

LASERGENE VERSION COMPARISON

Lasergene Molecular Biology

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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/ <i>de novo</i> assembly workflow			•
Assess read alignment, coverage, and SNPs	•	•	•
Assemble reads <i>de novo</i> 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.

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 Nanore 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	•	•	•
<i>De novo</i> 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

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 access protein modeling and design programs