DNASTAR LASERGENE

VERSION COMPARISON GUIDE

Lasergene Molecular Biology

	16	17	18
Pairwise and Multiple Sequence Alignment			
Easily build and manage custom databases for plasmid auto-annotation *new feature!*			•
Create local sequence databases or import and save BLAST databases from NCBI to enable lightning-fast local BLAST searches *now available in SeqBuilder Pro, too*			•
Create trees using any of three Maximum Likelihood methods: IQ-Tree, RAxML, or RAxML-NG			•
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		•	•
Align cDNA sequences to chromosomes using a specialized alignment method		•	•
Analyze variants in viral, mitochondrial, and chloroplast genomes		•	•
Perform BLAST and Entrez searches against a MegAlign Pro alignment	•	•	•
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 .pptx 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			
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.

608.258.7420 USA
866.511.5090 USA toll free
0.808.271.1041 UK
0.800.182.4747 Germany
1202 Ann Street
Madison, WI 53713
www.dnastar.com
info@dnastar.com

Lasergene Genomics

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Next-Gen Sequence Assembly and Alignment			
Align Iso-Seq data and visualize mRNA isoforms in a dedicated alignment track *new feature!*			•
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		•	•
Align PacBio HiFi and ONT long read data and locate variants		•	•
Assemble viral genomes using ARTIC protocol data		•	•
De novo 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			
Analyze variants in paired tumor/normal samples with GATK's MUTECT2 *new feature!*			•
Filter variants by chromosome and across tracks *new feature!*			•
Import SeqMan NGen assembly files and BAM, BED, and VCF files into the same GenVision Pro session for multi-sample variant comparison			•
Use an integrated genome browser to filter variants in a variety of ways (incl. by Venn diagram) and create and compare variant sets			•
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

	16	17	18
Macromolecular Structure, Motion, and Function			
Model protein interactions with DNA, RNA, and small molecules using the Boltz-2 algorithm*, a competitive analogue of AlphaFold 3 *new feature!*			•
Create local sequence databases or import and save BLAST databases from NCBI to enable lightning-fast local BLAST searches			•
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		•	•
Enjoy photo-realistic images in Protean 3D, thanks to a new rendering engine		•	•
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