DNASTAR®
Software for Life Scientists

LASERGENE VERSION COMPARISON

Lasergene Molecular Biology	15	16	17
Sanger Sequence Assembly and Analysis			
New 64-bit SeqMan Ultra application with better performance and increased capacity			●
Improved algorithms for increased accuracy of Sanger assemblies			●
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			
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		●	●
Access SeqBuilder Pro as a standalone application		●	●
Agarose gel simulation in SeqBuilder Pro	●	●	●
Automated clone verification workflow	●	●	●
Batch sequence editing built-in to SeqBuilder Pro	●	●	●
New SeqBuilder Pro application for sequence editing and analysis	●	●	●
Quick search and selection of enzymes	●	●	●
Collapsible and sortable feature and primer lists	●	●	●
Plasmid auto-annotation (single or batch) using curated database	●	●	●
Automated virtual cloning: site-directed, TA, TOPO, Gateway, InFusion, GeneArt and Gibson Assembly	●	●	●
Design customized primer pairs	●	●	●
Pairwise and Multiple Sequence 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	●	●	●
MAFFT, MUSCLE, Mauve, and Clustal Omega alignment algorithms	●	●	●
Align sequences and create phylogenetic trees	●	●	●

Add our Genomics & 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			
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	●	●	●
Visualization, browsing , isoform analysis and multi-sample comparison in GenVision Pro	●	●	●
RNA-Seq analysis for model and non-model organisms	●	●	●
Automatic mRNA annotation using RefSeq	●	●	●
Gene panel workflows with control validation	●	●	●
Reference-guided assembly for any size genome on a desktop computer	●	●	●
De novo genome and transcriptome assembly	●	●	●
Variant Detection and Analysis			
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	●	●	●
Access to allele and genotype frequencies for SNPs	●	●	●
SNP detection accuracy >99.8%	●	●	●
Direct comparison to dbSNP and GERP and dbNSFP databases	●	●	●

Lasergene Protein

	15	16	17
Macromolecular Structure, Motion, and Function			
Automated hot spot scanning to locate residues that are important for protein fold stability*		●	●
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	●	●	●
Protein composition analysis	●	●	●
Export editable images to PowerPoint and PDF	●	●	●
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 acess protein modeling and design programs*