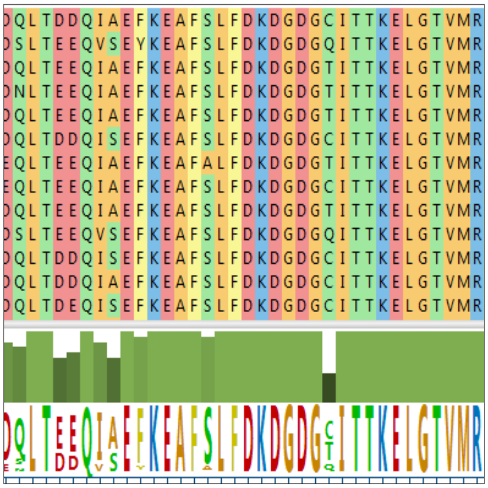
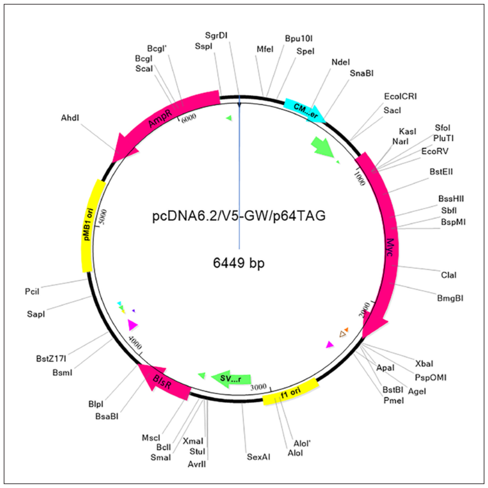
DNASTAR

LASERGENE

LASERGENE MOLECULAR BIOLOGY

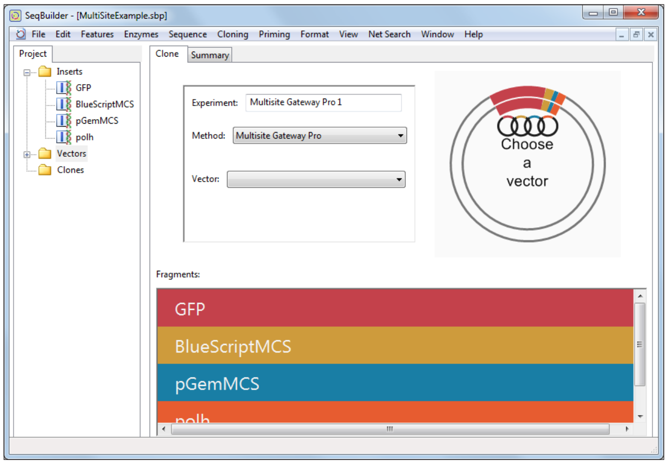
Essential software for sequence analysis





COMPREHENSIVE SEQUENCE ANALYSIS

- Create and organize sequence databases to enable lightning-fast local BLAST searches
- Edit sequences and discover genes
- Translate one or many sequences simultaneously
- Use the curated annotation database or create and manage your own databases for plasmid auto-annotation
- Simulate movement through an agarose gel
- Create flexible plasmid maps



Experiment: Multisite Gateway Pro 1

Method: Multisite Gateway Pro

Vector:

Fragments:

GFP

BlueScriptMCS

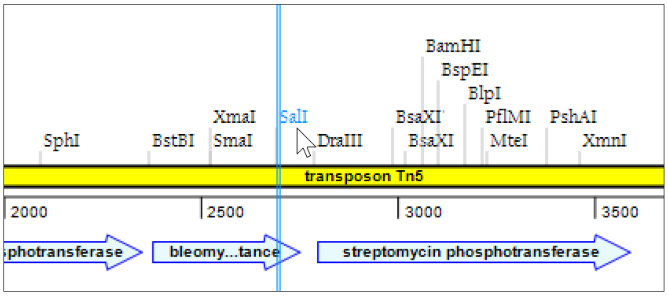
pGemMCS

polh

SeqBuilder Pro provides an easy-to-use wizard for setting up precise and scarless Golden Gate clones.

