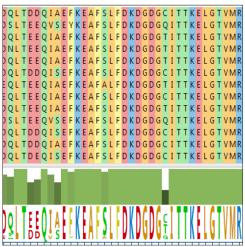


LASERGENE MOLECULAR BIOLOGY FOR STUDENTS AND EDUCATORS

Essential software for sequence analysis is now more easily accessible for students







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
- Integrated phylogenetic trees using RAxML, for Maximum Likelihood inference and bootstrapping calculations

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
- Easily visualize and compare multiple assemblies in a single project

COMPREHENSIVE SEQUENCE ANALYSIS

- Accurate and fast sequence auto-annotation
- Sequence editing, including automated and batch editing
- Agarose gel simulations
- Gene discovery

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