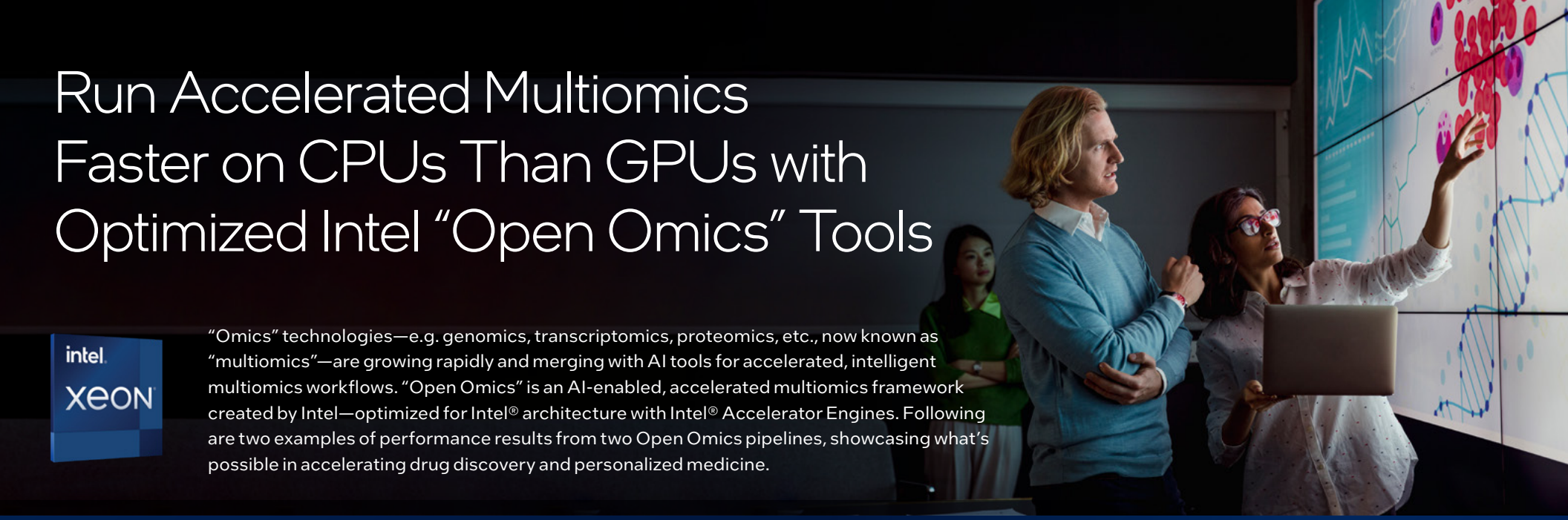
Run Accelerated Multiomics Faster on CPUs Than GPUs with Optimized Intel "Open Omics" Tools



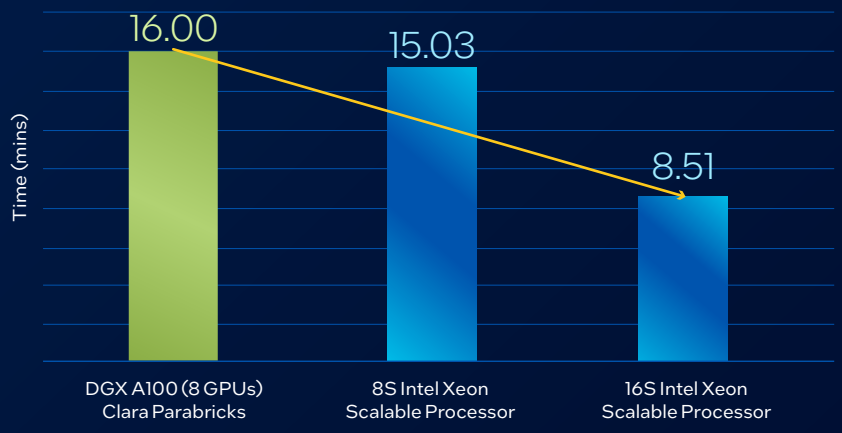
"Omics" technologies—e.g. genomics, transcriptomics, proteomics, etc., now known as "multiomics"—are growing rapidly and merging with AI tools for accelerated, intelligent multiomics workflows. "Open Omics" is an AI-enabled, accelerated multiomics framework created by Intel—optimized for Intel® architecture with Intel® Accelerator Engines. Following are two examples of performance results from two Open Omics pipelines, showcasing what's possible in accelerating drug discovery and personalized medicine.

Optimized DeepVariant Accelerates Variant Calling On Intel® CPUs

Accelerating variant calling (VC) pipelines delivers quicker insights and understanding for drug discovery and personalized medicine. The Open Omics optimized DeepVariant Germline pipeline accelerates VC on Intel® Xeon® Scalable processors completing in up to 53% less time compared to costly GPU-dependent infrastructure.

Time to Completion: DeepVariant Germline Pipeline

NVIDIA Clara Parabricks on DGX A100 (8 GPUs) vs.
Open Omics on Intel® Xeon® 8480+ processor (multi-socket configuration)



Up to
53%
faster time to completion

Open Omics Acceleration Framework for Digital Biology

The Open Omics framework offers accelerated tools for digital biology research running on performant Intel® processors. The Framework simplifies using these tools in on-premises and cloud computing running Intel CPUs with built-in Intel® Accelerator Engines. Open Omics tools are modular, allowing researchers to adapt them in ways they want to interact with the framework. Open Omics is free and open source.

