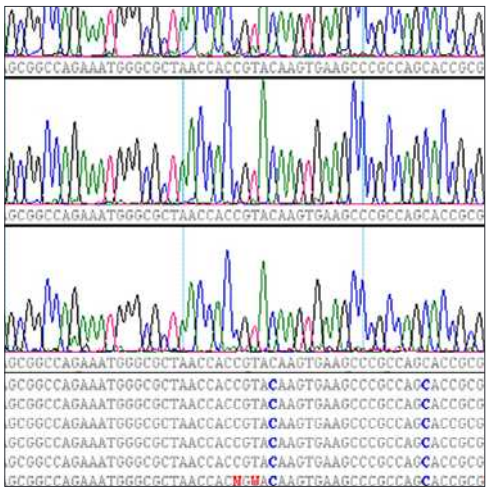
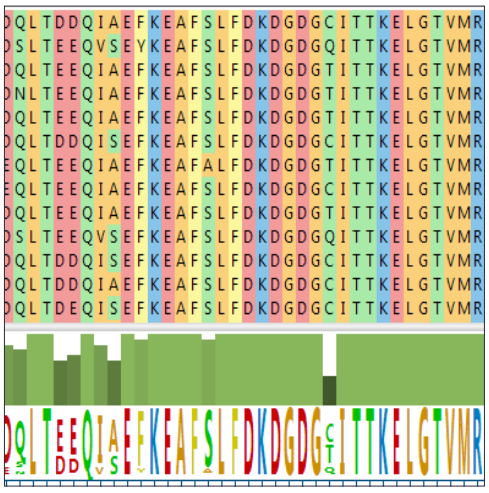
DNASTAR
Software for Life Scientists

LASERGENE MOLECULAR BIOLOGY

Essential software for sequence analysis





MULTIPLE SEQUENCE ALIGNMENT

- Many popular multiple and pairwise sequence alignment methods, including MUSCLE, MAFFT, Clustal Omega, Clustal W, and ParaSail
- Whole genome alignment using MAUVE
- Customizable phylogenetic trees

VIRTUAL CLONING AND PRIMER DESIGN

- Support for all major cloning methods, including Gibson Assembly, InFusion, Gateway, Multisite Pro Gateway, TOPO, TA Cloning and restriction enzyme techniques
- Design and customize primers and probes
- Create and share primer catalogs

SANGER SEQUENCE ASSEMBLY

- Assemble reads *de novo* or against one or more reference sequences
- Assess read alignment, coverage and SNPs
- Design sequencing primers to improve coverage

COMPREHENSIVE SEQUENCE ANALYSIS

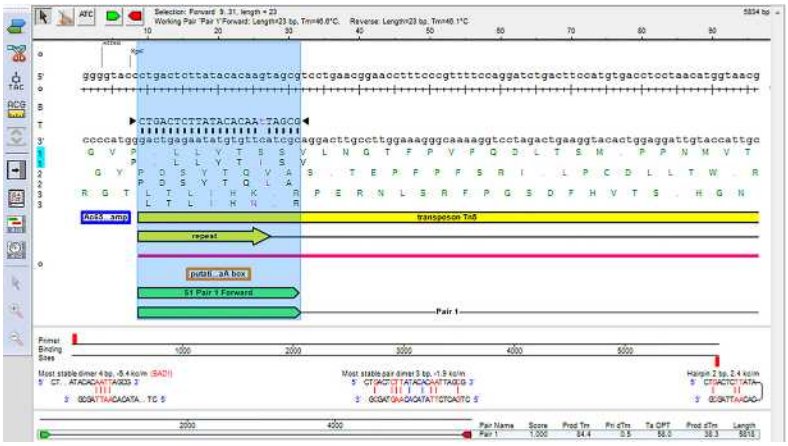
- Accurate and fast sequence auto-annotation
- Sequence editing, including automated and batch editing
- Agarose gel simulations
- Gene discovery
- Integrated BLAST searching
- Publication quality graphics

Flexible licensing and pricing options for any lab

SeqBuilder Pro

Just interested in the basics? Our flagship sequence editor lets you create sequence maps, perform virtual cloning, design primers, batch edit and annotate sequences, and much more!

