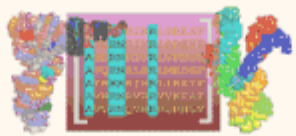
Back Forward Reload Home Search Netscape Print Security Shop Stop Netscape

Bookmarks Location: http://www.mbio.ncsu.edu/BioEdit/bioedit.html

Instant Interne MyPresario Search Activity Entertainment Retail Central Community Free Hotmail





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Tom Hall
Department of Microbiology
North Carolina State University

Biological sequence alignment editor for Windows 95/98/NT

BioEdit.zip (full installation 8.2 Mb)

Upgrade

Bug fixes / changes

BioEdit General information

BioDoc.pdf (pdf format help doc)

BioEdit.doc (MS Word document)

View Screenshots

BioEdit is a biological sequence alignment editor written for Windows 95/98/NT. A rich, intuitive multiple document interface with many convenient features makes alignment, manipulation and viewing of sequences relatively quick and easy on your desktop computer. Several sequence manipulation and analysis options and fully-automated links to local and WWW-based anaylsis programs facilitate an integrated working environment which allows you to view, align and analyze sequences from a single application with simple point-and-click operations.

BioEdit's features include:

- Several modes of hand alignment
- Automated ClustalW alignment
- Automated Blast searches (local and WWW)
- Plasmid drawing and annotation
- Accessory application configuration
- Restriction mapping
- RNA comparative analysis tools
- Graphical matrix data viewing tools
- Shaded alignment figures
- Translation-based nucleic acid alignment
- ABI trace viewing, editing and printing
- Highly customizable ... many more features

Note: Bug -- If you have version 5.0.0 or later, see here

Try PaperWorks, Tom's free journal article library/pdf organizer and viewer

VALUABLE Citeline Internet Research Software RESOURCE

Citeline.com

Enter disease, therapy or topic and click Search: Tips

Search

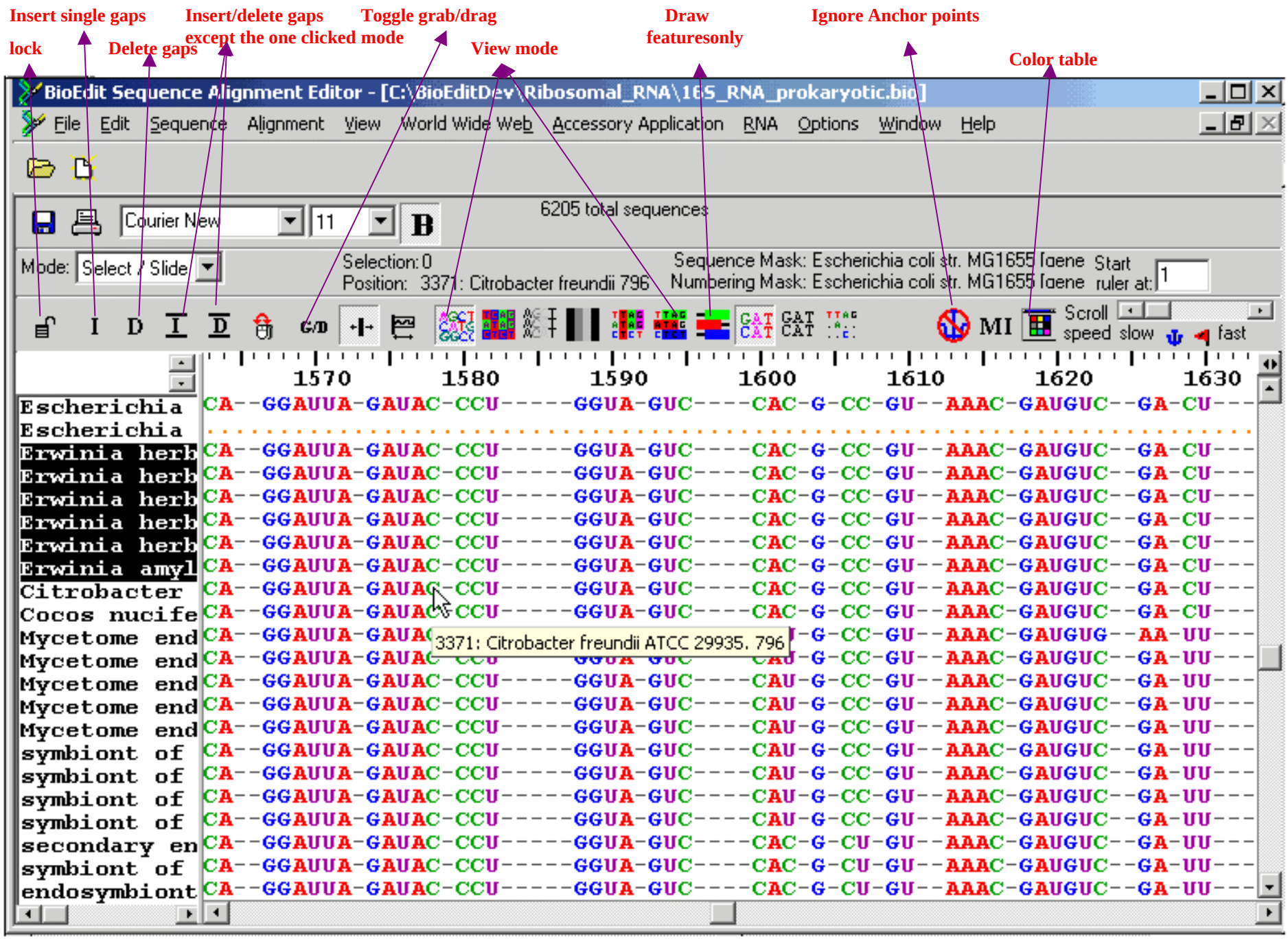
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Current version 5.0.9
Last updated 3/24/01
Tom Hall
tahall2@unity.ncsu.edu

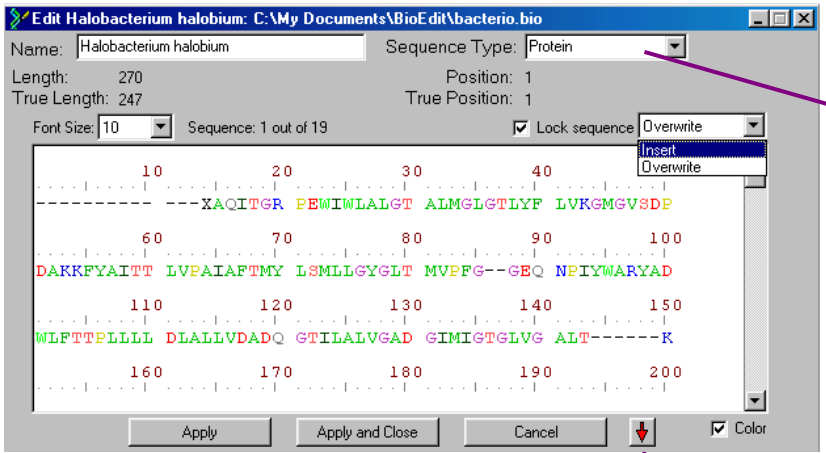
RNaseP database ReadMe file See screen shots Accessory applications Multi-file download email Tom

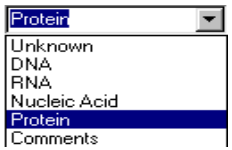
Introduction

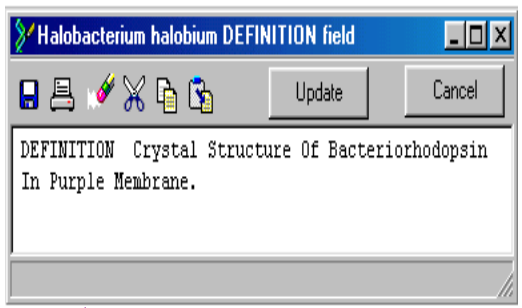
- **Developed by graduate student at North Carolina State University.**
- **C++ program written in Borland's C++ Builder with the Visual Component Library (VCL) of Delphi**
- **To provide basic functions for protein and nucleic acid editing, alignment, manipulation and analysis**
- **Not powerful sequence analysis program, but user friendly interface for sequence manipulation and linking to other, more scientific analysis programs, both local and WWW-based.**
- **Suitable for large alignments (≅ 20,000 sequences).**
- **Does not use excessive physical memory .**