Learn more at **github.com/IntelLabs/Open-Omics-Acceleration-Framework**

Open Omics AlphaFold2 on Intel Runs Faster Than FastFold on Expensive GPUs

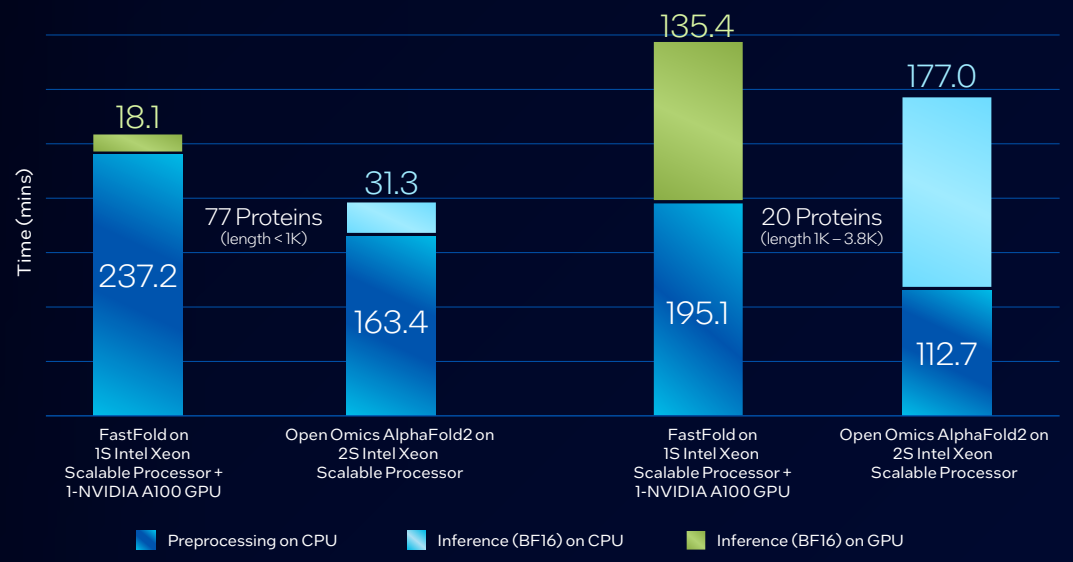
The faster you can simulate protein folding, the quicker you can begin to understand its function and interactions with other molecules for drug discovery. Open Omics optimized AlphaFold2 takes advantage of Intel Xeon processor acceleration technologies, enabling you to run faster on hardware you're familiar with, rather than complex and expensive GPU-dependent workstations.

Want More Information?

Visit intel.com/artificialintelligence to learn more about how Intel is innovating with AI.

Protein Folding (77 and 20 Proteins) Time to Completion (Preprocessing and Inference)

Open Omics AlphaFold2 on Intel® Xeon® 8480+ Processors vs.
FastFold on Intel Xeon 8480+ Processor + NVIDIA A100 GPU



CONFIGURATIONS

Protein Folding (77 and 20 proteins)

AlphaFold2 on 2 CPU sockets: Test by Intel as of 05/21/23. 1-node, 2x Intel® Xeon® Platinum 8480+, 56 cores, HT On, Turbo On, Total Memory 1024 GB (16 slots/ 64 GB/ DDR5 4800 MT/s [4800 MT/s]), bios: SE5C7411.86B.9525.D13.2302071332, ucode version: 0x2b000190, OS Version: Rocky Linux 8.7 (Green Obsidian), kernel version: 4.18.0-372.32.1.el8_6.crt2.x86_64, compiler version: g++ 9.4.0, workload version: Intel-python - 2022.1.0 JAX - v0.4.8, AlphaFold2, - v2.0, Hmmer (Our optimizations over v3.3.2), hh-suite (Our optimizations over v3.3.0), Kalign2 – v2.04, framework version: PyTorch - v1.11.0, model name & version: AlphaFold2

Best CPU + GPU: Open Omics preprocessing on 1 CPU socket + FastFold Model inference on 1 A100 for best CPU-GPU performance. Since preprocessing and model inference can be run independently, the time for this case was obtained by adding preprocessing on 1 CPU socket using Open Omics with model inference on GCP A100 instance using FastFold.

DeepVariant (variant calling)

Open Omics-optimized DeepVariant on CPU: Test by Intel as of 06/10/23. 1-node (1,2 socket), 2/4/8/16/32-nodes (4/8/16/32/64 sockets), Each socket is 1x Intel® Xeon® Platinum 8480+, 56 cores, HT On, Turbo On, Total Memory 256 GB (8 slots/ 32 GB/ DDR5 4800 MT/s [4800 MT/s]), bios: SE5C7411.86B.9525.D13.2302071332, ucode version: 0x2b000190, OS Version: Rocky Linux 8.7 (Green Obsidian), kernel version: 4.18.0-372.32.1.el8_6.crt2.x86_64, compiler version: g++ 9.4.0, workload version: bwa-mem2 v2.2.1, Samtools v. 1.16.1, Our optimized version of DeepVariant v1.5, framework version: Intel-tensorflow 2.11.0, model name & version: Inception V3

DeepVariant using Nvidia Clara Parabricks on DGX A100: Performance reported by Nvidia on 03/21/2023 on DGX A100 box running Nvidia Clara parabricks; reported here: https://developer.nvidia.com/blog/long-read-sequencing-workflows-and-higher-throughputs-in-nvidia-parabricks-4-1/

Performance varies by use, configuration, and other factors. Learn more at www.Intel.com/PerformanceIndex. Performance results are based on testing as of dates shown in configurations and may not reflect all publicly available updates. See backup for configuration details. No product or component can be absolutely secure. Your costs and results may vary. Intel does not control or audit third-party data. You should consult other sources to evaluate accuracy.

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