SeqBuilder Pro is included with Lasergene Molecular Biology, but can also be purchased separately, starting at **just $99** for academic and government researchers, making it the perfect fit for your lab and budget.



Complete Your DNASTAR Lasergene Software Package with our Genomics & Protein Applications

DNASTAR Lasergene includes tools for genomics and protein analysis that integrate seamlessly with the editing, analysis and visualization tools in Lasergene Molecular Biology. If you are working with next-generation sequencing or protein data, our full DNASTAR Lasergene package provides powerful and accurate results for all your analysis needs.

Contact Us

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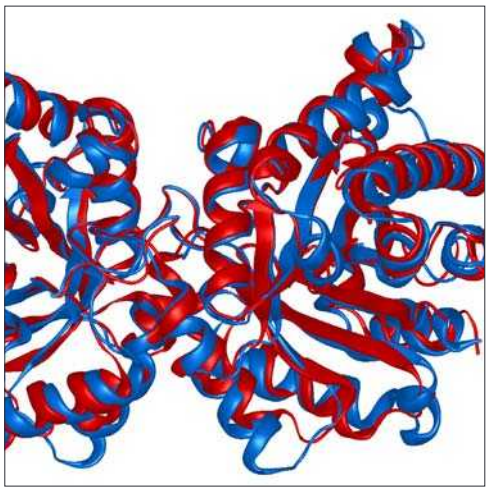
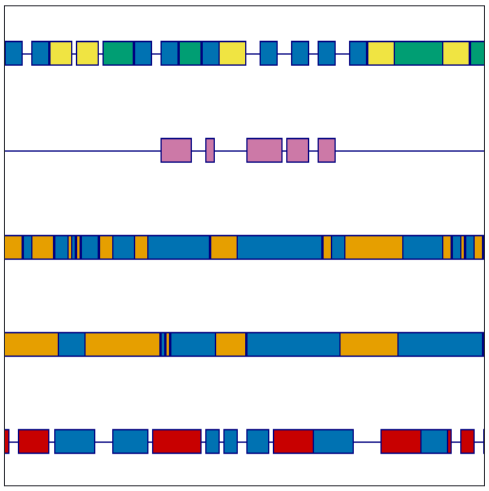
DNASTAR

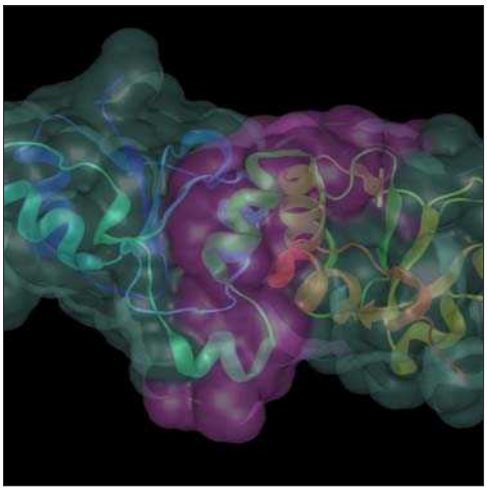
DNASTAR®
Software for Life Scientists

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

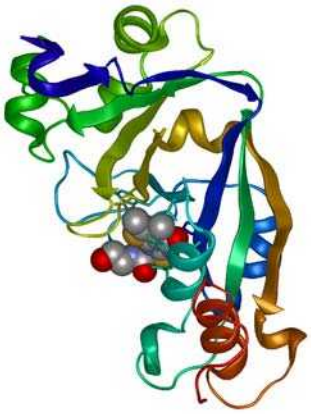
PROTEIN MODELING

- 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

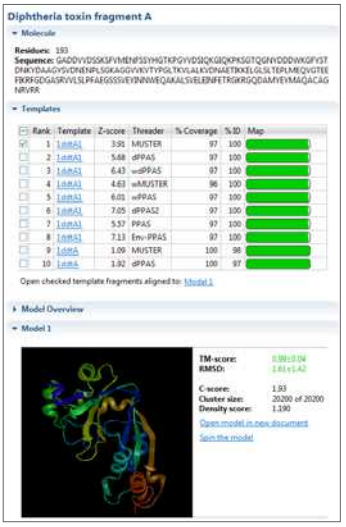
Comprehensive tools for protein modeling

