



DNASTAR LASERGENE SOFTWARE SITE LICENSE



Overview

All researchers at the Albert Einstein College of Medicine have access to the complete DNASTAR Lasergene software package. This includes a comprehensive set of tools for molecular biology, genomics and protein analysis. A detailed list of features is shown below.

Download Lasergene at:

<https://www.dnastar.com/albert-einstein-college-of-medicine-site-license/>

LASERGENE MOLECULAR BIOLOGY Essential sequence analysis software

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

MULTIPLE SEQUENCE ALIGNMENT

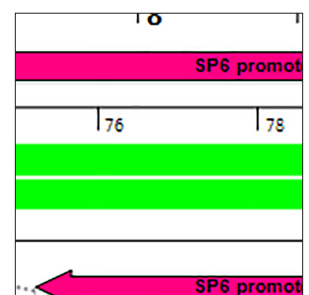
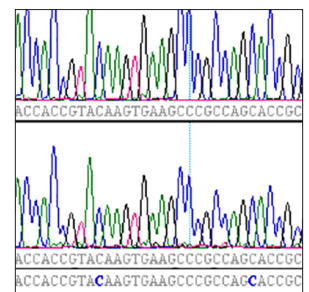
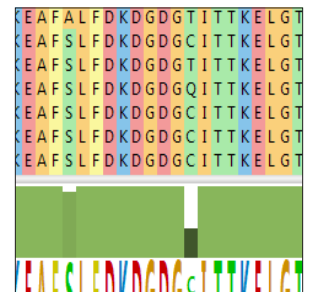
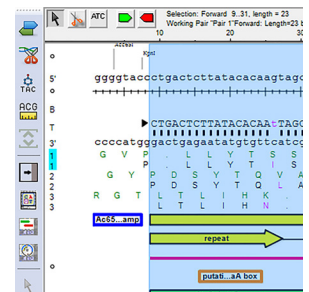
- Many popular multiple and pairwise sequence alignment methods, including MUSCLE, MAFFT, Clustal Omega, Clustal W, and ParaSail
- Whole genome alignment using MAUVE
- Customizable phylogenetic trees

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 annotation
- Sequence editing
- Agarose gel simulations
- Gene discovery
- Integrated BLAST searching
- Publication quality graphics



LASERGENE GENOMICS

Support for all major NGS 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 workflow for modeling impact of mutations on protein structure

GENOME ASSEMBLY AND EDITING

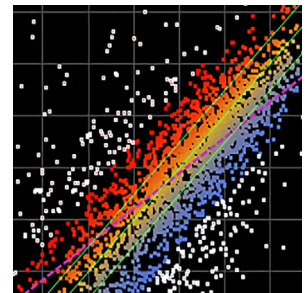
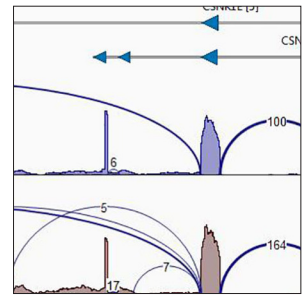
- *De novo* genome assembly and contig editing
- Editing and gap closure for reference-guided alignments

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



LASERGENE PROTEIN

Protein structure and sequence analysis

PROTEIN SEQUENCE ANALYSIS

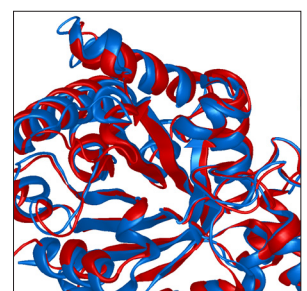
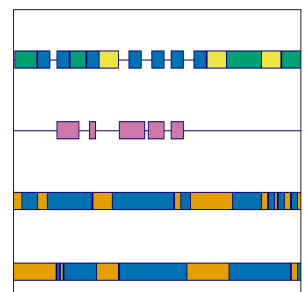
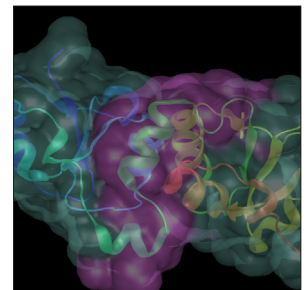
- Utilize integrated views and analysis methods for sequence, secondary structure, and tertiary structure
- Predict secondary structure characteristics

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



Learn More

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<https://www.dnastar.com/albert-einstein-college-of-medicine-site-license/>