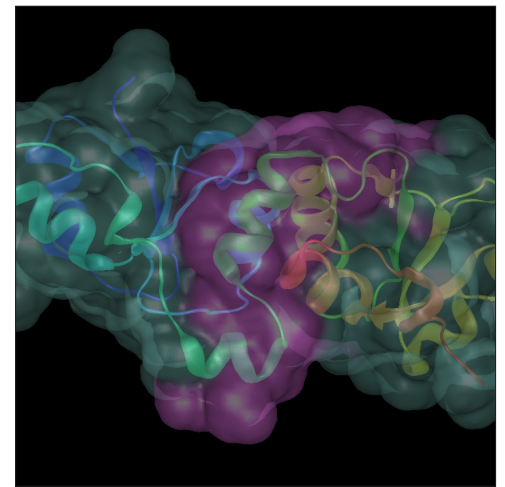
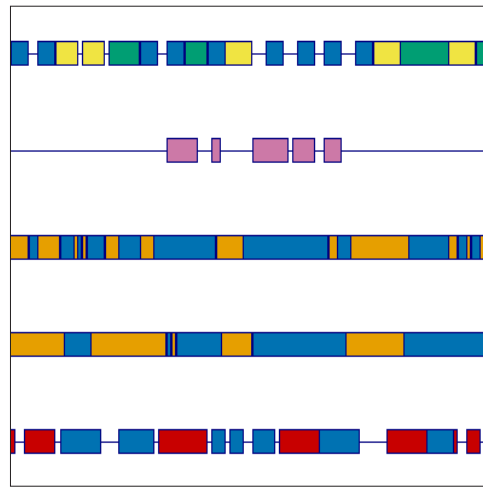
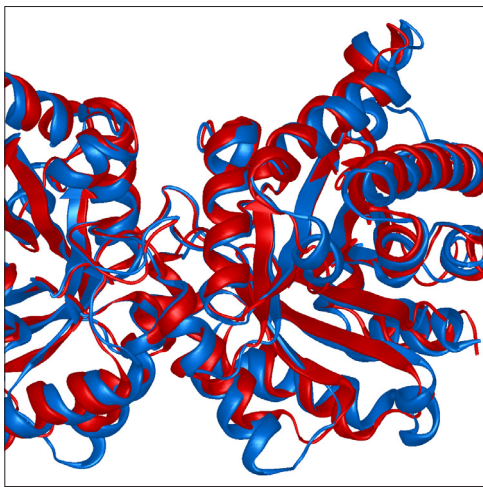


LASERGENE PROTEIN

Software for sequence analysis, protein design, and protein modeling prediction



PROTEIN SEQUENCE ANALYSIS

- Utilize integrated views and analysis methods for sequence, secondary structure, and tertiary structure
- Predict secondary structure characteristics

ADVANCED PROTEIN DESIGN

- Create, model, and analyze variants on a protein structure
- Perform hot-spot scans and improve fold stability with protein design tools
- Calculate energy changes caused by mutations
- Perform serine and alanine variant scans
- Improve protein fold stability
- Predict protein function, ligand binding sites, and enzyme activity

PROTEIN STRUCTURE ANALYSIS

- Predict B-cell epitopes
- Create molecular and solvent accessible surfaces to visualize predicted epitopes
- Align entire structures or selected regions
- Create publication quality graphics
- Visualize conformational changes of nearly 400 animated macromolecular structures

PROTEIN MODELING PREDICTION

- Predict protein structures and assemblies with confidence using a unified, guided structure prediction workflow that makes set-up fast and intuitive

See reverse for details.

