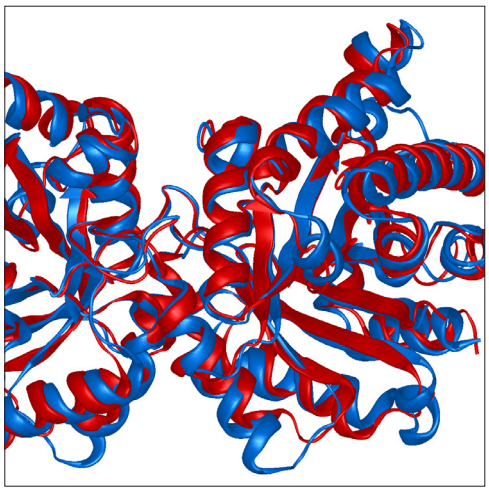
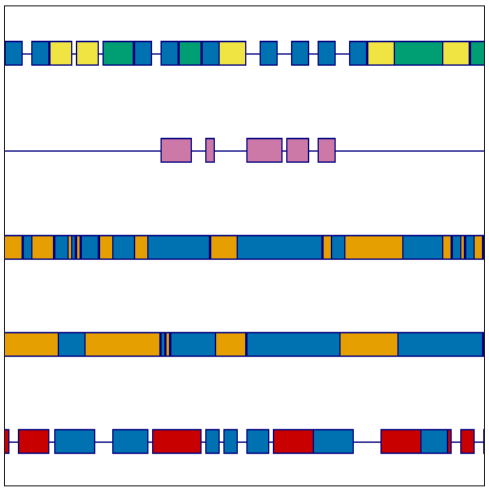
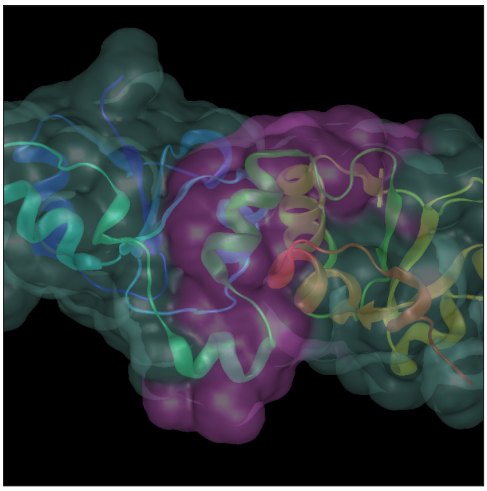
DNASTAR
SOFTWARE FOR LIFE SCIENTISTS

