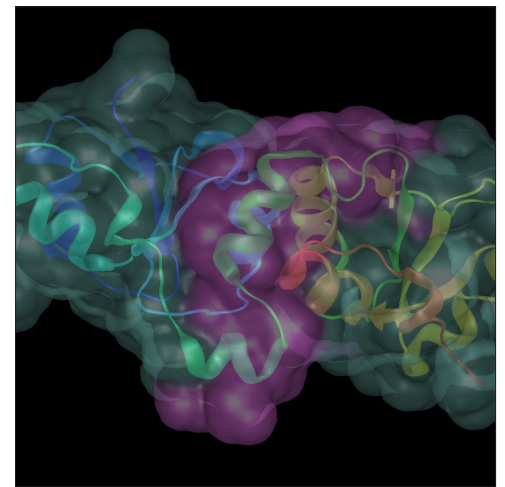
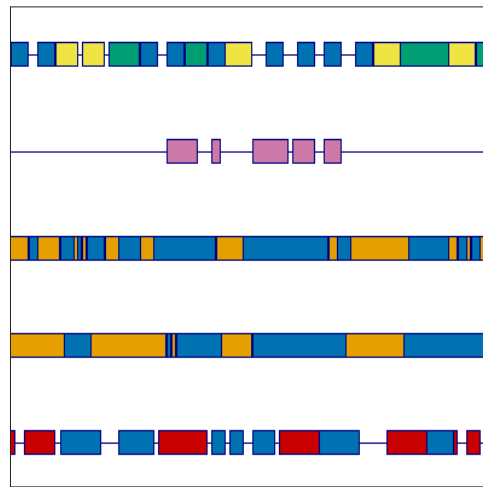
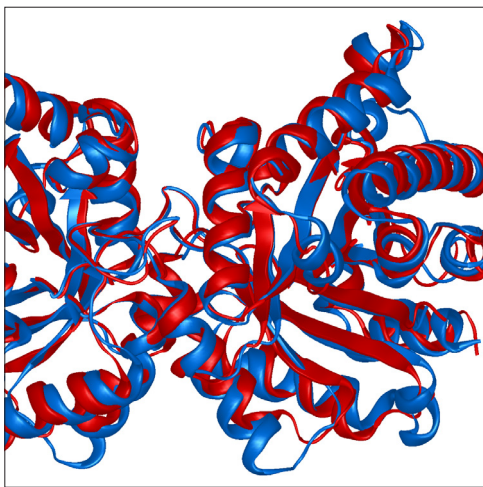


LASERGENE PROTEIN

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

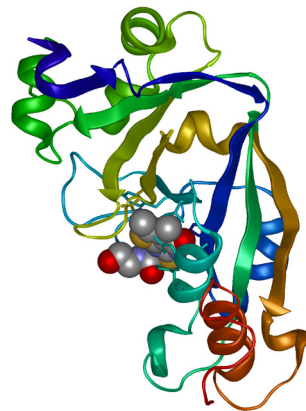
PROTEIN MODELING

- 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



Diphtheria toxin fragment A

Residues: 193
Sequence: GADVVDSKSPVMEVNSVHGTKPGVYDSIQKIQPKSGTQGNVDDWIKGPTF
DINIKDADSDYDNEPLNSKAGDQWVWYVSLTIVLALVKNATIKRELQSLSTPLAQEYGTTE
FKRFGDQASRVLSLFFAEGSSVYVNWVQKALSVLENFETRGRGDAMVEYMAQACAG
NRVRR

Rank	Template	Z-score	Threader	% Coverage	% ID	Map
1	1doAA	3.91	MUSTER	97	100	
2	1doAA	5.68	dPPAS	97	100	
3	1doAA	6.43	wdPPAS	97	100	
4	1doAA	4.83	wMUSTER	96	100	
5	1doAA	6.01	wPPAS	97	100	
6	1doAA	7.05	dPPAS2	97	100	
7	1doAA	5.57	PPAS	97	100	
8	1doAA	7.13	Env-PPAS	97	100	
9	1doAA	1.09	MUSTER	100	98	
10	1doAA	1.92	dPPAS	100	97	

Open checked template fragments aligned to: [Model 1](#)

Model Overview

Model 1

TM-score: 0.99±0.04
RMSD: 1.61±1.42
C-score: 1.93
Cluster size: 20200 of 20200
Density score: 1.190
[Open model in new document](#)
[Spin the model](#)

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

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

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!**

Model Overview

[Open checked in new document](#)
[Export as image...](#)

Model	Energy	Cluster size	Ligand conta
<input checked="" type="checkbox"/> 1	-26.73	6	232
<input checked="" type="checkbox"/> 2	-22.29	3	224
<input checked="" type="checkbox"/> 3	-21.98	5	308
<input checked="" type="checkbox"/> 4	-19.84	5	208
<input checked="" type="checkbox"/> 5	-18.66	3	233
<input checked="" type="checkbox"/> 6	-16.50	1	223
<input checked="" type="checkbox"/> 7	-16.45	1	221
<input checked="" type="checkbox"/> 8	-15.56	1	229
<input checked="" type="checkbox"/> 9	-15.01	4	277
<input checked="" type="checkbox"/> 10	-14.62	1	163

Model 1

Molecule: Model 1
Energy: -26.73
Cluster Size: 6
Cluster Energy: -21.68 +/- 3.28
Ligand atom contacts: 232

Chains: [1](#) [A](#)

[Open model in new document](#)
[Spin the model](#)

Resi
<input checked="" type="checkbox"/> 1:CY
<input checked="" type="checkbox"/> 1:VA
<input checked="" type="checkbox"/> 1:ILQ
<input checked="" type="checkbox"/> 1:AS
<input checked="" type="checkbox"/> 1:GL
<input checked="" type="checkbox"/> 1:AS
<input checked="" type="checkbox"/> 1:TR
<input checked="" type="checkbox"/> 1:LY
<input checked="" type="checkbox"/> 1:PH
<input checked="" type="checkbox"/> 1:AL
<input checked="" type="checkbox"/> 1:CY

NovaDock report

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