

LASERGENE VERSION COMPARISON

Lasergene Molecular Biology

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Pairwise and Multiple Sequence Alignment

Create phylogenetic trees using the IQ-Tree maximum likelihood method			•
Create and search local sequence databases, including BLAST databases imported from NCBI			•
Analyze gene homology in bacterial genomes or eukaryotic chromosomes		•	•
Add, remove, or shuffle gaps in an alignment		•	•
Create multiple phylogenetic trees for one alignment using different methods		•	•
Create trees using two new Maximum Likelihood methods: RAXML and RAXML-NG		•	•
Align cDNA sequences to chromosomes using a specialized alignment method		•	•
See molecular wt, charge, aliphatic index, instability index and more for amino acid selections		•	•
Analyze variants in viral, mitochondrial, and chloroplast genomes		•	•
Perform BLAST and Entrez searches against a MegAlign Pro alignment	•	•	•
Enjoy updated views and enhanced user controls in MegAlign Pro	•	•	•

Sanger Sequence Assembly and Analysis

Manually trim Sanger trace file sequences more efficiently		•	•
Save and share default project parameters for Sanger assemblies		•	•
Easily export an image of your assembly in PDF, BMP, or PPT format		•	•
Trim vectors and take advantage of an extensive, built-in vector database		•	•
Easily analyze and visualize variants in multiple samples		•	•

Cloning, Primer Design, and Gene Detection

Use a simple wizard to create precise and scarless Golden Gate clones with automated domestication			•
Automatically clone one or more fragments simultaneously using batch cloning		•	•
Import VectorNTI, Geneious, and Clone Manager Suite file types	•	•	•
Perform PCR site-directed mutagenesis and predict the impact of a mutation on protein structure	•	•	•

Add our Genomics and Protein Applications to Complete Your Lasergene Package!

See reverse side for details.



Next-Gen Sequence Assembly and Alignment

Assemble and analyze phased variants using long-read data up to human genome length			•
Access Gene Set Enrichment (GSEA) data for differential expression assemblies created with RNA-Seq data			•
Auto-generate PCA/Volcano plots for differential gene expression using EdgeR or DESeq2	•		•
Access updated human genome templates for whole exome/genome variant analysis	•		•
Import BAM files	•		•
Enjoy improved reporting for metagenomics data	•		•
Align PacBio HiFi and ONT long read data and locate variants	•		•
Assemble viral genomes using ARTIC protocol data	•		•
<i>De novo</i> assemble genomes using PacBio HiFi reads	•		•
Polish Canu or Spades assemblies of PacBio and Oxford Nanopore long read data	•		•
Quantitate and analyze miRNA gene expression levels	•		•
Use integrated DNASTAR Cloud Assembly for projects exceeding your hardware capacity	•	•	•

Variant Detection and Analysis

Import SeqMan NGen assembly files and BAM, BED, and VCF files into the same GenVision Pro session for multi-sample variant comparison			•
Filter variants in numerous useful ways, and create and compare variant sets			•
During downstream analysis, compare results to local sequence databases, including databases imported from NCBI			•
Cross-reference variant data in genomic literature using integrated access to Mastermind	•		•
Use our updated Variant Annotation Database, which now includes dbNSFP version 4.1	•		•
View updates to the variants table in real-time as filters are applied	•		•
Compare and analyze multiple VCF files from other NGS software pipelines	•		•
Model detected variants on protein structure with updated protein design workflow*	•	•	•

Lasergene Protein

Macromolecular Structure, Motion, and Function

Create and search local sequence databases, including BLAST databases imported from NCBI			•
Enjoy photo-realistic images in Protean 3D, thanks to a new rendering engine	•		•
Predict the structure of a multimeric assembly using AlphaFold-Multimer*	•		•
Make precision selections on a structure in Protean 3D's Structure view	•		•
Create custom labels for atoms, residues, and other structural components	•		•
Export 3D models for use in other applications	•		•
Improve fold stability and developability using new protein design tools*	•	•	•
Search the BLAST and Entrez databases from within Protean 3D	•	•	•

* Additional subscription may be required to access protein modeling and design programs