PRIMER DESIGN AND VIRTUAL CLONING

- Use any major cloning method, including Golden Gate, Gibson Assembly, InFusion, Gateway, Multisite Pro Gateway, TOPO cloning, TA cloning, and restriction enzyme techniques
- Design and customize primers and probes
- Create and share primer catalogs



SeqBuilder Pro lets you customize the appearance and types of restriction sites, features, translations, and more.

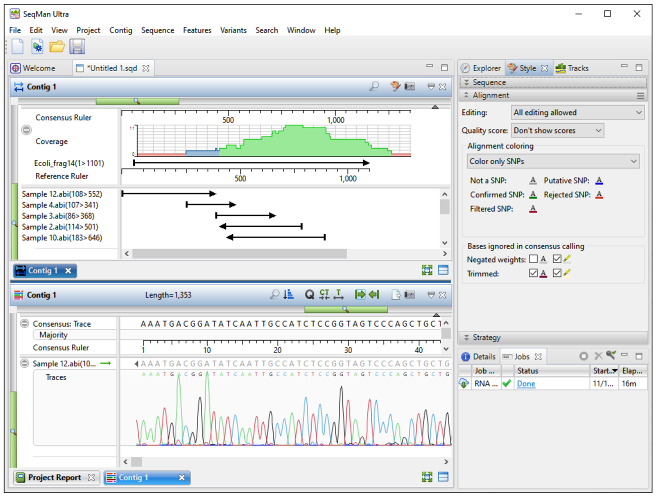
MULTIPLE SEQUENCE ALIGNMENT AND PHYLOGENETIC ANALYSIS

- Align DNA, RNA, or protein using Clustal Omega, Clustal W, MAFFT, MUSCLE, or Mauve
- Analyze gene homology in bacterial genomes or eukaryotic chromosomes
- Align cDNA sequences to chromosomes
- Evaluate variants across genomic strains
- Calculate trees using four popular algorithms, including Neighbor Joining (BIONJ), Maximum Likelihood: RAxML and RAxML-NG, and IQ-Tree

A MegAlign Pro project displaying three of its interactive views: the alignment view, the variants table, and the phylogenetic tree view.

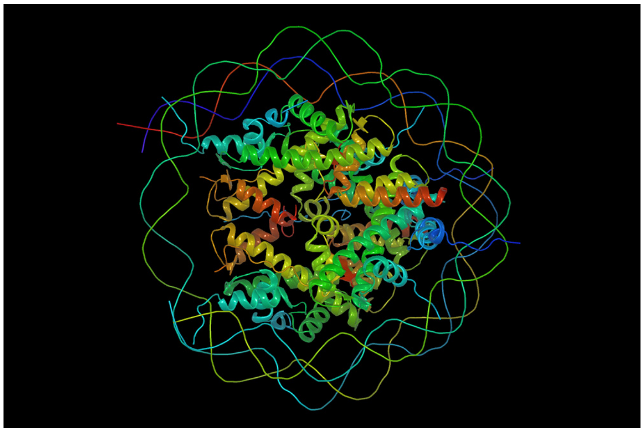
SANGER SEQUENCE ASSEMBLY AND ANALYSIS

- Assemble reads *de novo* or against one or more reference sequences
- Assess read alignment, coverage, and SNPs
- Analyze and visualize variants across samples
- Design sequencing primers to improve coverage
- Efficiently trim trace sequences using manual or automated trimming options



SeqMan Ultra lets you assemble and analyze Sanger data and can also perform downstream analysis for NGS and long-read assemblies created using Lasergene Genomics (see below).

For a complete bioinformatics solution, add Lasergene Genomics and Lasergene Protein



DNASTAR Lasergene includes tools for genomics and protein analysis that integrate seamlessly with the editing, analysis, and visualization tools in **Lasergene Molecular Biology**.

If you are working with next-generation sequencing or protein data, our full **DNASTAR Lasergene** package provides powerful tools and accurate results for all your bioinformatics analysis needs.

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