LASERGENE PROTEIN AND NOVA APPLICATIONS

Software for protein modeling and analysis







PROTEIN SEQUENCE ANALYSIS

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

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

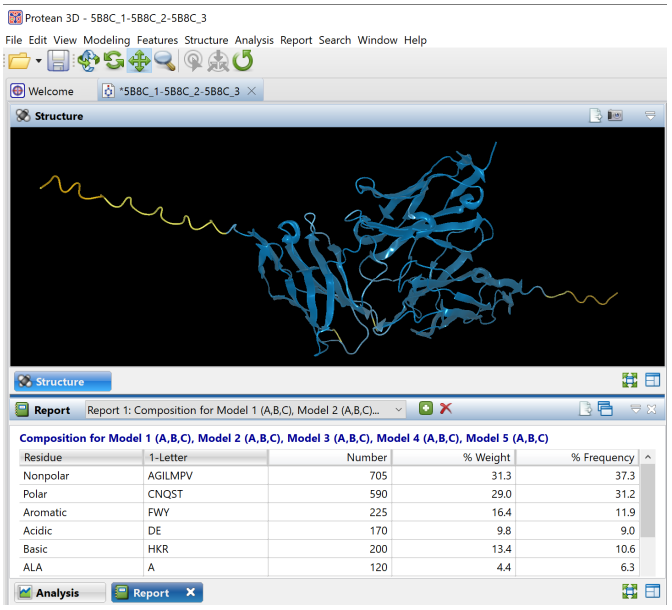
PROTEIN MODELING

- Predict 3D structure for any protein sequence using the award-winning **AlphaFold 2**, **AlphaFold-Multimer**, or **I-TASSER** algorithms
- Model antibody structures and identify antibody/antigen binding sites
- Predict protein function, ligand binding sites, and enzyme activity
- Model docking for any receptor and ligand pair
- Predict binding interactions and energy
- Create and model variants on protein structures
- Perform hot-spot scans and improve fold stability with protein design tools

Comprehensive tools for protein modeling

Structure Prediction with NovaFold, NovaFold AI, and NovaFold AI-Multimer

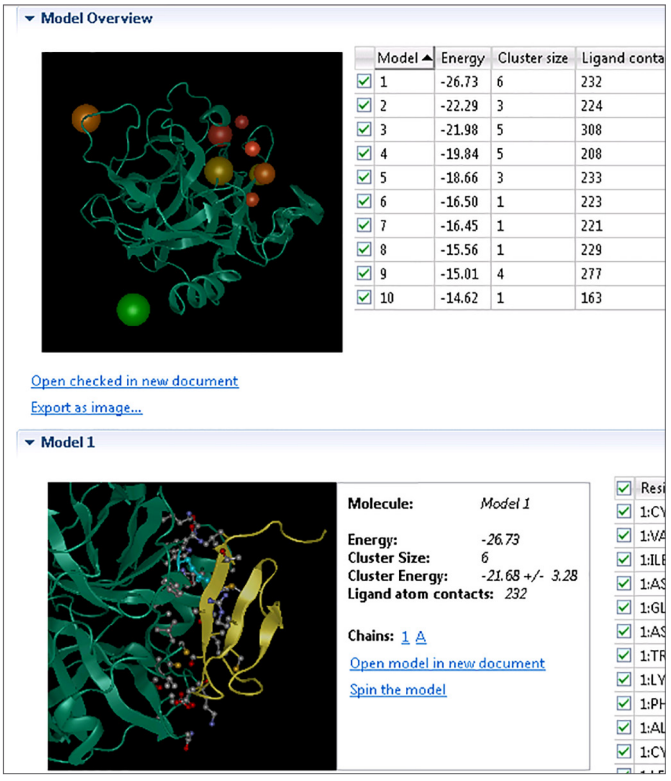
- **NovaFold** utilizes the award-winning **I-TASSER** protein structure prediction algorithm, which combines threading and *ab initio* folding technologies.
- **NovaFold AI** uses the **AlphaFold 2** algorithm from DeepMind to predict distance and create dihedral maps using deep multiple sequence alignments as input.
- **NovaFold AI-Multimer** uses the AlphaFold-Multimer algorithm to predict the structure of a multimeric protein assembly.



The structure view and the compolsition report for a NovaFold AI-Multimer prediction. Many other customizable views and reports are available.

Protein-Protein Docking with NovaDock

- Based on SwarmDock, a high-resolution docking algorithm
- Model protein docking and binding interactions
- Explore protein flexibility during docking



The NovaDock report showing the top ligand-receptor docking models for a completed prediction.

Antibody Modeling with NovaFold Antibody

- Model Fv, Fab, VH, sdAb in minutes
- Search a library of antibody frameworks, or provide custom templates
- *Ab initio* loop modeling for H3 - up to 15 residues
- Automated annotation of CDR loops

Advanced Protein Design

- Create, model, and analyze variants on structure
- Calculate energy changes caused by mutations
- Perform serine and alanine variant scans
- Improve protein fold stability

608.258.7420 USA
866.511.5090 toll free
0.808.271.1041 UK
0.800.182.4747 Germany
1202 Ann Street
Madison, WI 53713
www.dnastar.com
info@dnastar.com