

LASERGENE VERSION COMPARISON

Lasergene Molecular Biology

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Pairwise and Multiple Sequence Alignment

User-customized layouts to quickly apply preferred styling and view organization <i>New in Lasergene 17.2</i>	•	•	•
Improved distance table with more statistical options and easier customization <i>New in Lasergene 17.2</i>	•	•	•
RAxML, for Maximum Likelihood phylogenetic inference calculation	•	•	•
Support for multiple phylogenetic trees in a single alignment	•	•	•
Expanded sequence and alignment editing capabilities	•	•	•
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 <i>New in Lasergene 17.2</i>	•	•	•
Easily export an image of your assembly in PDF, Bitmap, or PPT format <i>New in Lasergene 17.2</i>	•	•	•
Improved vector trimming with built-in extensive vector database <i>New in Lasergene 17.2</i>	•	•	•
Easy multiple-sample variant analysis and visualization	•	•	•
Live variant report updates variants in real-time, as filters are applied	•	•	•
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 & Protein Applications to Complete Your Lasergene Package!
 See reverse side for details.

Next-Gen Sequence Assembly and Alignment

Full integration of SeqMan NGen into SeqMan Ultra for streamlined assembly <i>New in Lasergene 17.2</i>			●
Jobs panel allows for convenient management of local and cloud assemblies <i>New in Lasergene 17.2</i>			●
Unique, multi-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			●
Redesigned SeqMan NGen with better guidance for project setup			●
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 <i>New in Lasergene 17.2</i>			●
Updated Variant Annotation Database includes dbNSFP version 4.1 <i>New in Lasergene 17.2</i>			●
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

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 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