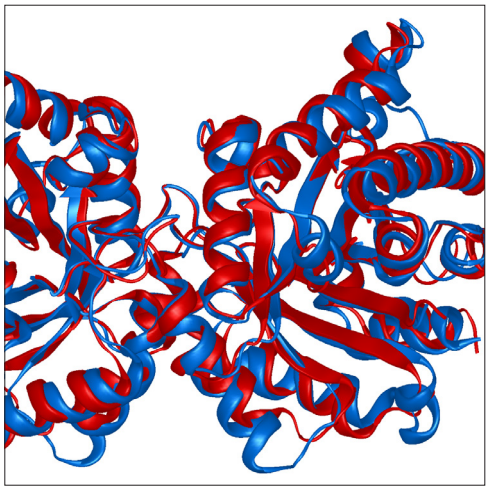
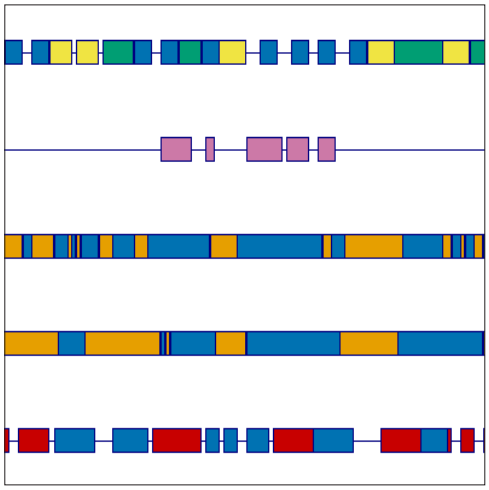
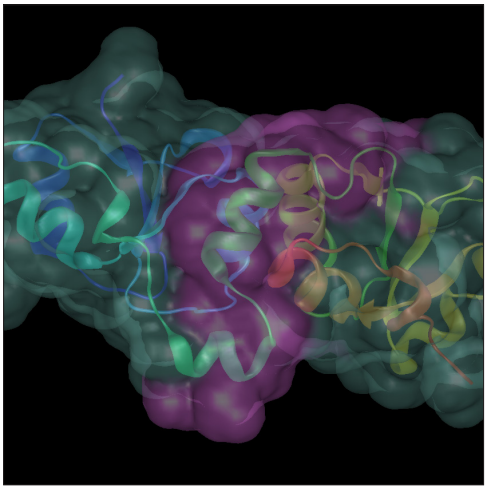
DNASTAR LASERGENE

LASERGENE PROTEIN AND NOVA APPLICATIONS







Protean 3D: Our flagship application for protein analysis and protein design

PROTEIN SEQUENCE ANALYSIS

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

ADVANCED PROTEIN DESIGN

- Use protein design tools to perform hot-spot scans and improve fold stability
- Predict binding interactions and energy
- Create, model, and analyze the effects of variants on structure
- Calculate energy changes caused by mutations
- Perform serine and alanine variant scans
- Improve protein fold stability

PROTEIN STRUCTURE ANALYSIS

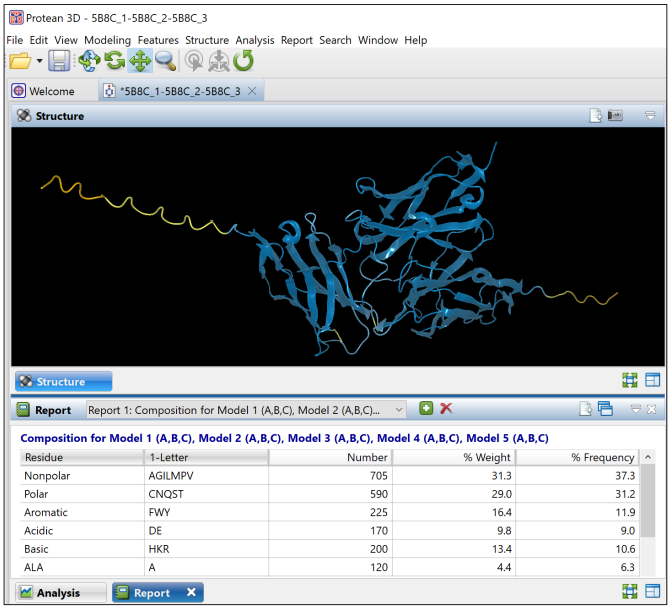
- Predict B-cell epitopes
- Create molecular and solvent accessible surfaces to visualize predicted epitopes
- Align entire structures or selected regions
- Predict protein function, ligand binding sites, and enzyme activity
- Visualize conformational changes of nearly 400 animated macromolecular structures
- Create publication quality graphics
- Predict tertiary structures using the integrated Nova Applications (see reverse)

Nova Applications: Protein modeling and structure prediction within the Protean 3D interface

PROTEIN STRUCTURE PREDICTION

Predict 3D structure for any protein sequence using your choice of three award-winning algorithms.

- **NovaFold** utilizes the **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** features 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

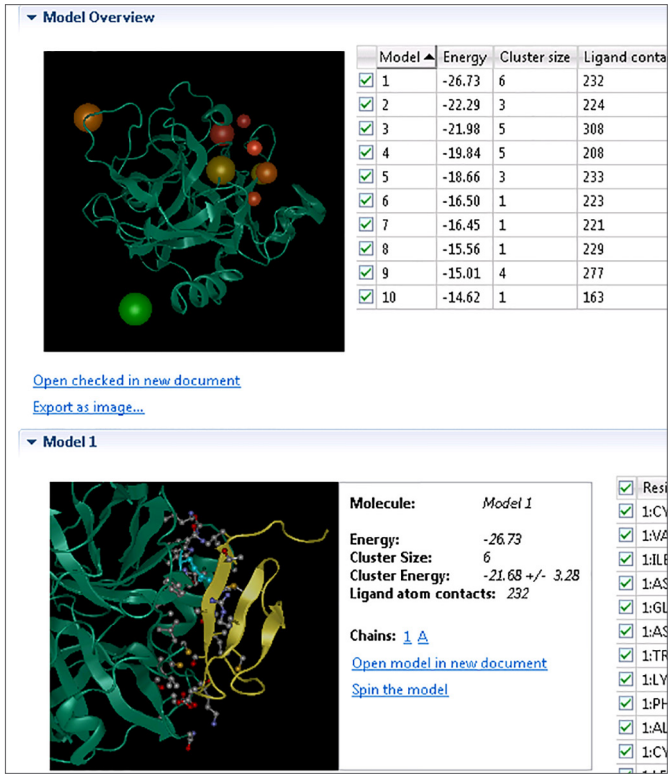
Model protein docking and binding interactions for any receptor and ligand pair using **NovaDock**.

- Based on SwarmDock, a high-resolution docking algorithm
- Explore protein flexibility during docking

ANTIBODY MODELING

Model antibody structures and identify antibody/antigen binding sites with **NovaFold Antibody**.

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



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

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