Klein and J. E. Stone. Cray Users Group, Lugano Switzerland, May 2014.
- **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.
- **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.



# Related Publications

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

- **GPU-Accelerated Molecular Visualization on Petascale Supercomputing Platforms.** J. Stone, K. L. Vandivort, and K. Schulten. *UltraVis'13: Proceedings of the 8th International Workshop on Ultrascale Visualization*, pp. 6:1-6:8, 2013.
- **Early Experiences Scaling VMD Molecular Visualization and Analysis Jobs on Blue Waters.** J. Stone, B. Isralewitz, and K. Schulten. In proceedings, *Extreme Scaling Workshop*, 2013.
- **Lattice Microbes: High-performance stochastic simulation method for the reaction-diffusion master equation.** E. Roberts, J. Stone, and Z. Luthey-Schulten. *J. Computational Chemistry* 34 (3), 245-255, 2013.
- **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.
- **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.



# Related Publications

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- **Quantifying the Impact of GPUs on Performance and Energy Efficiency in HPC Clusters.**  
J. Enos, C. Steffen, J. Fullop, M. Showerman, G. Shi, K. Esler, V. Kindratenko, J. Stone, J Phillips. International Conference on Green Computing, pp. 317-324, 2010.
- **GPU-accelerated molecular modeling coming of age.**  
J. Stone, D. Hardy, I. Ufimtsev, K. Schulten. J. Molecular Graphics and Modeling, 29:116-125, 2010.
- **OpenCL: A Parallel Programming Standard for Heterogeneous Computing.**  
J. Stone, D. Gohara, G. Shi. Computing in Science and Engineering, 12(3):66-73, 2010.
- **An Asymmetric Distributed Shared Memory Model for Heterogeneous Computing Systems.** I. Gelado, J. Stone, J. Cabezas, S. Patel, N. Navarro, W. Hwu. *ASPLOS '10: Proceedings of the 15<sup>th</sup> International Conference on Architectural Support for Programming Languages and Operating Systems*, pp. 347-358, 2010.



# Related Publications

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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.
- **Long time-scale simulations of in vivo diffusion using GPU hardware.** E. Roberts, J. Stone, L. Sepulveda, W. Hwu, Z. Luthey-Schulten. In IPDPS'09: Proceedings of the 2009 IEEE International Symposium on Parallel & Distributed Computing, pp. 1-8, 2009.
- **High Performance Computation and Interactive Display of Molecular Orbitals on GPUs and Multi-core CPUs.** J. Stone, J. Saam, D. Hardy, K. Vandivort, W. Hwu, K. Schulten, 2nd Workshop on General-Purpose Computation on Graphics Processing Units (GPGPU-2), ACM International Conference Proceeding Series, volume 383, pp. 9-18, 2009.
- **Probing Biomolecular Machines with Graphics Processors.** J. Phillips, J. Stone. Communications of the ACM, 52(10):34-41, 2009.
- **Multilevel summation of electrostatic potentials using graphics processing units.** D. Hardy, J. Stone, K. Schulten. J. Parallel Computing, 35:164-177, 2009.



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- **Adapting a message-driven parallel application to GPU-accelerated clusters.** J. Phillips, J. Stone, K. Schulten. Proceedings of the 2008 ACM/IEEE Conference on Supercomputing, IEEE Press, 2008.
- **GPU acceleration of cutoff pair potentials for molecular modeling applications.** C. Rodrigues, D. Hardy, J. Stone, K. Schulten, and W. Hwu. Proceedings of the 2008 Conference On Computing Frontiers, pp. 273-282, 2008.
- **GPU computing.** J. Owens, M. Houston, D. Luebke, S. Green, J. Stone, J. Phillips. Proceedings of the IEEE, 96:879-899, 2008.
- **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.