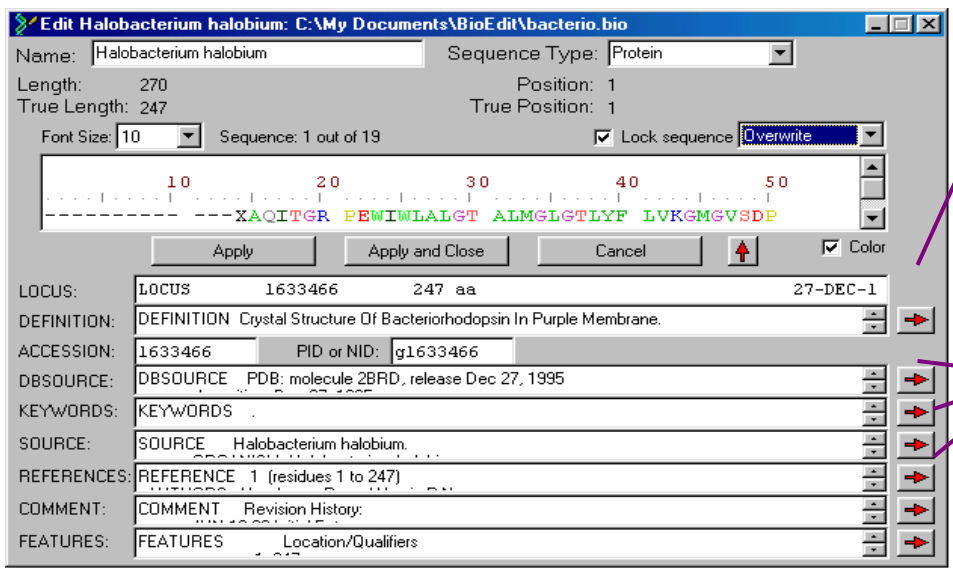

Insert single gaps lock
Delete gaps
Insert/delete gaps except the one clicked mode
Toggle grab/drag
View mode
Draw featuresonly
Ignore Anchor points
Color table
BioEdit Sequence Alignment Editor - [C:\BioEditDev\Ribosomal_RNA\16S_RNA_prokaryotic.bio]
File Edit Sequence Alignment View World Wide Web Accessory Application RNA Options Window Help
Courier New
11
6205 total sequences
Mode: Select / Slide
Selection: 0
Position: 3371: Citrobacter freundii 796
Sequence Mask: Escherichia coli str. MG1655 [gene
Numbering Mask: Escherichia coli str. MG1655 [gene
Start ruler at: 1
Scroll speed slow fast
1570 1580 1590 1600 1610 1620 1630
Escherichia
Escherichia
Erwinia herb
Erwinia herb
Erwinia herb
Erwinia herb
Erwinia herb
Erwinia amyl
Citrobacter
Cocos nucife
Mycetome end
Mycetome end
Mycetome end
Mycetome end
Mycetome end
symbiont of
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secondary en
symbiont of
endosymbiont
3371: Citrobacter freundii ATCC 29935, 796