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



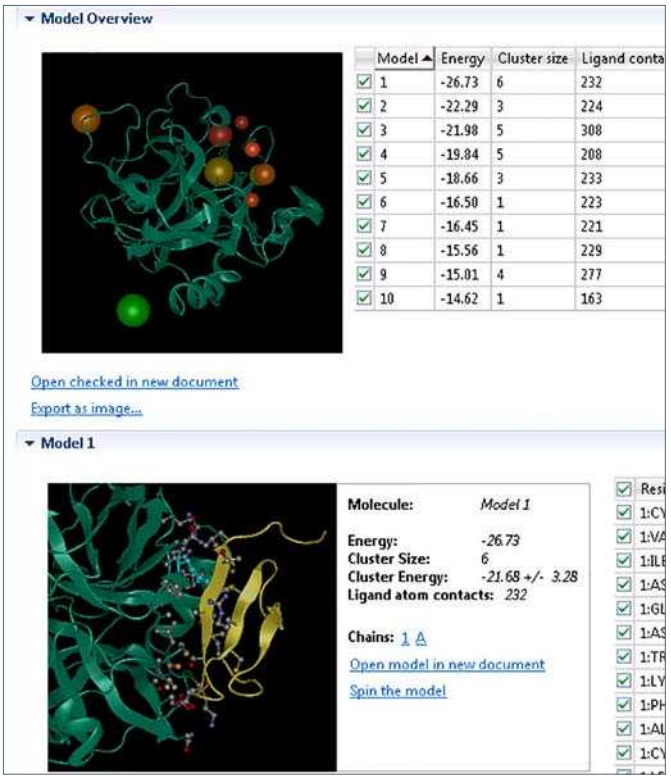
NovaFold model with predicted ligand binding TM-Score: 0.99±0.04; RMSD: 1.61±1.42



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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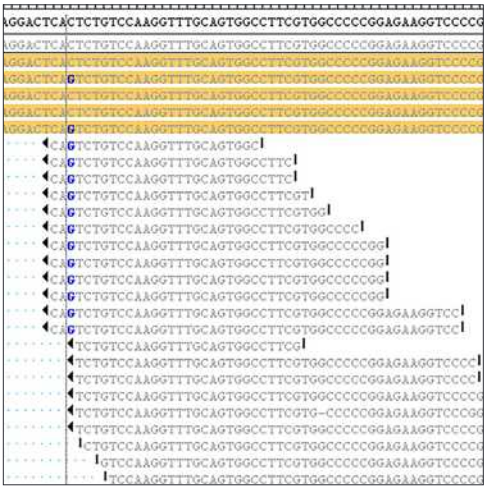
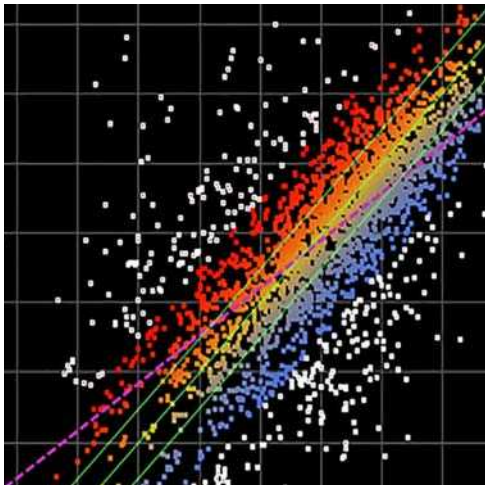
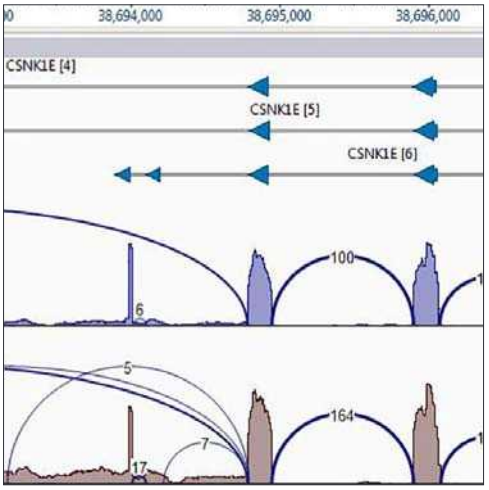
LASERGENE GENOMICS

