

LASERGENE VERSION COMPARISON

Lasergene Molecular Biology	15	16	17
Pairwise and Multiple Sequence Alignment			
RAxML, for Maximum Likelihood phylogenetic inference calculation New in Lasergene 17·1			•
Support for multiple phylogenetic trees in a single alignment New in Lasergene 17-1			•
Expanded sequence and alignment editing capabilities New in Lasergene 17-1			•
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	•	•	•
MAFFT, MUSCLE, Mauve, and Clustal Omega alignment algorithms	•	•	•
Sanger Sequence Assembly and Analysis			
Easy multiple-sample variant analysis and visualization New in Lasergene 17-1			•
Option for quick "Run Now" to bypass step-by-step wizard New in Lasergene 17-1			•
Live variant report updates variants in real-time, as filters are applied New in Lasergene 17-1			•
New 64-bit SeqMan Ultra application with better performance and increased capacity			•
Access to data from dbNSFP, 1000 Genomes, and ESP's Exome Variant Server for variant analysis			•
New hybrid reference-guided/de novo assembly workflow			•
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 New in Lasergene 17-1			•
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	•	•	•
Automated clone verification workflow	•	•	•
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.

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Next-Gen Sequence Assembly and Alignment Unique, multi-sample visualization to view and compare assembled sequences New in Lesergene 17-1 • New retrovirus integration workflow New in Lesergene 17-1 • Support for combining multiple projects of the same type into a single project New in Lesergene 17-1 • Od bit SegMan Willra application for project analysis with better puriormanne and increased capacity • Redesigned SegMan Noam with better guidance for project study • Auto-analysis of hardware and data to determine it assembly should be run locally or on the Cloud • Auto-analysis of hardware and data to determine it desembly should be run locally or on the Cloud • Ability to polish Canu or Spades assemblies of Poello and Oxford Nanopore long read data • Ability to polish Canu or Spades assemblies of Poello and Oxford Nanopore long read data • Ability to polish Canu or Spades assembles for projects that is exceed the capacity of your hardware • Outcome 18-18 and	Lasergene Genomics	15	16	17
Unique, mutil-sample visualization to view and compare assembled sequences New in Lesergene 17:1 Support for combining mutiple projects of the same type into a single project New in Lesergene 17:1 Support for combining mutiple projects of the same type into a single project New in Lesergene 17:1 Support for combining mutiple projects of the same type into a single project New in Lesergene 17:1 Support for combining mutiple projects of the same type into a single project New in Lesergene 17:1 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 Pacibia and Oxford Nanopore long read dota 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 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 OR RNA-Seq analysis for model and non-model organisms De novo genome and transcriptome assembly Variant Detection and Analysis Live variant betection and Analysis Live variant report updates variants in real-time, as fifters are applied New in Lesergene 17:1 Ability to compare and analyze multiple VCF files from other NCS software pipelines Model detected variants on protein structure with updated protein design workflow* Ornbine SNP and CNV analyzes with any workflow SNP detection accuracy -99-8% Direct comparison to dbSNP and SERP and dbNSFP databases Lasergene Protein Lasergene Protein Lasergene Protein Support for exporting data used to generate Analysis View tracks New in Lesergene 17:1 Support for exporting data used to generate Analysis View tracks New in Lesergene 17:1 Protein design tools to improve fold stability and developability* Integrated BLAST and Entrez searching	Next-Gen Sequence Assembly and Alignment			
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DNASTAR