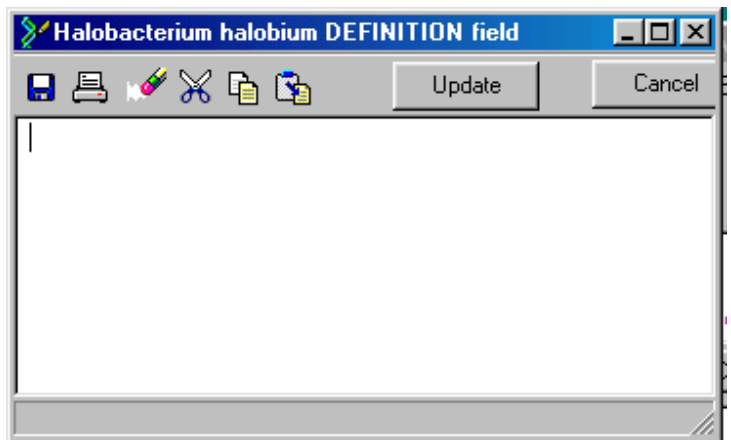
Editing /Adding sequences in Edit Box



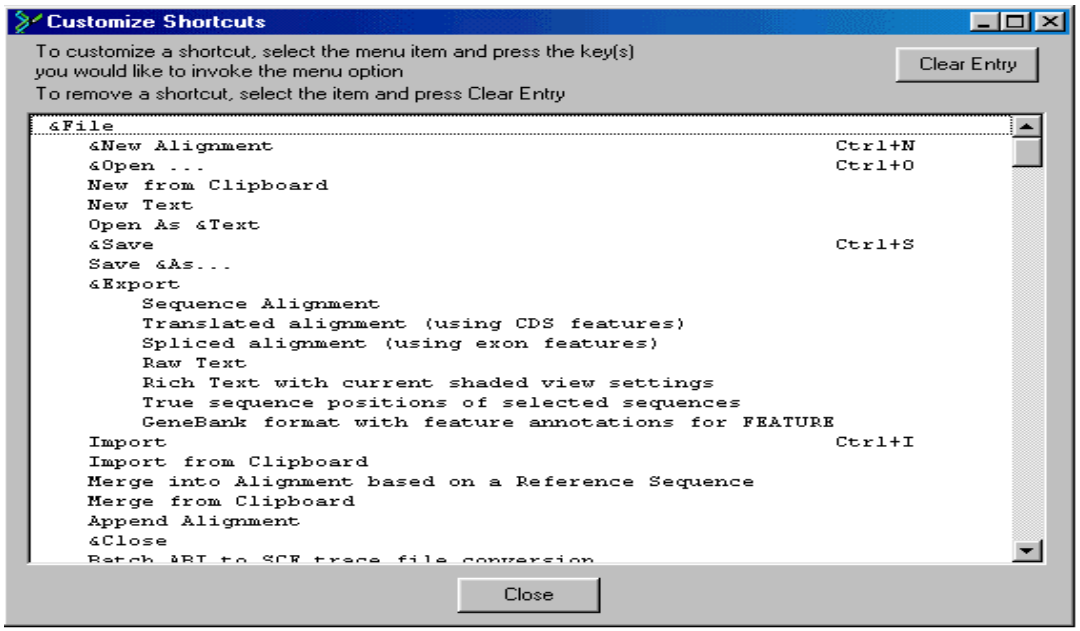




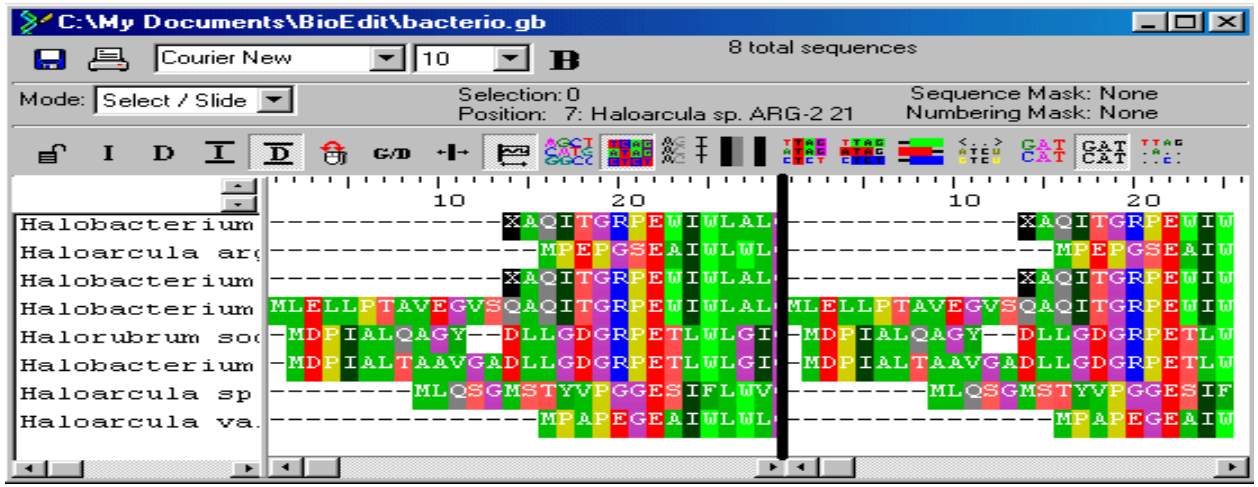




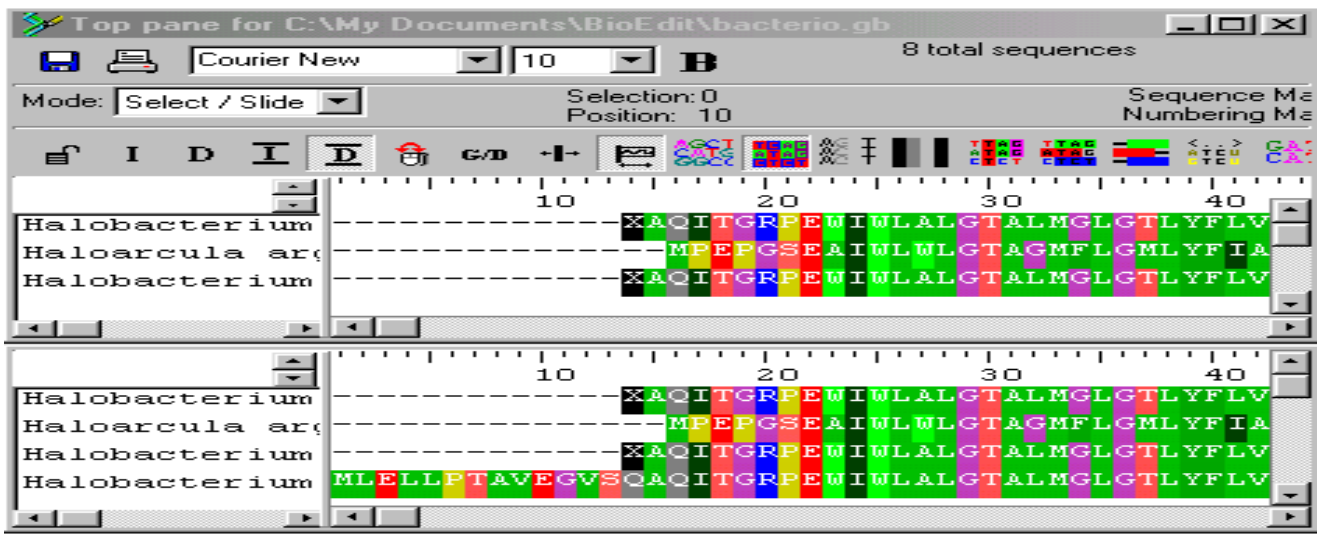
Customising shortcuts



Vertical split Window



Horizontal split window



Sorting Sequences

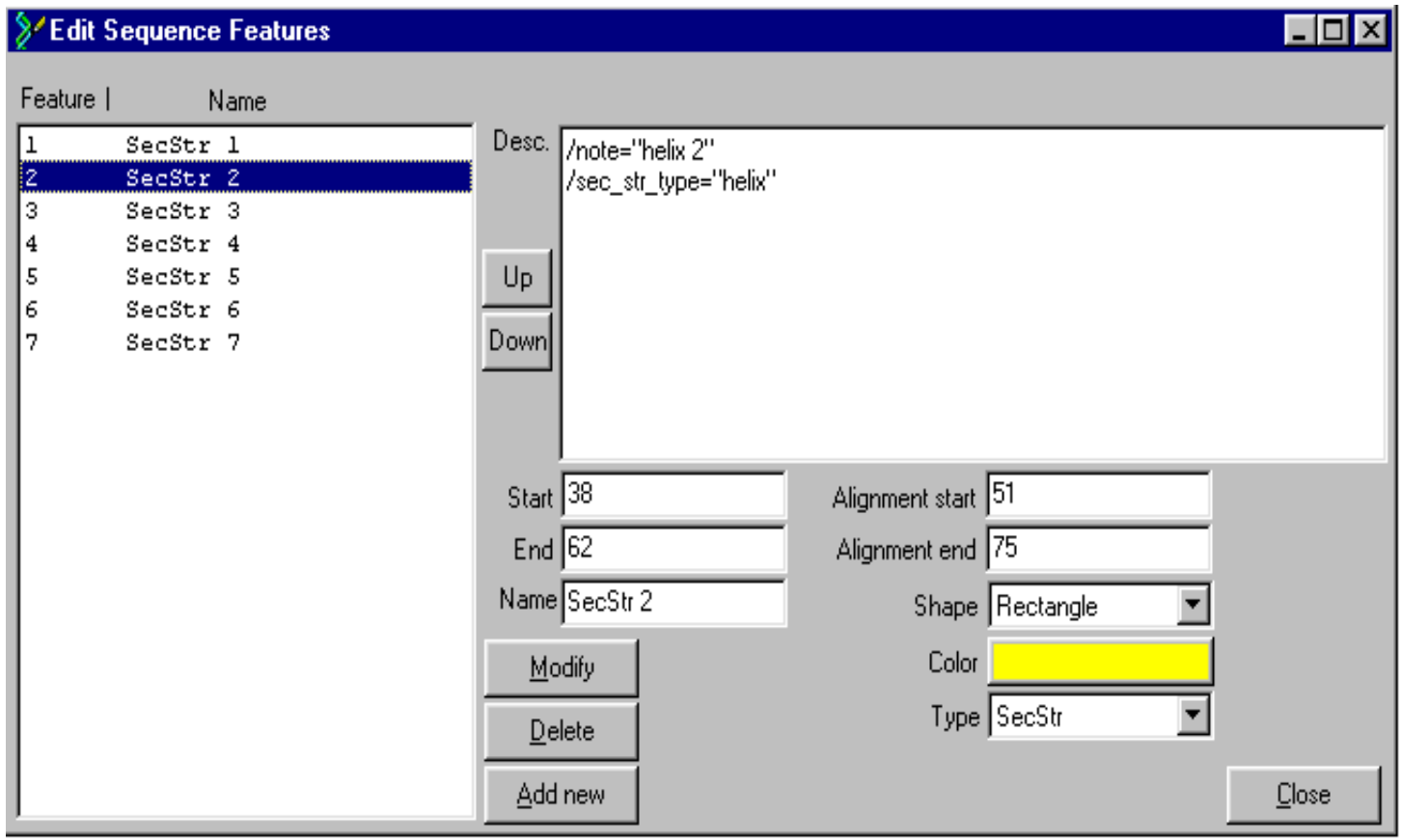
Sequences in an alignment document may be sorted by the following criteria:

- Title
- LOCUS
- DEFINITION
- REFERENCES
- COMMENT
- ACCESSION
- PID/NID
- residue frequency in a selected column(s)

To sort sequences, choose "Sequence->Sort-><sort type>

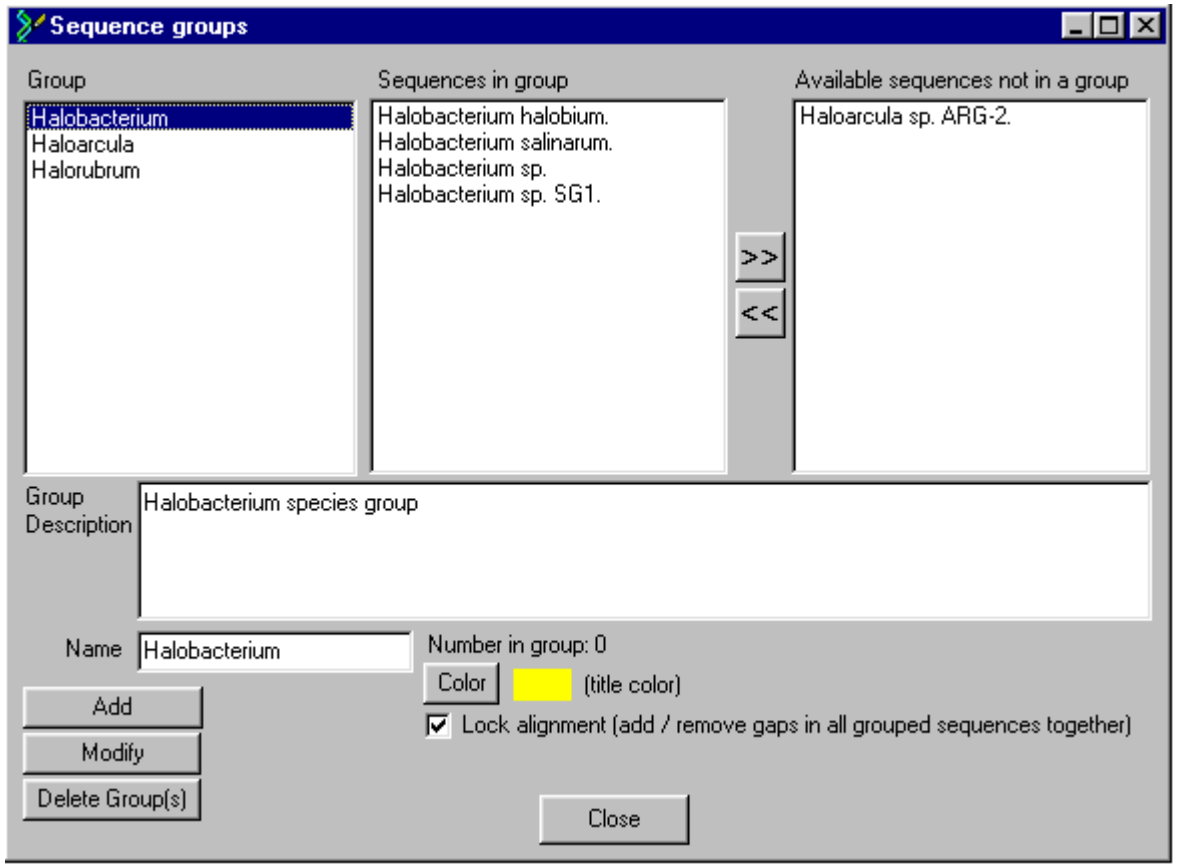
The first six sort types are alphabetical.

