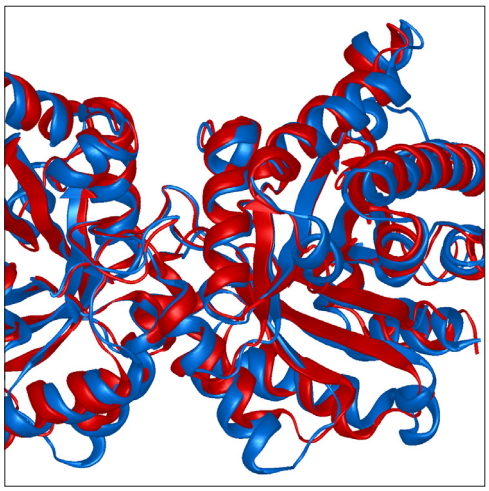
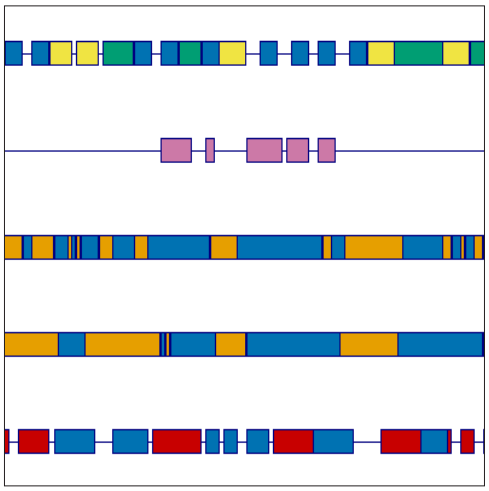
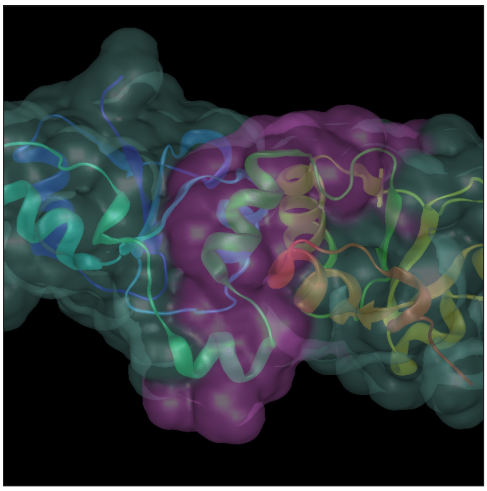
DNASTAR
SOFTWARE FOR LIFE SCIENTISTS

LASERGENE PROTEIN

Software for protein structure and sequence 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

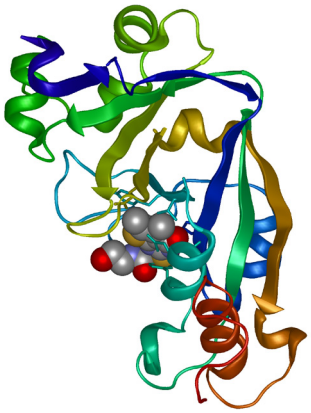
PROTEIN MODELING

- Predict 3D structure for any protein sequence
- 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

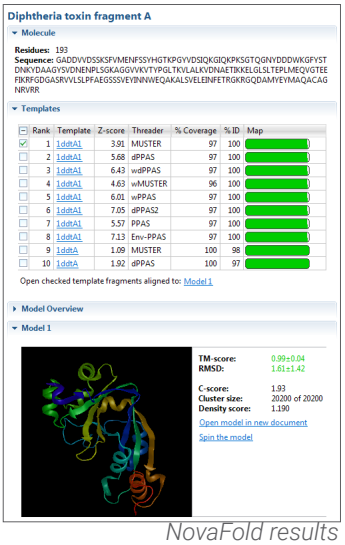
Comprehensive tools for protein modeling

Protein Structure Prediction with NovaFold

- Based on the top-rated algorithm: I-TASSER
- Large molecule support, up to 2000 residues
- Predict protein structure, function, ligand binding, and enzyme activity
- Advanced user restraint controls & custom templates



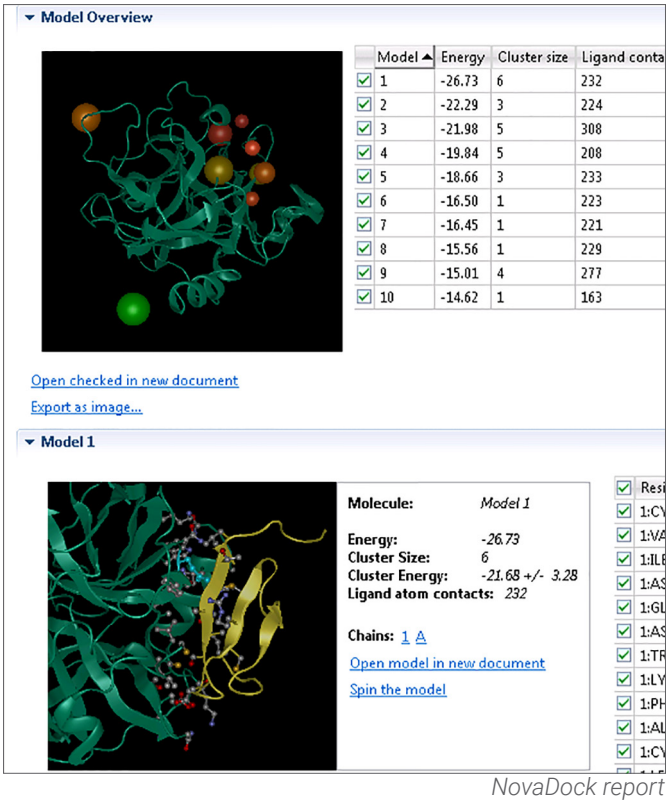
NovaFold model with predicted ligand binding TM-Score: 0.99±0.04; RMSD: 1.61±1.42



NovaFold results

Protein-Protein Docking with NovaDock

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



NovaDock report

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

Protein Design with NovaDesign - NEW!

- Create, model, and analyze variants on structure
- Calculate energy changes of mutations
- Perform serine and alanine variant scans
- Improve protein fold stability with an automated workflow **- COMING SOON!**

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