

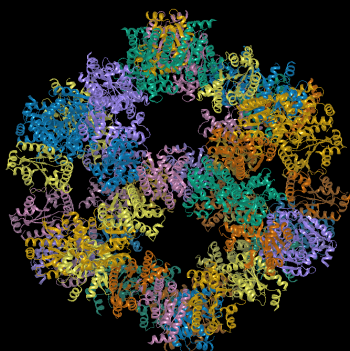
NovaLocal: Secure, Local Protein Structure Prediction at Scale

NovaLocal provides local access to advanced protein structure prediction and modeling workflows, giving you complete control over sensitive data and computational resources.

✓ Streamlined Access to Multiple Prediction Methods

Many state-of-the-art protein prediction algorithms require installation, command-line tools, and workflow configuration. NovaLocal provides access to these methods through an easy-to-use assistant within Protean 3D.

Configure a prediction in about a minute by selecting a prediction method, choosing input sequences, adjusting optional parameters, and submitting the job. Six algorithms are available:



- Model multi-chain protein structures with **AlphaFold-Multimer**
- Predict biomolecular complex structures with **Boltz**
- Model antibody and antibody fragment structures with **NovaFold Antibody**
- Predict protein-protein interactions through docking with **NovaDock**
- Model protein structures from a single sequence with **ESMFold2**
- Predict protein complex structures with **ColabDock** (coming in Lasergene 19.1)

✓ Secure, Local, and Cloud-Free

NovaLocal performs the entire prediction workflow within your organization's computing environment*, making it well suited for proprietary, confidential, or regulated biological data. Sequence data and prediction results remain on your local computer throughout the workflow, eliminating the need to transfer sensitive data to external cloud services.

*Boltz prediction has one step that requires MMseqs2. One option is to run that step on DNASTAR's secure, no-data-collection server. If your organization requires maximum performance and fully local execution, DNASTAR can assist with local MMseqs2 installation and deployment.

✓ Fast and Scalable, with Unlimited Predictions Included

NovaLocal supports both individual predictions and large batch workflows using the same streamlined setup process. Because predictions run locally, NovaLocal can deliver faster performance than cloud-based solutions.

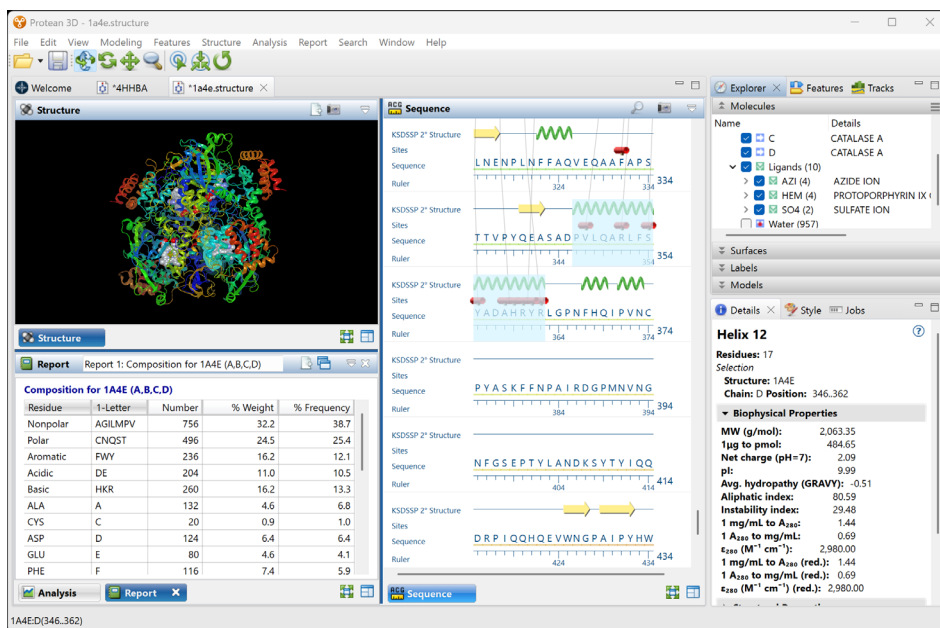
Each NovaLocal license includes unlimited predictions, enabling everything from individual analyses to large-scale batch workflows without token or usage restrictions.

✓ Integrated Visualization and Analysis in Protean 3D

Prediction results open directly in Protean 3D for interactive visualization, structural analysis, and generation of fully customizable, publication-quality figures.

By combining prediction and downstream analysis within a single workflow, NovaLocal helps you move efficiently from sequence to structural insight.

Right: Top-ranked protein complex predicted by Boltz, displayed in multiple customizable Protean 3D visualization and analysis views.



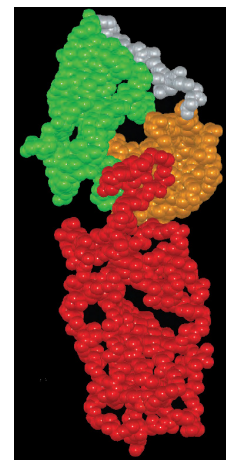
Case Study: Rapid AI-Driven Antibody Screening

Identifying the antigen targets of antibodies within the highly diverse human antibody repertoire has traditionally required extensive experimental screening. To evaluate a more efficient approach, DNASTAR used Protean 3D's biophysical modeling tools and its Boltz structure modeling algorithm to perform an entirely *in silico* screen of a highly abundant memory B-cell clonotype against a panel of 55 common pathogen antigens.

The analysis identified the SARS-CoV-2 spike receptor binding domain (RBD) as the target antigen and predicted an epitope overlapping the ACE2 binding interface. Experimental bio-layer interferometry subsequently confirmed high-affinity binding to multiple recent SARS-CoV-2 variants, with dissociation constants as low as 1 nM. The complete virtual screen was completed in approximately one hour. This demonstrates how rapid computational screening can substantially reduce the number of candidate interactions requiring experimental validation, lowering both time and cost while accelerating antibody characterization, therapeutic discovery, and studies of the human antibody repertoire.

Request a PDF of the complete poster for additional methods, results, and validation data.

Right: Protean 3D visualization of a Boltz structure prediction for the scCt1-Fv – S-RBD complex.



Questions About NovaLocal? We're Here to Help.

To find out whether NovaLocal is a good fit for your research environment, contact us with questions or to request a demonstration.

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