Adding, modifying and selecting sequence feature manually -Annotating



Highlight the sequence title and choose the menu option "Sequence->Features->Edit Features"

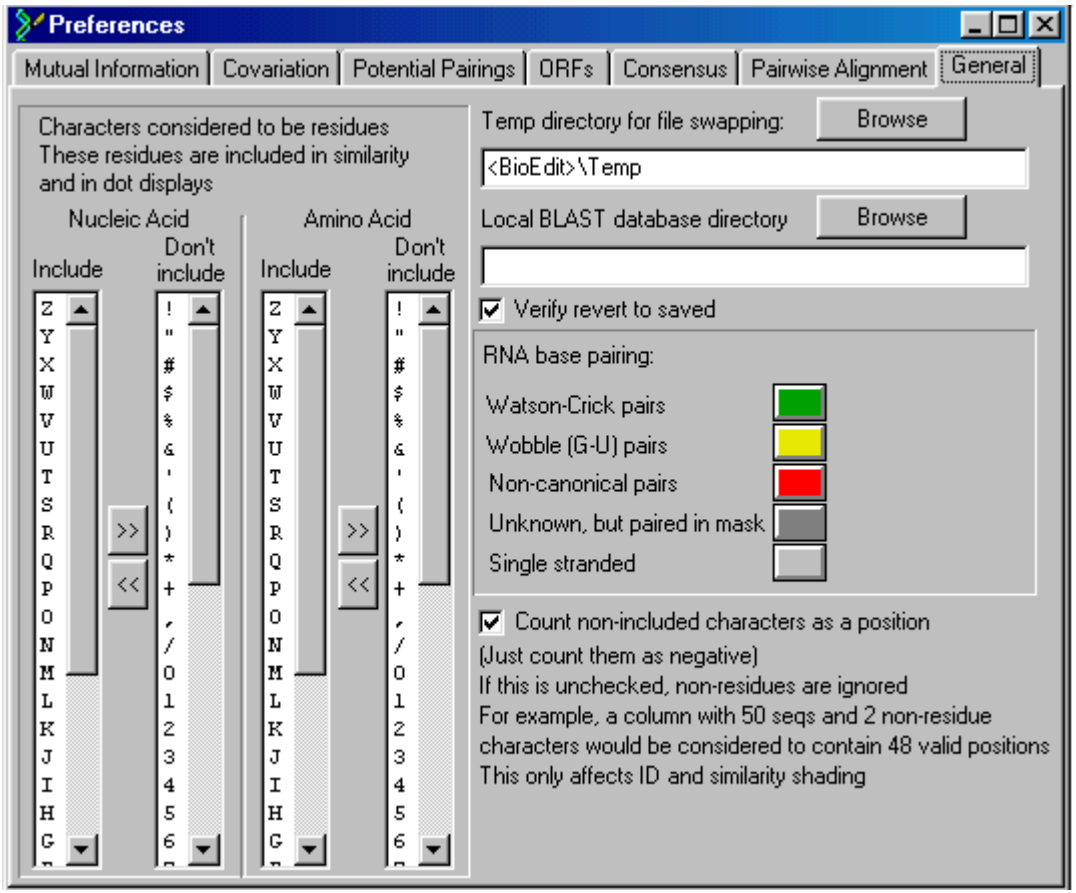
Grouping sequences into groups or families



To edit sequence groups, choose

"Sequence->Sequence groups (or families)".

User-defined valid residue characters
General Preferences

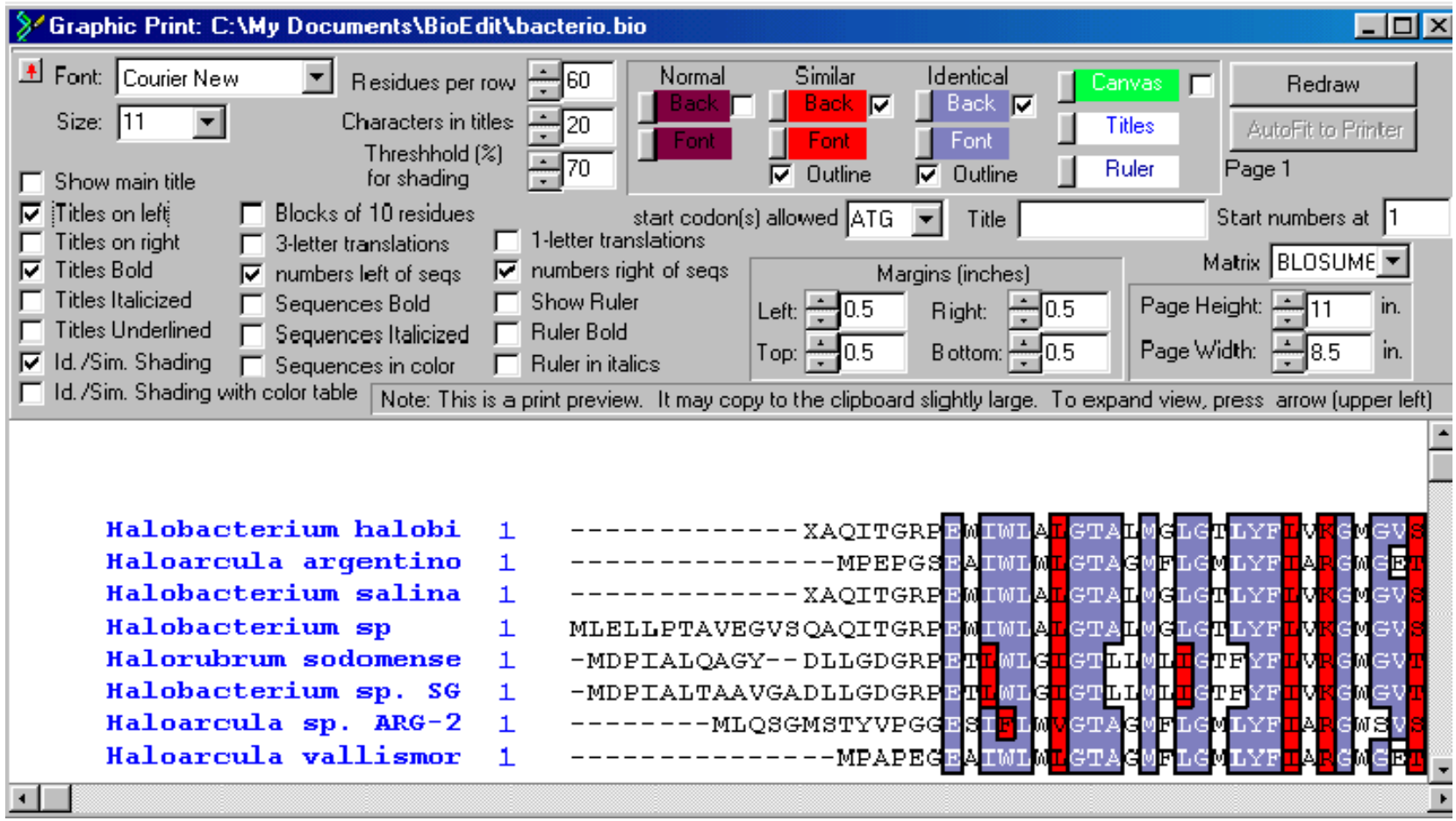


To see or change the current settings for what is considered a "true" residue, choose "Options->Preferences->General.

File formats read and written by BioEdit

- BioEdit
- Genbank
- Fasta
- NBRF/PIR
- Phylip3.2/2
- Phylip 4
- IG/Stanford
- EMBL
- GCG (single sequence only)
- DNAStrider
- Fitch
- Zuker (import only)
- Olsen (import only)
- Plain or raw (single sequence only)
- PIR/CODATA
- MSF (multiple sequence format)
- ASN.1 (NCBI)
- PAUP/NEXUS

Shaded graphic view of Alignment



Choose ‘Graphic View’ from ‘File’ menu of open document

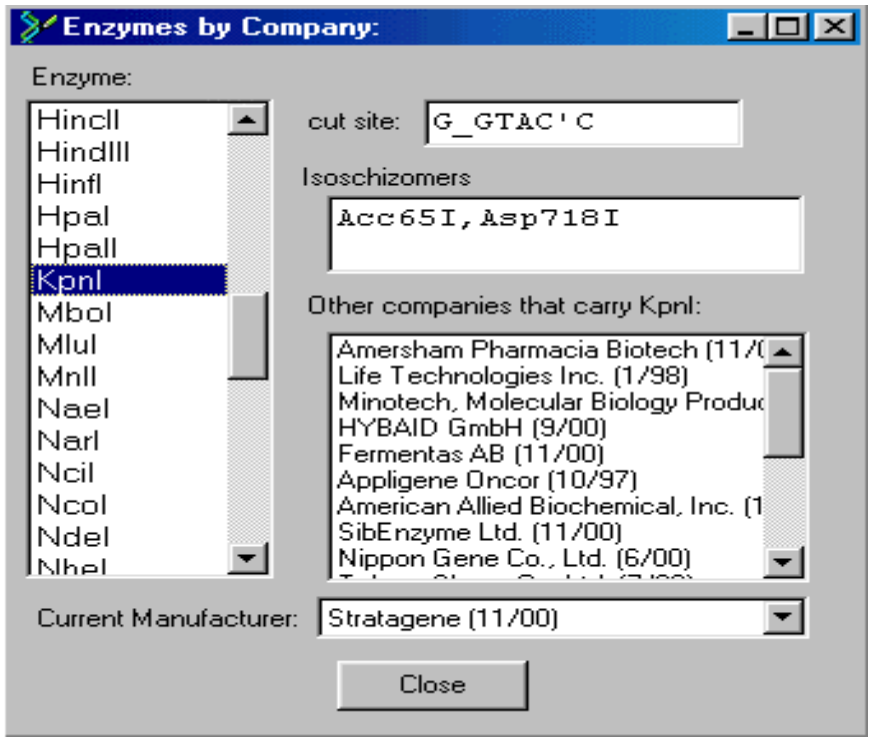
Restriction Maps

BioEdit offers two ways to generate restriction maps of nucleic acid sequences.