Supporting all major NGS workflows and technologies







RESEQUENCING AND GENOTYPING

- Reference guided alignment for any size project
- Cancer genomics
- Copy number variation (CNV) calculation
- Sanger validation of NGS assemblies and variant calls
- Variant detection accuracy >99%
- SNP to structure worklfow for modeling impact of mutations on protein structure

GENOME ASSEMBLY AND EDITING

- *De novo* genome assembly and contig editing
- Editing and gap closure for reference-guided alignments

TRANSCRIPTOME ANALYSIS

- *De novo* transcriptome assembly with auto-mRNA annotation
- RNA-Seq gene expression analysis and statistics, including DESeq2 and EdgeR
- ChIP-Seq peak detection
- Microarray analysis
- miRNA discovery and quantification
- Combined analysis and visualization of gene expression data from multiple technologies

METAGENOMICS

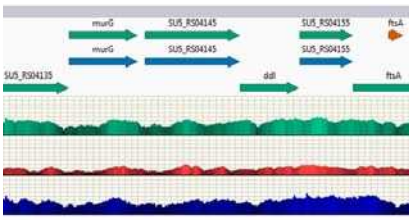
- Alignment of metagenomic sequencing data to biome genomes and gene databases
- *De novo* assembly of novel sequences

Perform NGS assembly, alignment, and variant calling quickly and accurately

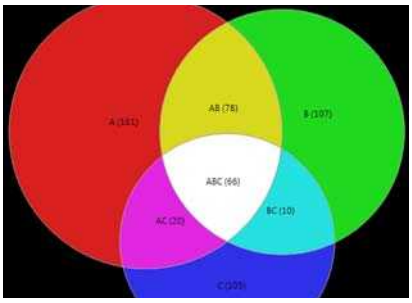
Accuracy and Speed Benchmarks

REFERENCE-GUIDED ALIGNMENT BENCHMARKS				
Data Set	**Number of Samples**	**Input Data (Gbases)**	**Assembly Time**	**Per-Sample Assembly Time**
Salmonella Genome	18	7	69 minutes	2.7 minutes
Human RNA-Seq	11	69	11 hours	55 minutes
Human Exome	10	68	8 hours	49 minutes
Human Genome	1	112	17 hours	17 hours
Human Genome	3	335	43 hours	14 hours

DE NOVO TRANSCRIPTOME ASSEMBLY BENCHMARKS				
Data Set	**Number of Reads (Millions)**	**Transcripts**	**Average Transcript Length**	**Assembly Time**
Human	100	30,342	975	15 hours
Water Bear	45	24,960	1,680	30 hours



Multiple genome assemblies



Venn diagram used to compare SNPs, genes & peaks

ACCURACY COMPARISONS FOR HUMAN EXOME VARIANT ANALYSIS USING NA12878							
Workflow	**Sensitivity**	**Specificity**	**False Discovery Rate**	**True Positives**	**False Positives**	**False Negatives**	**Elapsed Time**
Lasergene Genomics Suite	**99.56%**	**99.999%**	**1.29%**	**15,272**	**200**	**67**	**1.3 hr**
CLC Bio's Genomics Work-bench 8.0	99.18%	99.995%	7.41%	15,553	1,245	288	3.1 hr
Geneious 8.1	91.68%	99.995%	7.82%	14,827	1,257	1,346	2.9 hr
BWA Mapper / GATK Unified Genotyper	99.09%	99.999%	1.08%	15,161	166	139	6.0 hr
BWA Mapper / GATK Haplotype Base Caller	99.14%	99.999%	0.97%	15,168	149	132	6.3 hr

Sequencing Platforms

Illumina
Ion Torrent
PacBio

Operating Systems

Windows
Macintosh

DNASTAR Cloud

Hardware Requirements

16-32 GB RAM
Quad-Core 3 GHz processor
Two 1-4 TB hard drives*
**For ref-guided alignments on local computers*

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