



DRUG DISCOVERY PLATFORM EXPLORES NOVEL CHEMICAL SPACE WITH HIGHER ACCURACY

"There are an estimated 10^{60} possible drug compounds—an intractable problem. We aim to help the industry discover the most promising molecules through physics-based and machine learning approaches to ultimately deliver better medicines to patients."

— Patrick Lorton, CTO, Schrödinger

Discovering and Designing Novel Drugs

It can cost billions of dollars to bring a new medicine to market. The process of finding a novel compound, predicting its efficacy, and ensuring its safety is time-consuming and resource-intensive. Of the trillions of promising molecules that get tested each year, only a handful will make the cut. These days the medical field demands ever safer, more selective drugs for patients. Yet drug discovery has fewer ready candidates: the obvious areas of chemical space have been explored. The problems have become more complex and the solutions harder to find in chemical space.

Every decade, the tools become more powerful. Leveraging NVIDIA's accelerated computing platform as the computational engine, Schrödinger's suite of tools makes it possible for researchers to deploy accurate digital simulations of promising compounds and model how they react to target proteins in the human body. Using proven physics-based platforms in combination with machine learning techniques, scientists can discover and design more novel drugs more efficiently than ever before.

Chemistry Meets Digitalization

Over the past ten years, Schrödinger has engaged in an ambitious scientific development initiative to improve a crucial tool for drug discovery: free energy perturbation (FEP). FEP allows researchers to predict how proteins will interact with distinct molecules in a human body. It allows them to pose questions like, will these two molecules bind together in a stable way? Is the resulting compound potent enough, or is there a similar ligand molecule that would be more effective?

A lot has happened since the FEP methodology was first created in 1954. Sampling algorithms, force fields, and parallel-processing supercomputers have changed how biopharma companies calculate free energy in molecular dynamics. Schrödinger researchers embarked on a large-scale project to create a new free energy calculation technology called FEP+. Their goals were to update existing protocols and improve the tool's accuracy, reliability, ease of use, and performance.



Schrödinger is a pioneer and industry leader in physics-based computational methods to evaluate and accelerate drug discovery.

INDUSTRY

- > Preclinical research
- > Life sciences
- > Pharmaceutical

PRODUCTS USED

- > NVIDIA DGX Systems
- > NVIDIA-Certified Systems™
- > NVIDIA CUDA
- > NVIDIA CUDA-X
- > NVIDIA Clara Discovery
- > DeepOps automation tools

FEATURED PRODUCTS

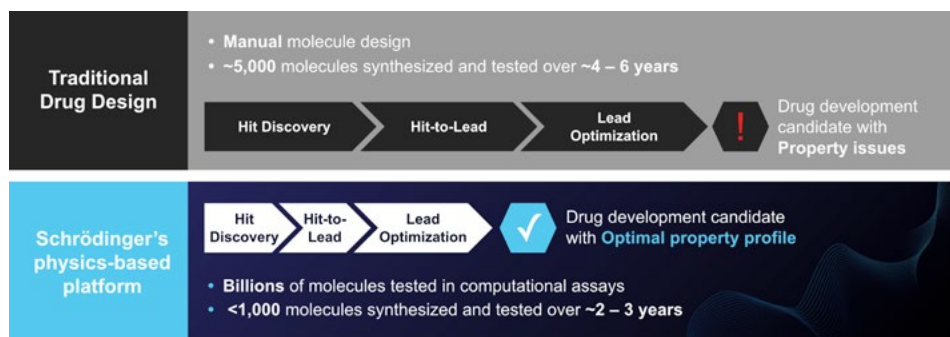
- > FEP+ to predict protein-ligand binding of on- and off-targets
- > Desmond for molecular dynamics
- > DeepAUTOQSAR for automated machine learning
- > LiveDesign for collaborative design and informatics



PREFERRED
PARTNER

Amplify Your Insights, Improve Discovery Speed

Reduces time and cost and increases quality vs. traditional drug design



RESULTS

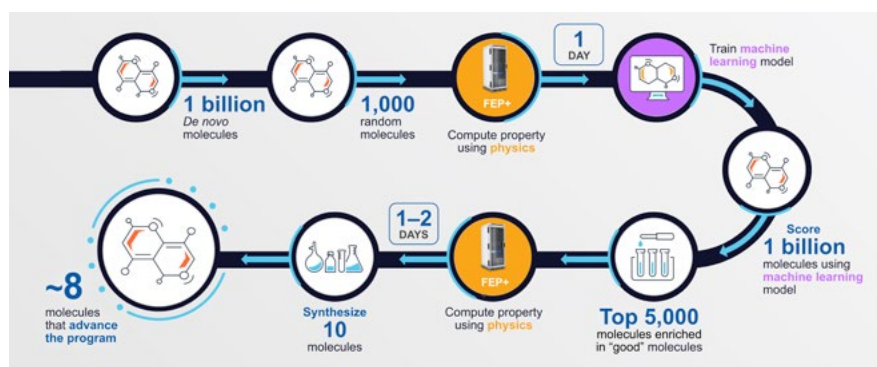
- > Able to accurately evaluate billions of virtual compounds a week
- > Can predict compound properties with an accuracy comparable to physical experiments
- > Have the ability to perform precision design of new molecules and efficient multi-parameter optimization
- > Can scale computational resources easily using GPU-based tools

Staying Ahead of Demanding Applications

Using FEP+, researchers can now predict chemical properties with the same accuracy as laboratory experiments, and gain the speed and lower cost of modeling drug activity in-silico vs. in-vitro. The ability to accurately evaluate potential drug candidates computationally is critical for assessing thousands or more molecules at a time. Combining the accuracy of FEP+ with the addressable scale of machine learning enables biopharma researchers to expand the volume of calculations to millions and billions of compounds in search of novel matter. With this process and enough compute resources, companies can better identify quality drug candidates in less time.