- **WebCutter:** Highlight the title of the sequence you wish to map and choose “Auto-fed WebCutter Restriction Mapping” from the “World Wide Web” menu.

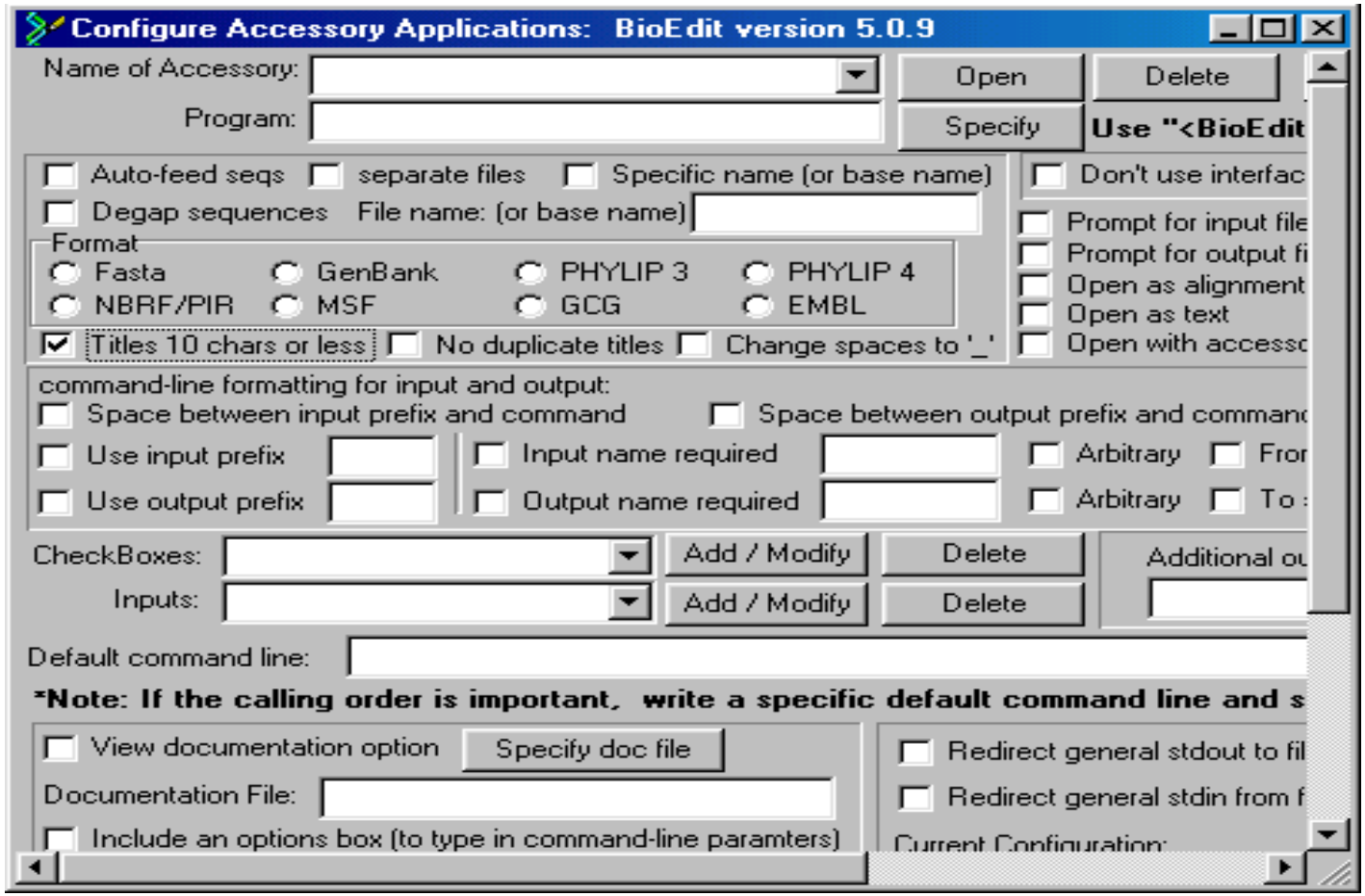
- **BioEdit:** Highlight the title of the sequence you wish to map and choose “Restriction Map” from the “Sequence” menu. An interface window will appear with the following options:

Restriction Enzyme Browser



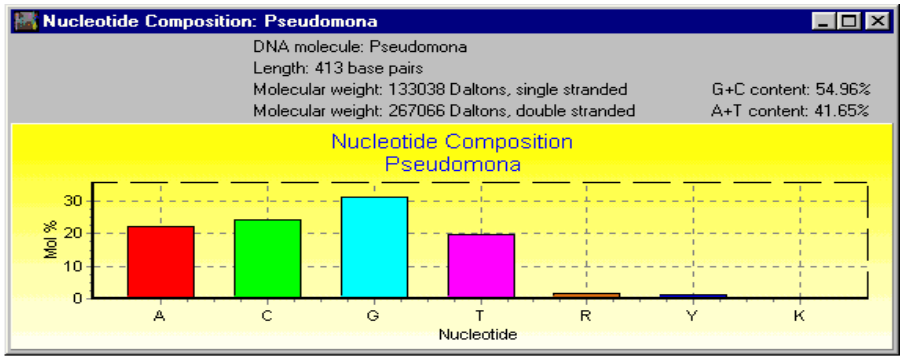
Restriction enzymes may be browsed by manufacturer by choosing a manufacturer and pressing the button on the restriction map dialog. You may also examine restriction enzymes at any time by choosing “View Restriction Enzymes by Manufacturer” from the “Options” menu.

Adding and configuring a new application



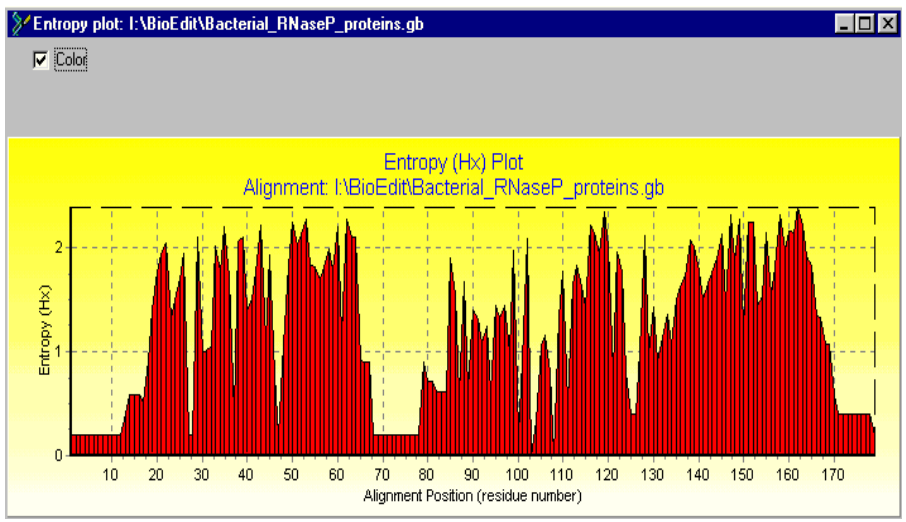
To add a new application to be included in the “Accessory Applications” menu, choose “Add / Modify / Remove an Accessory Application” from the “Accessory Applications” menu.

Amino acid and Nucleotide Composition



Choose “Amino Acid Composition” from the “Protein” submenu of the “Sequence” menu, or “Nucleotide Composition” form the “Nucleic Acid” submenu of the “Sequence” menu, respectively.