Comprehensive tools for protein modeling

Protein Structure Prediction with Boltz

- The Boltz algorithm delivers fast, accurate structure predictions using an open-source AlphaFold 3-style architecture
- Protean 3D's guided setup experience streamlines the process of running even complex modeling predictions
- Boltz excels at predicting ligand binding, multimeric protein assemblies and complexes
- Set up and run predictions in large batches

Structure Prediction with AlphaFold-Multimer

- AlphaFold-Multimer excels at predicting multimeric protein assemblies and protein complexes

Antibody Modeling with NovaFold Antibody

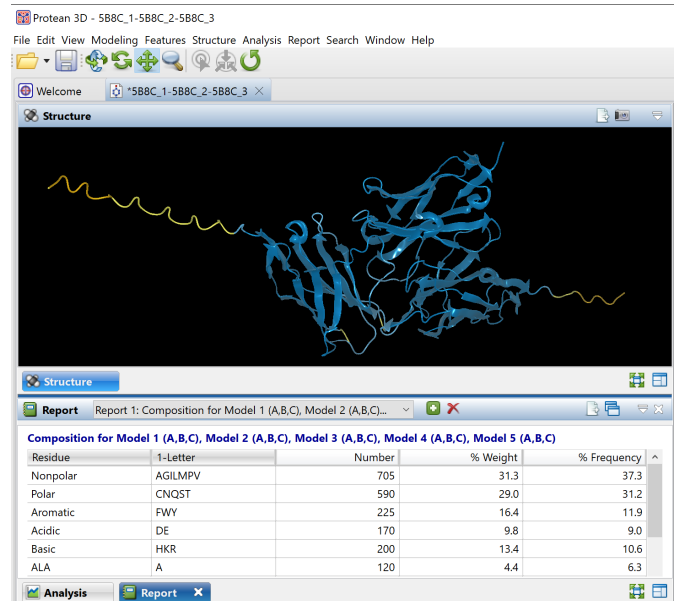
- Rapidly model antibody structures and identify antibody-antigen binding sites.
- Generate Fv, Fab, VH, and single-domain antibody (sdAb) models in minutes
- Search built-in antibody framework libraries or use custom templates
- *Ab initio* loop modeling for H3 - up to 15 residues
- Automated annotation of CDR loops
- Configure multiple local structure predictions using a common target structure and a set of variable structures

Protein-Protein Docking with NovaDock

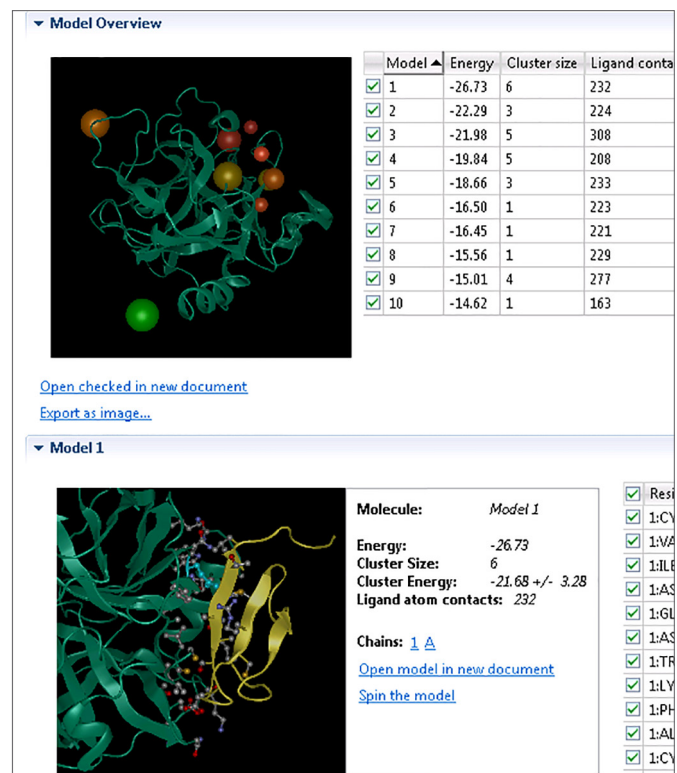
- Model protein interactions and binding modes with a high-resolution docking workflow based on SwarmDock
- Configure multiple local structure predictions using a common target structure and a set of variable structures

Flexible Cloud and Local Deployment

- Choose cloud-based execution for convenience and to free up local computer resources
- Cloud-based predictions are included with your Lasergene Protein license; purchase additional capacity as needed
- Choose local execution (separately licensed) for enhanced data security and unrestricted usage



Above: The structure view and the composition report for an AlphaFold-Multimer prediction. Many other customizable views and reports are available.



Above: The NovaDock report shows the top ligand-receptor docking models for a completed prediction.



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