“The predictive modeling built into our platform is designed to dramatically expand and accelerate the search for high-quality therapeutic molecules, and NVIDIA is a key technology partner in this work,” Lorton said. “Our advanced computational software helps the world’s biggest pharma companies explore more of the chemical space and reach high-quality candidates more quickly, with far less compute cost, than traditional methods.”

As improvements to FEP+ continue, researchers are seeing faster and more performant synthesis queues and potency scoring, which has the potential to significantly accelerate the entire lead optimization process. Better predictive modeling means researchers can move forward with strong candidates and deprioritize weak binders with higher confidence. It also gives teams the ability to run multi-parameter optimization by combining FEP+ with other predictive models for ADMET properties (absorption, distribution, metabolism, excretion, and toxicity), which is key in late-stage projects.



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For years, Schrödinger has relied on NVIDIA GPUs to run its commercial applications, including:

- > FEP+
- > Desmond for simulating molecular dynamics
- > DeepAutoQSAR / DeepChem for machine learning

Calculating properties of novel molecules requires massive amounts of GPU cycles. For instance, it can take thousands of GPU hours to run a series of FEP+ calculations. Running workloads in parallel and using the most powerful GPUs, Schrödinger is able to accelerate the time to identify candidates in their own drug discovery pipeline.

Collaborating to Accelerate Drug Discovery

NVIDIA and Schrödinger worked together to simplify, automate, and accelerate the deployment of Schrödinger software on NVIDIA DGX™ A100's with the **DeepOps project**. The DGX A100 can deliver best-of-breed AI infrastructure for workloads that demand the highest performance possible. The two companies focused on deployment and configuration to improve GPU utilization, while also increasing the performance and scale of Schrödinger workflows at the scheduler level. With those optimizations in place, Schrödinger was able to maximize throughput for its FEP+ calculations.

Part of the DGX experience is a white-glove implementation service that can ensure streamlined deployment and efficient operation. Working together on an infrastructure design, NVIDIA and Schrödinger were able to further minimize the time between infrastructure deployment and effective research using a DeepOps playbook. Following the technical documentation, the teams set up the Schrödinger suite and jobserver alongside the **Slurm** scheduler to maximize the throughput of computational chemistry workflows. This also provides the best user experience for system administrators and scientists. Once deployed, scientists can launch applications and workflows on the cluster from the command-line or Schrödinger's Maestro graphical-user interface.

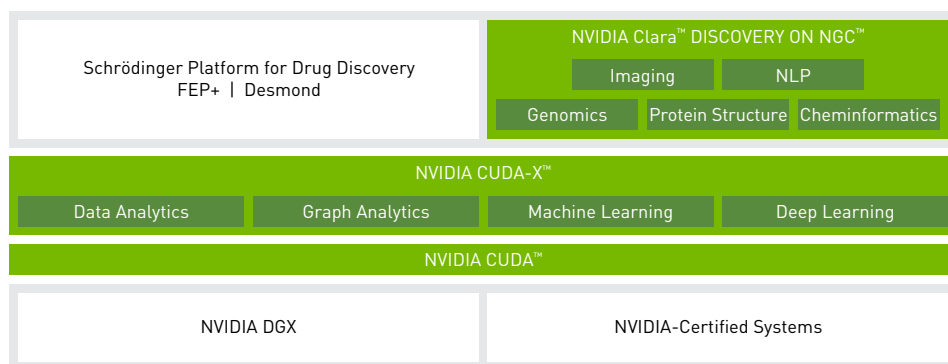
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Conclusion

Collaboration is an excellent way to create new and more performant technologies that can solve some of the world's most complex challenges. Schrödinger and NVIDIA have succeeded in:

- > Accelerating drug discovery timelines with powerful simulation software that can evaluate billions of molecules a week.
- > Enabling biopharma companies to identify top-scoring compounds with more confidence for high-quality pipelines.
- > Using machine learning techniques to amplify physical modeling across vast chemical space and model structure-activity relationships, i.e. for ADMET properties.
- > Optimizing GPU-based infrastructure tools to schedule jobs more efficiently, and improve performance and scale.

GPU-accelerated computing delivers dramatic increases in computational power, enabling researchers and biopharma companies to create more accurate models of virtual novel compounds that could become tomorrow's life-saving medicines. It's now possible to design large numbers of synthesizable virtual molecules, predict their properties, and set up pipelines with confidence.



Ready to Get Started?

Contact Schrödinger at info@schrodinger.com

Learn more about NVIDIA DGX Systems: nvidia.com/dgx-systems