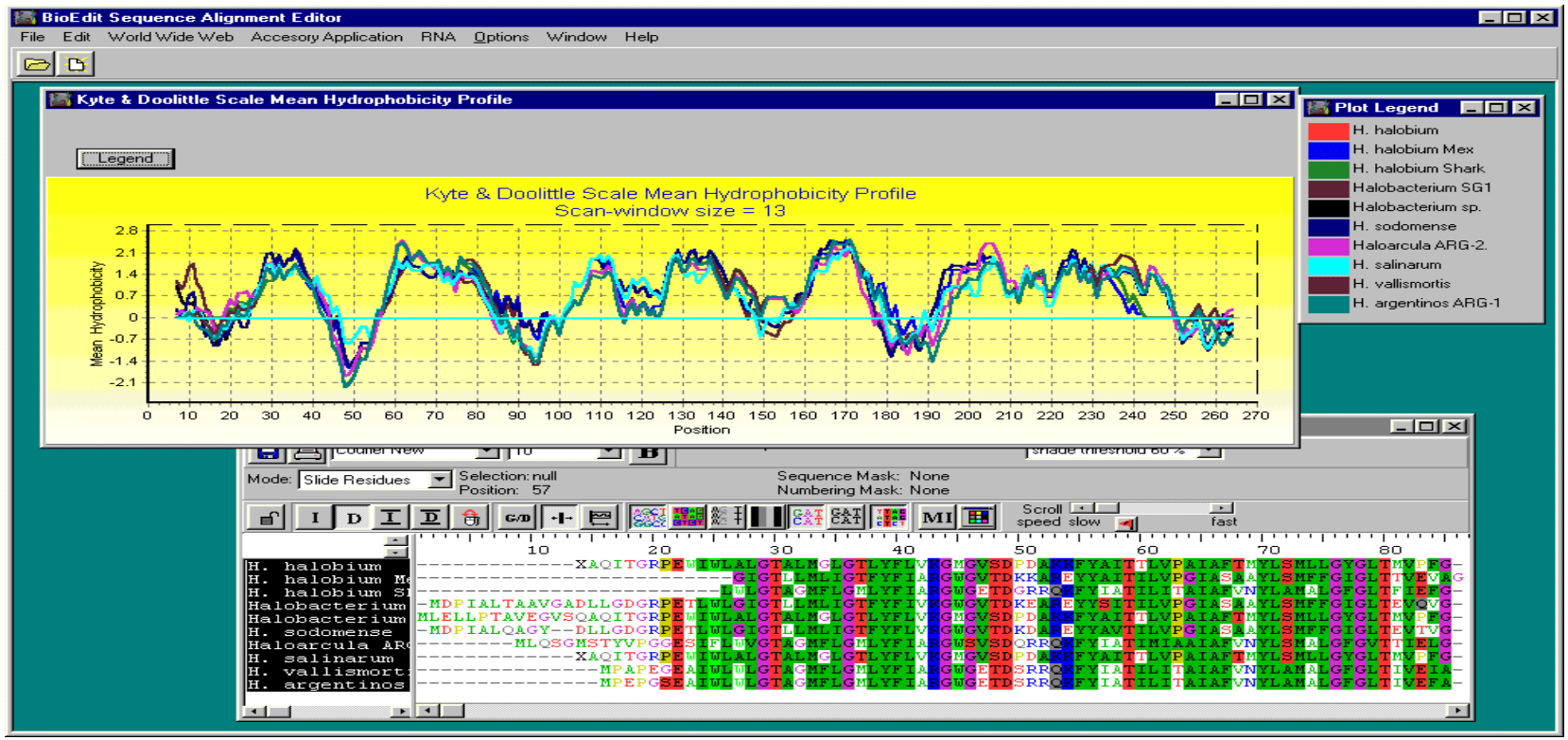
Entropy plots



a measure of the lack of predictability for an alignment position

choose “Entropy (Hx) Plot” from the “Alignment” menu

Hydrophobicity Profiles



Kyte & Doolittle Mean Hydrophobicity Profile

Boyko Scale Mean Hydrophobicity profile

Eisenberg Scale Mean Hydrophobicity profile

Hoop & Woods Scale Mean Hydrophobicity profile

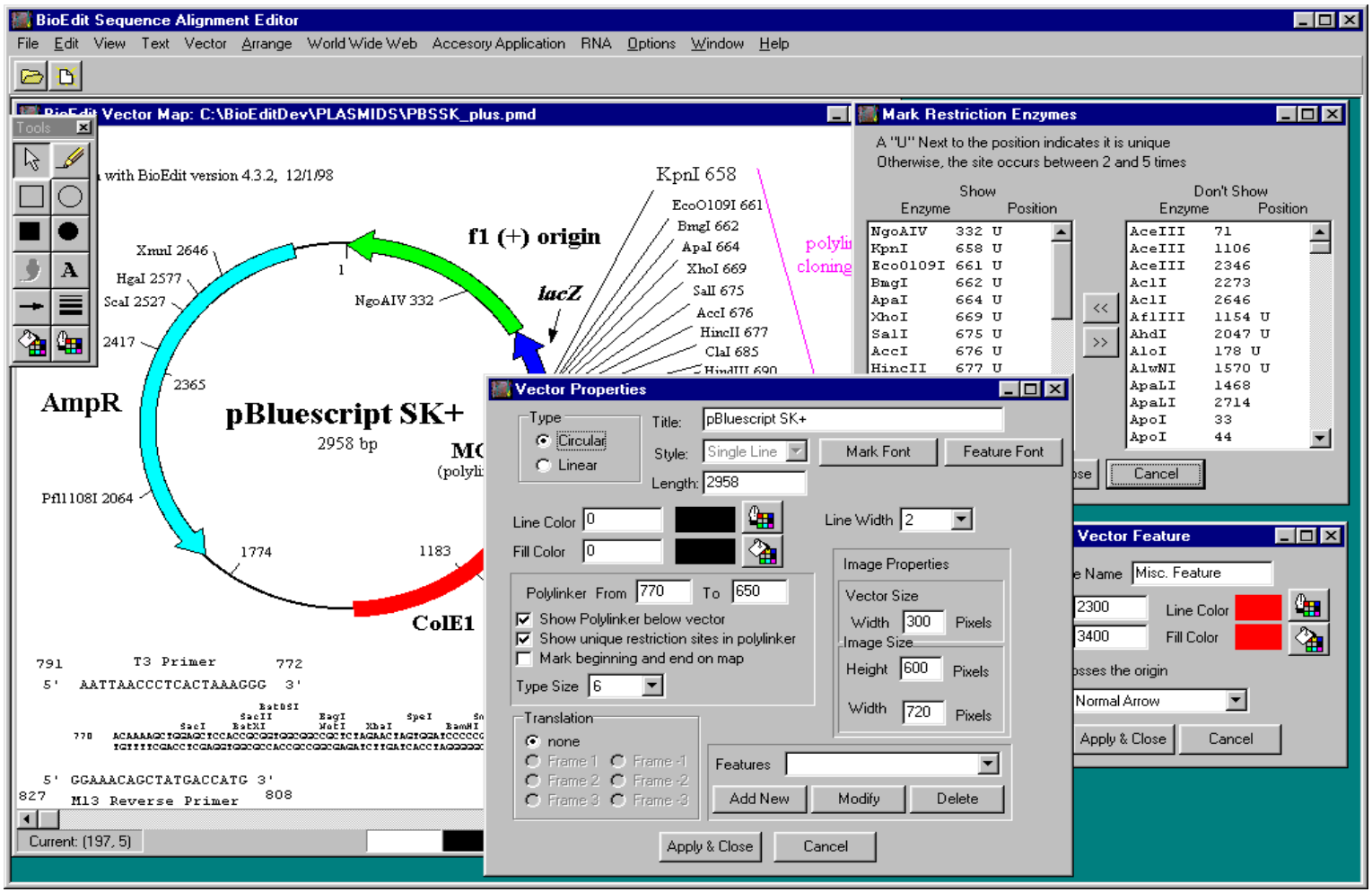
Cornette Scale Mean Hydrophobicity profile

Eisenberg Hydrophobicity Moment profile.

