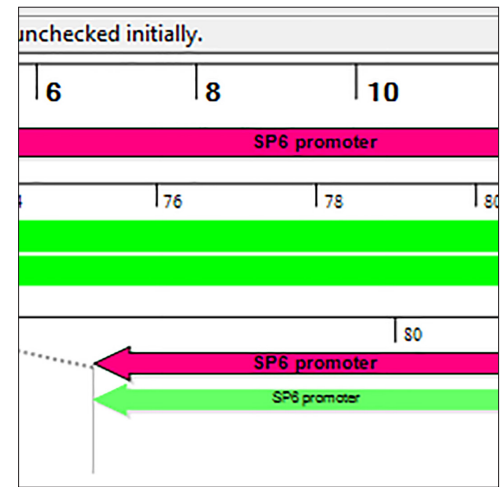
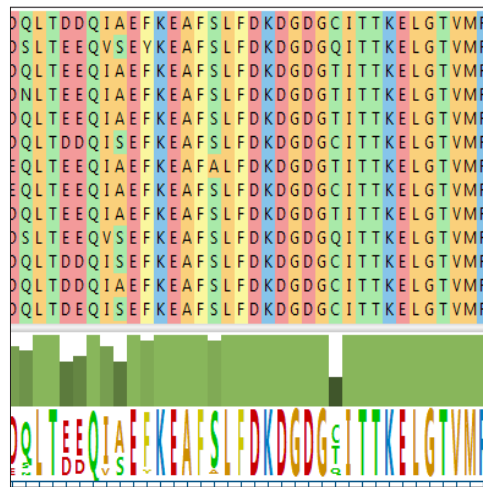
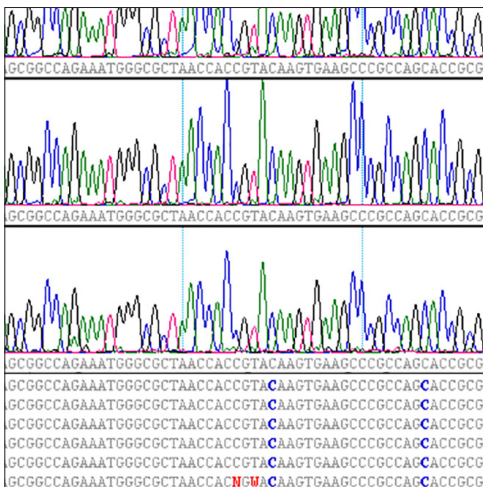


LASERGENE MOLECULAR BIOLOGY

Essential software for sequence analysis



MULTIPLE SEQUENCE ALIGNMENT

- Many popular multiple and pairwise sequence alignment methods, including MUSCLE, MAFFT, Clustal Omega, Clustal W, and ParaSail
- Whole genome alignment using MAUVE
- Customizable phylogenetic trees

VIRTUAL CLONING AND PRIMER DESIGN

- Support for all major cloning methods, including Gibson Assembly, InFusion, Gateway, Multisite Pro Gateway, TOPO, TA Cloning and restriction enzyme techniques
- Design and customize primers and probes
- Create and share primer catalogs

SANGER SEQUENCE ASSEMBLY

- Assemble reads *de novo* or against one or more reference sequences
- Assess read alignment, coverage and SNPs
- Design sequencing primers to improve coverage

COMPREHENSIVE SEQUENCE ANALYSIS

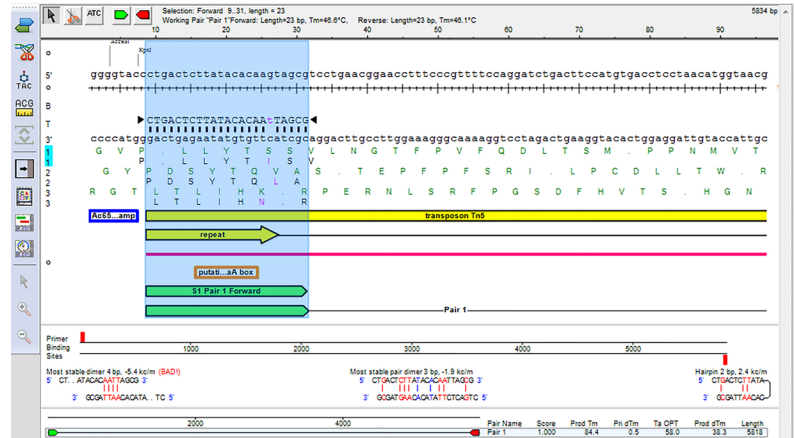
- Accurate and fast sequence auto-annotation
- Sequence editing, including automated and batch editing
- Agarose gel simulations
- Gene discovery
- Integrated BLAST searching
- Publication quality graphics

Flexible licensing and pricing options for any lab

SeqBuilder Pro

Just interested in the basics? Our flagship sequence editor lets you create sequence maps, perform virtual cloning, design primers, batch edit and annotate sequences, and much more!

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