

# Lasergene<sup>®</sup>

## EditSeq

### A UTILITY FOR EDITING AND IMPORTING UNUSUAL FILE TYPE

EditSeq is provided with every Lasergene system to enable you to work on nucleic acid and protein sequences of all sizes from a variety of formats, including GenBank, FASTA, MacVector, GCG<sup>®</sup>, Text, ABI<sup>®</sup>, and data from the clipboard. You can even access NCBI's databases by accession number or utilizing the integrated internet interface to search BLAST and Entrez text databases.\* With EditSeq you can manually edit sequence, comments and annotations, conveniently separated into three panes. Dynamic links between sequence and annotations exhibit automatic updating of feature coordinates with sequence editing and inclusion of features with copying/pasting of sequences. Available functions include reverse complement, invert, translate, back-translate, and ORF identification.

### MAIN EditSeq WINDOW

The screenshot shows the EditSeq window for a file named 'tethis21.seq : SEQUENCE'. The window is divided into three main panes:

- Target sequence sections:** The top pane displays a DNA sequence with a scale bar at the top indicating positions 10, 20, 30, and 40. The sequence is shown in 8-line blocks, with line numbers 40, 80, 120, 160, 200, 240, and 280 on the right. A blue circle highlights a specific position in the sequence.
- Sequence comments pane:** The middle pane contains metadata for the sequence:
 

```

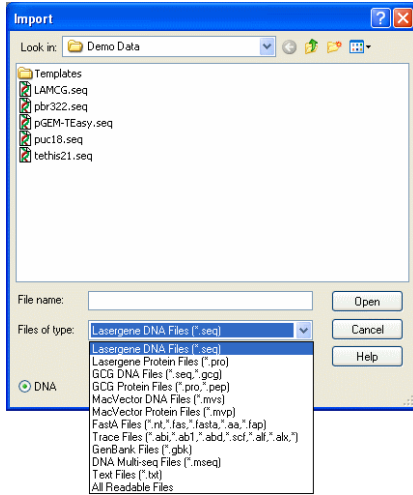
      LOCUS      TETHIS21MA          906 bp    D
      DEFINITION T.thermophila macronuclear histone H
      ACCESSION  M31332
      
```
- Annotation pane:** The bottom pane shows source and organism information:
 

```

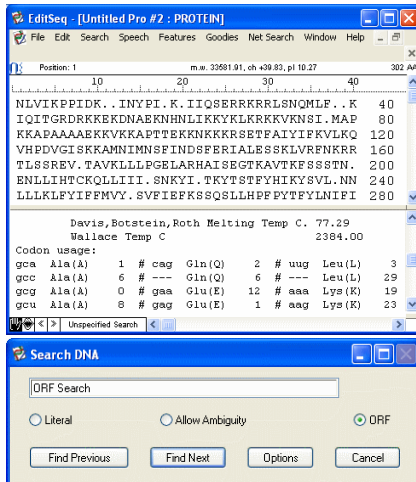
      source      1..906
      /organism="Tetrahymena thermophila"
      /mol_type=genomic DNA
      /db_xref="taxon:5911"
      
```

Three callout boxes with blue circles point to specific elements in the window: 'Target sequence sections' points to the sequence text, 'Sequence comments pane' points to the LOCUS/DEFINITION/ACCESSION block, and 'Annotation pane' points to the source/organism block.

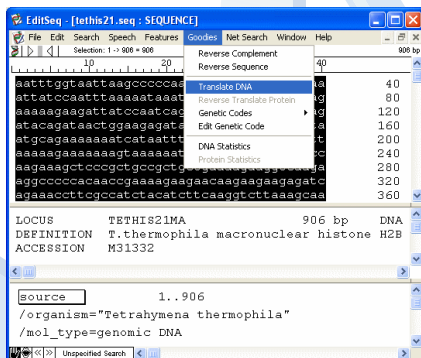
# EditSeq FEATURES



Enter a variety of file formats



Search for ORFs



Translate to Protein or view DNA statistics

## Sequence Entry

- I.U.B. nucleotide and protein codes fully supported Import Data from many other programs
- Download directly from NCBI\* using accession numbers, BLAST or Entrez text searches
- Proof reading by voice read back
- Keyboard entry and configuration for alphabetical or numeric control
- Feature coordinates automatically updated with sequence editing
- Sequences saved using EditSeq may be opened in other Lasergene modules for additional analysis

## Analysis

- Reverse complement sequence
- Translate DNA
- Back translate proteins
- Control and customize expression-specific codes
- Integrated BLAST and Entrez text searches\* search tools
- Copy/paste sequence includes contained annotations
- View statistics about any sequences or portion of a sequence

## Display

- Sequence, comments and annotations in separate, editable panes
- Feature creation utilizing NCBI's applicable feature keys
- Exon selection by triplet indicator
- ORF identification, selection and translation
- Sequence and annotations dynamically linked