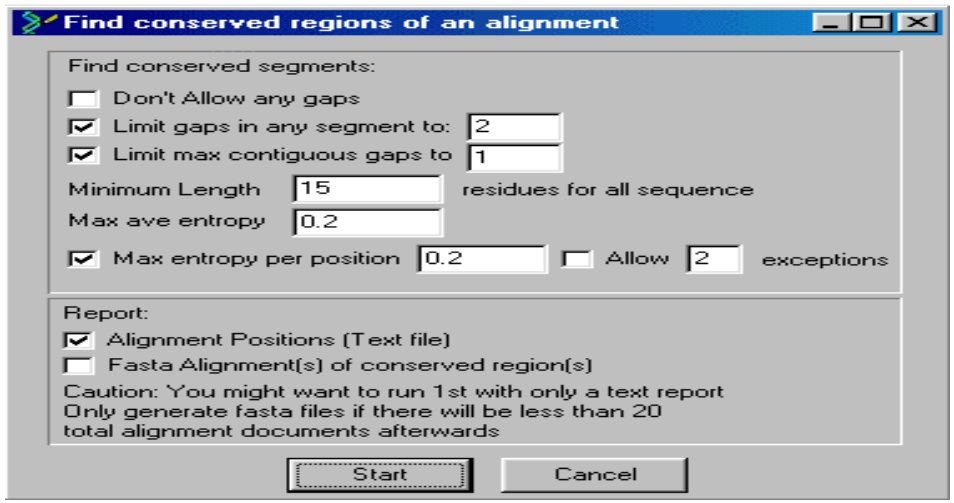
Parker HPLC Scale Mean Hydrophobicity profile

Mean Eisenberg Moment Profile.

Plasmid Drawing and Anotation

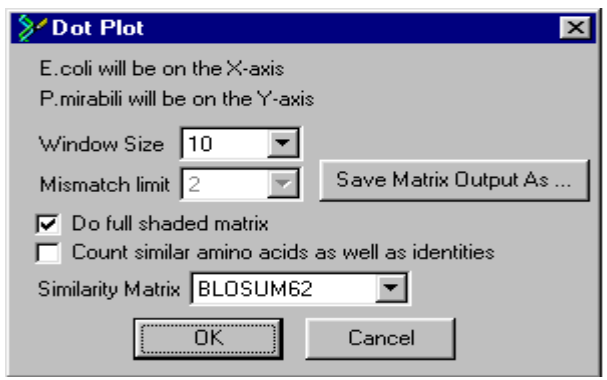


Search for conserved regions in an alignment



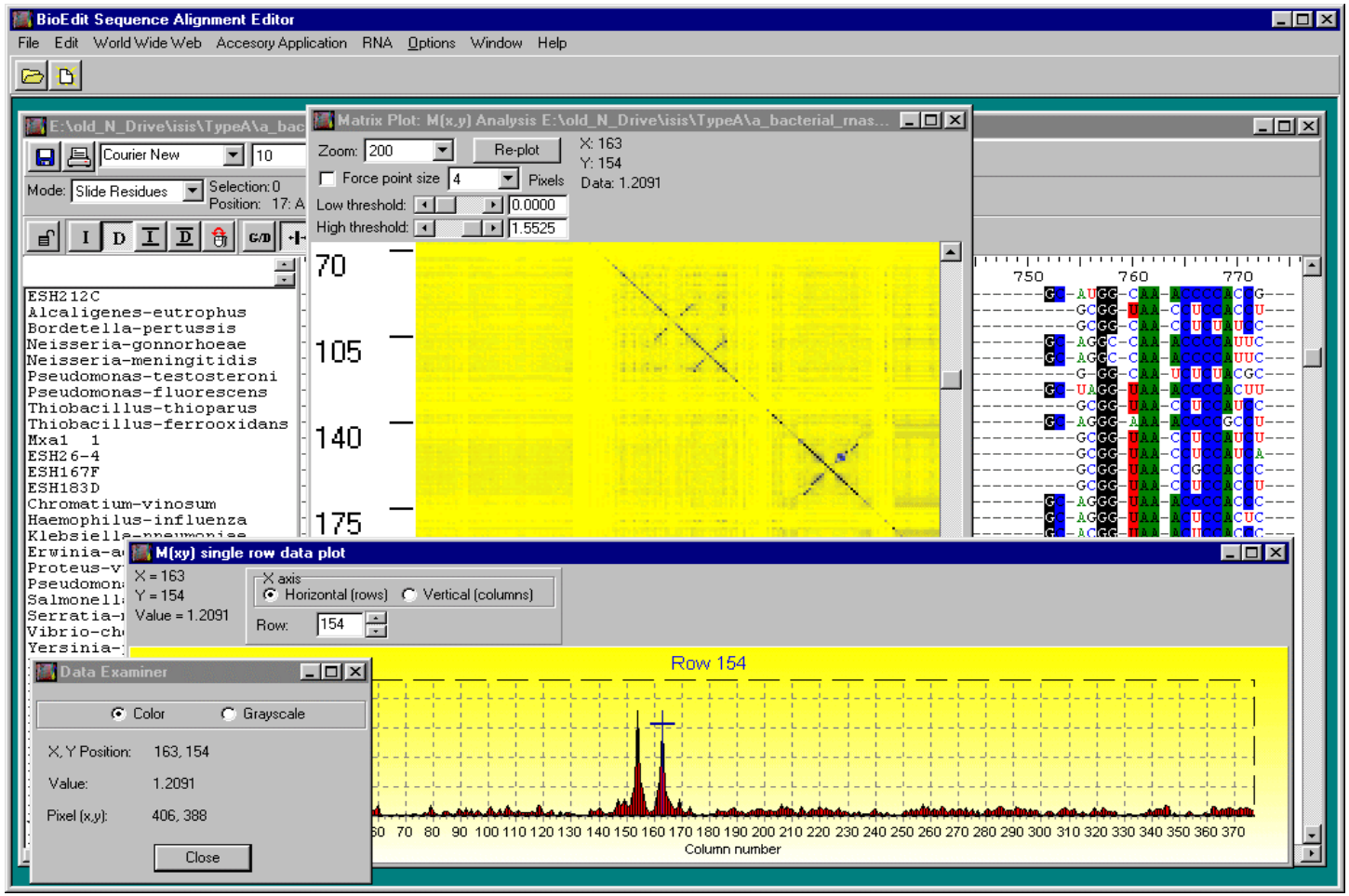
choose Alignment->Find Conserved Regions.

Dot Plot

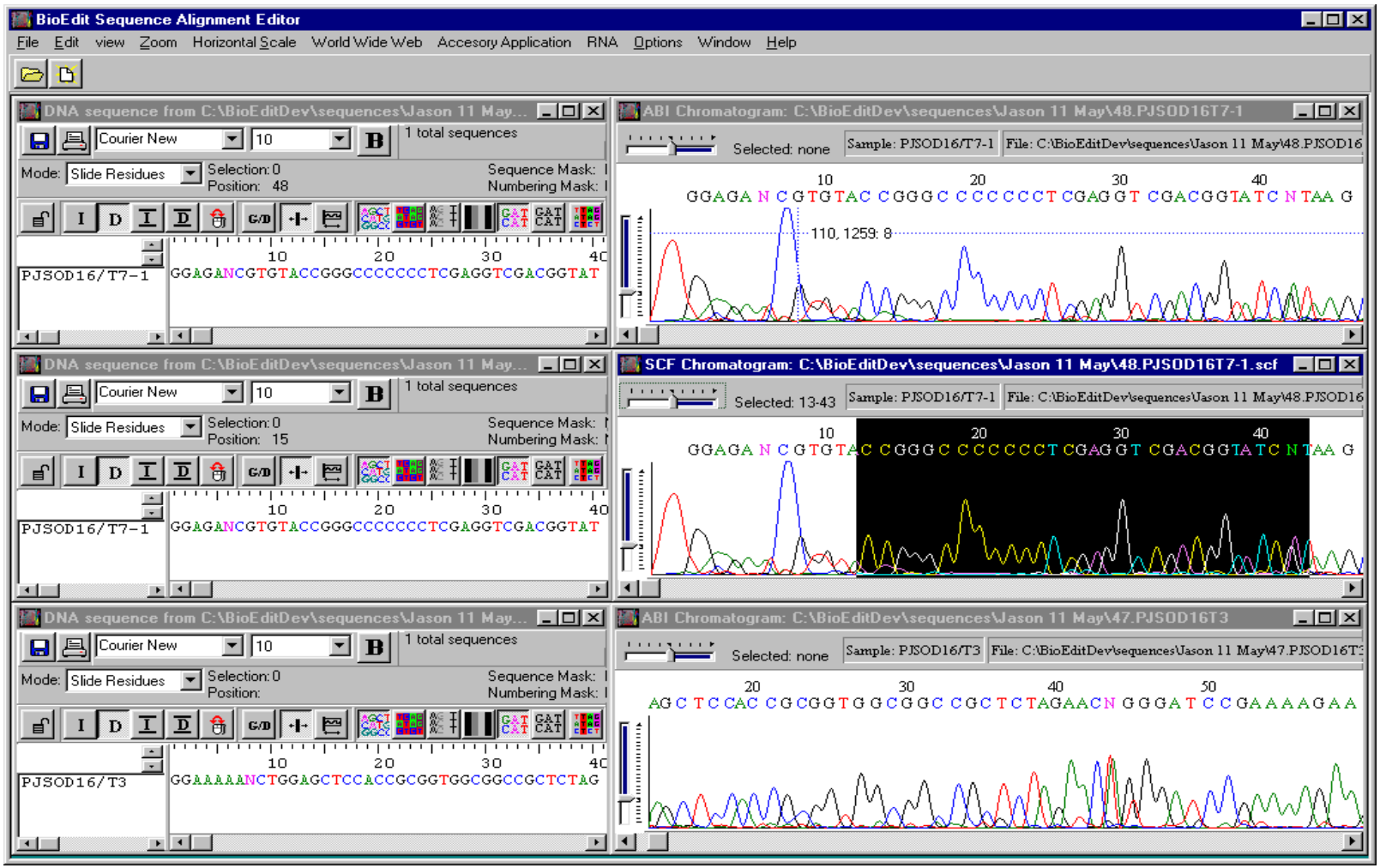


choose "Sequence-> Dot Plot (pairwise comparison)"

