

VERSION COMPARISON GUIDE

Lasergene Molecular Biology

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Cloning, Primer Design, and Sequence Analysis

Save files, images and tables from SeqBuilder Pro to your SciNote electronic lab notebook (ELN), improving data organization, collaboration, traceability, and regulatory compliance			•
Identify a microbial strain using PubMLST data via a utility in the DNASTAR Navigator			•
Create precise and scarless Golden Gate clones with automated domestication		•	•
Automatically clone one or more fragments simultaneously using batch cloning	•	•	•

Pairwise and Multiple Sequence Alignment

Hear nucleotide and amino acid residues spoken aloud while entering sequences manually or configuring BLAST search queries (multiple Lasergene packages)			•
Easily build and manage custom databases for plasmid auto-annotation		•	•
Create local sequence databases or import and save BLAST databases from NCBI to enable lightning-fast local BLAST searches		•	•
Create trees using any of three Maximum Likelihood methods: IQ-Tree, RAxML, or RAxML-NG		•	•
Analyze gene homology in bacterial genomes or eukaryotic chromosomes	•	•	•
Add, remove, or shuffle gaps in an alignment	•	•	•
Create multiple phylogenetic trees for one alignment using different methods	•	•	•
Align cDNA sequences to chromosomes using a specialized alignment method	•	•	•
Analyze variants in viral, mitochondrial, and chloroplast genomes	•	•	•

Sanger Sequence Assembly and Analysis

Manually trim Sanger trace file sequences more efficiently	•	•	•
Save and share default project parameters for Sanger assemblies	•	•	•
Easily export an image of your assembly in .pdf, .bmp, or .pptx format	•	•	•
Trim vectors and take advantage of an extensive, built-in vector database	•	•	•
Easily analyze and visualize variants in multiple samples	•	•	•

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

See reverse side for details.



Lasergene Genomics

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Next-Gen Sequence Assembly and Analysis

Automatically annotate FASTA files or annotate during <i>de novo</i> assembly in SeqMan NGen using AUGUSTUS and Swiss-Prot information				•
Quickly find ORFs, splice sites, and transcription factor binding sites using automated data tracks that detect and mark each feature with unique visual indicators				•
Assemble and analyze data generated on the Element sequencing platform				•
Characterize B-cell clonotypes and recover paired antibody chain sequences from 10x Genomics immune profiling data with a new beta workflow for single-cell V(D)J antibody repertoire analysis				•
Align Iso-Seq data and visualize mRNA isoforms in a dedicated alignment track			•	•
Access Gene Set Enrichment (GSEA) data for differential expression assemblies created with RNA-Seq data			•	•
Auto-generate PCA/Volcano plots for differential gene expression using EdgeR or DESeq2	•	•	•	

Variant Detection and Analysis

Experience optimized SeqMan NGen assembly performance for up to 2x faster processing compared to Lasergene 18.1				•
Analyze variants in paired tumor/normal samples with GATK's MUTECT2			•	•
Filter variants by chromosome and across tracks			•	•
Import SeqMan NGen assembly files and BAM, BED, and VCF files into the same GenVision Pro session for multi-sample variant comparison			•	•
Use an integrated genome browser to filter variants in a variety of ways (incl. by Venn diagram) and create and compare variant sets			•	•
Align PacBio HiFi and ONT long-read data and locate variants	•	•	•	
Cross-reference variant data in genomic literature using integrated access to Mastermind	•	•	•	

Lasergene Protein

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Macromolecular Structure, Motion, and Function

Set up Boltz, AlphaFold-Multimer, NovaDock, and NovaFold Antibody predictions through a guided structure prediction wizard				•
Easily configure multiple structure predictions using a common fixed input and a series of variable protein or ligand binders				•
Run Boltz, NovaDock, and NovaFold Antibody predictions locally* for enhanced data security and unrestricted usage				•
Choose from multiple Amber force fields in the protein design workflow				•
Model protein interactions with Boltz, a competitive analogue of AlphaFold 3			•	•
Create local sequence databases or import and save BLAST databases from NCBI to enable lightning-fast local BLAST searches			•	•
Predict the structure of a multimeric assembly using AlphaFold-Multimer	•	•	•	
Create custom labels for atoms, residues, and other structural components	•	•	•	

* NovaLocal licensed separately