

LIFE AND MATERIAL SCIENCE APPLICATION PERFORMANCE

Critical COVID-19 Research Accelerated on NVIDIA GPUs

NVIDIA GPUs accelerate today's most critical global health research efforts. In just under two weeks, researchers determined the first high resolution structure of the 2019-nCoV spike protein using Structura Bio application, cryoSPARC. The turnaround time came by ongoing improvements in computational throughput and more accurate methods. Over the past 5 years, today's cryo-EM pipelines take days rather than months.

From real-time processing as data is acquired to advanced molecular simulations using HPC and AI, future vaccines and therapies will be ready to fight global health threats.



END TO END GPU ACCELERATED CRYO-EM

Single Compute Platform for AI, HPC, Visualization



GPU-accelerated apps

- AMIRA
- BioEM
- cryoSPARC
- cyYOLO
- Dynamo

- EMAN2
- emClarity
- GCTF
- IMOD
- MotionCor2

- RELION
- Tomviz
- Topaz
- VMD
- Warp

Cryo-EM Performance White Paper



Overview of Life & Material Accelerated Apps



MD

All key codes are GPU-accelerated

Great multi-GPU, multi-node (dense) performance

GPU-accelerated apps

ACEMD, AMBER, BAND, CHARMM, DESMOND, ESPResso, Folding@Home, GPUgrid.net, GROMACS, HALMD, HOOMD-Blue, LAMMPS, Lattice Microbes, mdcore, MELD, miniMD, NAMD, OpenMM, PolyFTS, SOP-GPU & more



All key codes are ported or optimizing

GPU-accelerated math libraries, OpenACC directives

GPU-accelerated apps

ABINIT, ACES III, ADF, BigDFT, CP2K, GAMESS, GAMESS-UK, GPAW, LATTE, LSDalton, LSMS,

MOLCAS, MOPAC2012, NWChem, NWChemEx, OCTOPUS, PEtot, QUICK, Q-Chem,

QMCPack, Quantum Espresso, QUICK, TeraChem, VASP

Active acceleration projects

CASTEP, GAMESS, Gaussian, ONETEP, Quantum Supercharger Library, & more



AMBERMD 2020



Cellulose 408,609 atoms



Performance Comparison - Cellulose 4fs



Factor IX 90,906 atoms

Performance Comparison - FactorIX 4fs



DHFR 23,558

atoms

Performance Comparison - JAC 4fs



Performance Comparison - STMV 4fs



Benefit of NVSWITCH and NCCL - Average benchmark performance



AmberMD recommended usage

Motherboard and CPU	Dual-socket CPU with server
System memory	>=16GB
GPUs	V100 or A100 NVSWITCH
GPUs per socket	4 or 8
GPUs per task	1 - 4



GROMACS 2020



GROMACS - 2020





GROMACS recommended usage

Motherboard and CPU	Dual-socket CPU server
System memory	>=16GB
GPUs	V100 / A100 with SXM2/3/4
GPUs per socket	1 to 4
GPUs per task	1 - 4



LAMMPS PATCH_20NOV2019



Performance Comparison - Atomic-Fluid Lennard-Jones 2.5 Cutoff



Bulk Cu lattice





Performance Comparison - ReaxFF/C



Performance Comparison - Rhodopsin



Si crystallization 🎆





Performance Comparison - SNAP



LAMMPS recommended usage

Motherboard and CPU	Dual-socket CPU
System memory	>=32GB
GPUs	V100 / A100
GPUs per socket	1 to 4
GPUs per task	4



NAMD 3.0A



NAMD - 3.0a1

Performance Comparison - Average Performance



NAMD - 3.0a1

ApoA1 92,224 atoms



Performance Comparison of APOA1 benchmarks



NAMD - 3.0a1

STMV 1,067,095 atoms





NAMD recommended usage

v3.0a has strong single GPU performance

Motherboard and CPU	Dual-socket CPU server
System memory	>=16GB
GPUs	V100 / A100
GPUs per socket	1 to 4
GPUs per task	1



RELION 3.0.8



RELION - 3.0.8

Performance Comparison - 3D Refinement



RELION RECOMMENDED USAGE

Motherboard and CPU	Dual-socket CPU
System memory	>=32GB
GPUs	RTX 6000 / RTX 8000 / V100 / A100
GPUs per socket	1 to 4
GPUs per task	1 to 4



VASP 6.1.0





VASP RECOMMENDED USAGE

Motherboard and CPU	Dual-socket CPU
System memory	>=32GB
GPUs	V100 / A100
GPUs per socket	1 to 4
GPUs per task	1 to 4