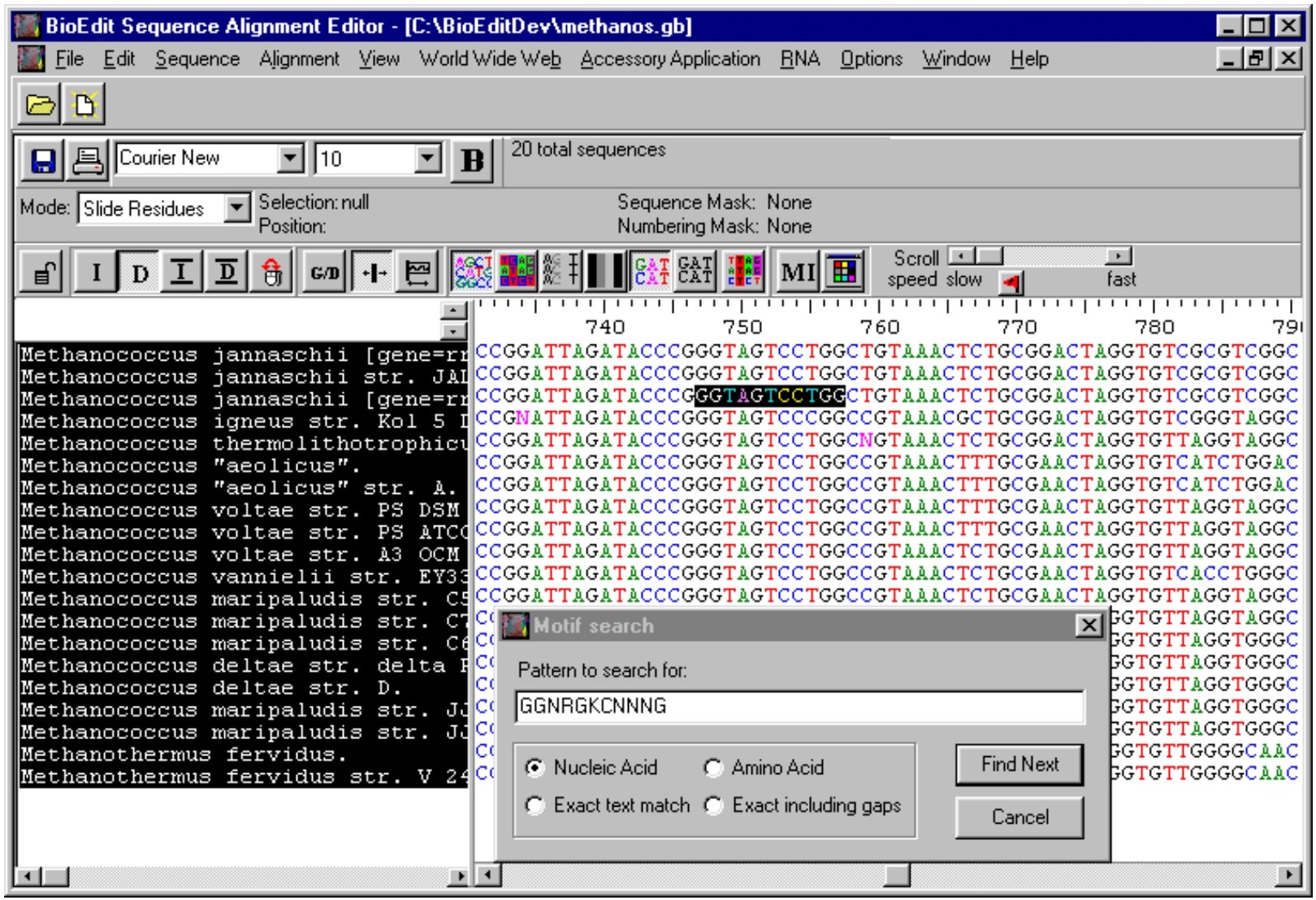
Mutual Information analysis and Graphical Data Examination



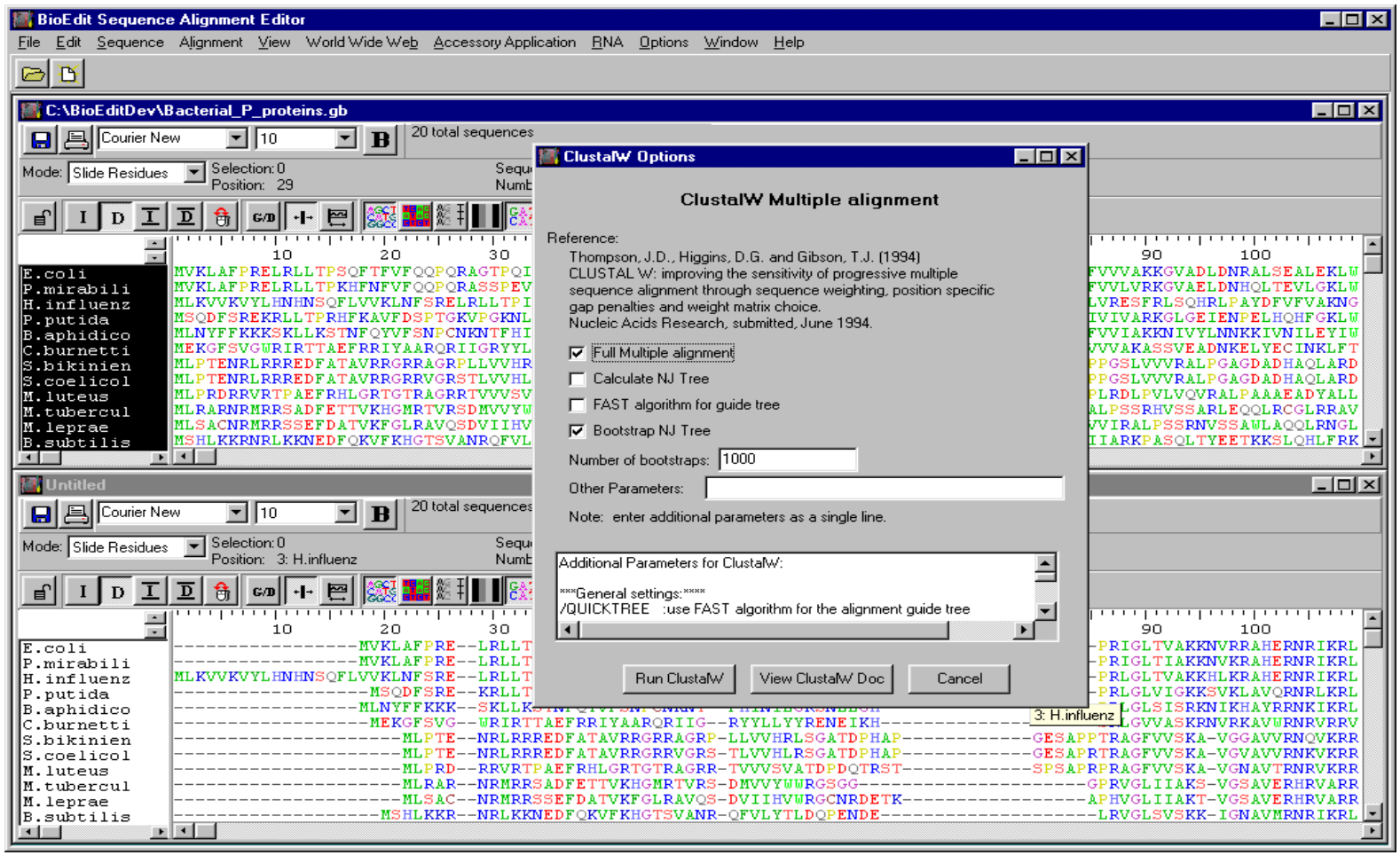
ABI and SCF trace viewing, editing and conversion



User-defined Motif Searching



Automated link to ClustalW with command line options available



Other Features of BioEdit

- Codon table
- Six frame translation
- Anchoring a column
- Identity Matrix
- Position of nucleotide numerical summary
- Pairwise sequence alignment
- Nucleotide translation with codon usage
- Local Blast
- Clustal W
- Web based accessories