DNASTAR

LASERGENE VERSION COMPARISON

Lasergene Molecular Biology	15	16	17
Pairwise and Multiple Sequence Alignment			
Variant analysis for viral, mitochondrial, and chloroplast genomes *New in Lasergene 17.4*			●
MAFFT7 algorithm for faster alignments of viral genomes and 16S data sets			●
High-capacity, customizable distance tables that support large data sets			●
Improved alignment report that can be configured and exported			●
RAxML, for Maximum Likelihood phylogenetic inference calculation			●
Support for multiple phylogenetic trees in a single alignment			●
Perform BLAST and Entrez searching from **MegAlign Pro** alignments		●	●
Updated views and enhanced user controls in **MegAlign Pro**		●	●
Export editable images to PowerPoint	●	●	●
Profile alignment functionality to merge alignments or additional sequences	●	●	●
Sanger Sequence Assembly and Analysis			
Full integration of **SeqMan NGen** into **SeqMan Ultra** for streamlined assembly			●
Easily export an image of your assembly in PDF, BMP, or PPT format			●
Improved vector trimming with extensive, built-in vector database			●
Easy multiple-sample variant analysis and visualization			●
New 64-bit **SeqMan Ultra** application with better performance and increased capacity			●
Assess read alignment, coverage, and SNPs	●	●	●
Assemble reads *de novo* or against one or more reference sequences	●	●	●
Cloning, Primer Design, and Gene Detection			
Batch cloning to automatically clone one or more fragments simultaneously			●
Enhanced support for VectorNTI, Geneious, and Clone Manager Suite file types		●	●
PCR site-directed mutagenesis with ability to predict impact of mutation on protein structure		●	●
Agarose gel simulation functionality	●	●	●
Plasmid auto-annotation (single or batch) using curated database	●	●	●
Automated virtual cloning: site-directed, TA, TOPO, Gateway, InFusion, GeneArt, and Gibson Assembly	●	●	●
PCR primer design	●	●	●

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

See reverse side for details.

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Lasergene Genomics

	15	16	17
Next-Gen Sequence Assembly and Alignment			
Expanded viral genome assembly to support data from ARTIC protocols			●
Support for *de novo* genome assembly with PacBio HiFi reads			●
Full integration of **SeqMan NGen** into **SeqMan Ultra** for streamlined assembly			●
Unique, mutli-sample visualization to view and compare assembled sequences			●
Support for combining multiple projects of the same type into a single project			●
64-bit **SeqMan Ultra** application for project analysis with better performance and increased capacity			●
Auto-analysis of hardware and data to determine if assembly should be run locally or on the Cloud			●
Ability to polish Canu or Spades assemblies of PacBio and Oxford Nanopore long read data			●
miRNA quantitation workflow to quantitate and analyze miRNA gene expression levels			●
Integrated **DNASTAR Cloud Assemblies** for projects that exceed the capacity of your hardware		●	●
Quick access to NGS and Sanger project setup in the new **DNASTAR Navigator**		●	●
Enhanced RNA-Seq statistics with DESeq and edgeR from Bioconductor	●	●	●
RNA-Seq analysis for model and non-model organisms	●	●	●
Gene panel workflows with control validation	●	●	●
De novo genome and transcriptome assembly	●	●	●
Variant Detection and Analysis			
Mastermind integration to cross-reference variant data in genomic literature			●
Updated **Variant Annotation Database** includes dbNSFP version 4.1			●
Live variant report updates variants in real-time, as filters are applied			●
Ability to compare and analyze multiple VCF files from other NGS software pipelines			●
Model detected variants on protein structure with updated protein design workflow*		●	●
Combine variant and PDB annotations to predict potential effects on protein structure*	●	●	●
Combine SNP and CNV analysis with any workflow	●	●	●
Direct comparison to dbSNP and GERP and dbNSFP databases	●	●	●

Lasergene Protein

	15	16	17
Macromolecular Structure, Motion, and Function			
Ability to import UniProt files, with full support for displaying annotations			●
Support for exporting data used to generate Analysis View tracks			●
Protein design tools to improve fold stability and developability*		●	●
Integrated BLAST and Entrez searching in Protean 3D		●	●
Mutation modeling and neighbor search to analyze SNP impact on protein structure	●	●	●
Access to **NovaDock** protein-protein docking, analysis and visualization*	●	●	●
Access to **NovaFold** and **NovaFold Antibody** structure prediction*	●	●	●
Protein function and ligand binding site prediction*	●	●	●
B-cell epitope prediction	●	●	●

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