



DNAMAN for Windows

DNAMAN uses advanced features of Microsoft Windows and offers versatile visual tools for sequence analysis.

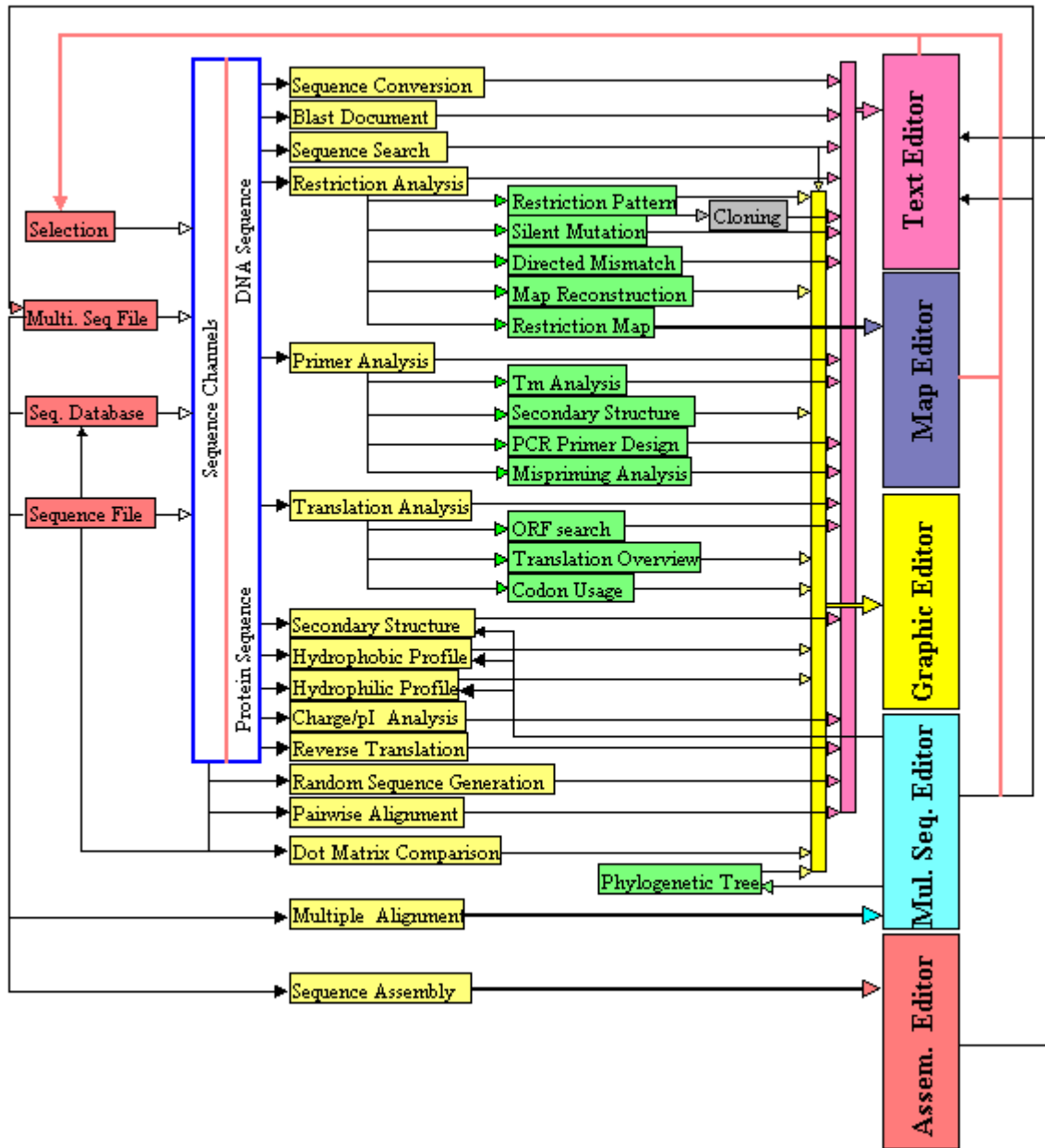
The screenshot displays the DNAMAN software interface with the following components:

- Example1.seq:** A linear DNA sequence of 886 bp. It features a red arrow labeled "Promoter" and a blue bar labeled "EXAMPLE1". Restriction sites for BamHI and ApaBI are indicated.
- Example.dmp:** A circular plasmid map of 4237 bp. It includes a green arrow for "Ampr", a blue arrow for "Gene 1", and a red arrow for "Lac". A red segment is labeled "Deletion". A Multiple Cloning Site (MCS) is shown with various restriction sites: NotI (2574), KpnI (2562), XbaI (2550), SmaI (2543), PstI (2531), SacI (2513), and EcoRI (2502). Other sites include BamHI (1731) and KpnI (1740).
- Multiple Alignment:** A window showing a sequence alignment. The "Output" section lists sequences: Lyn, Lyn-1, Lyn-2, Lyn-e, Lynb, Lync, Lyn-3, and Lyn-d. The "Consensus" sequence is shown as "tccacatcaactccttattt". A graph above the alignment shows a peak at position 150.
- Sequence Editor:** A text area at the bottom with a "Lock" checkbox and a sequence: "CACCTTCCTT GACGAGGGCT TTA CTG CCAA GGATATCCTC GACCAAAAAA TAAACGAAGT" and "61 GTCATCTTCT GATGATAAAG ATGCCCTTCTA TGGTGCTGAC CTCGGGGATA TTGTAAAGAA".

System Requirements

- Intel Pentium III 800 MHz or higher
- Windows 2000/XP
- At least 256MB memory
- A hard drive with at least 20MB of available disk space

DNAMAN: Integrated System for Sequence Analysis



Sequence Manipulation

[Sequence input](#)

[Information exchange](#)

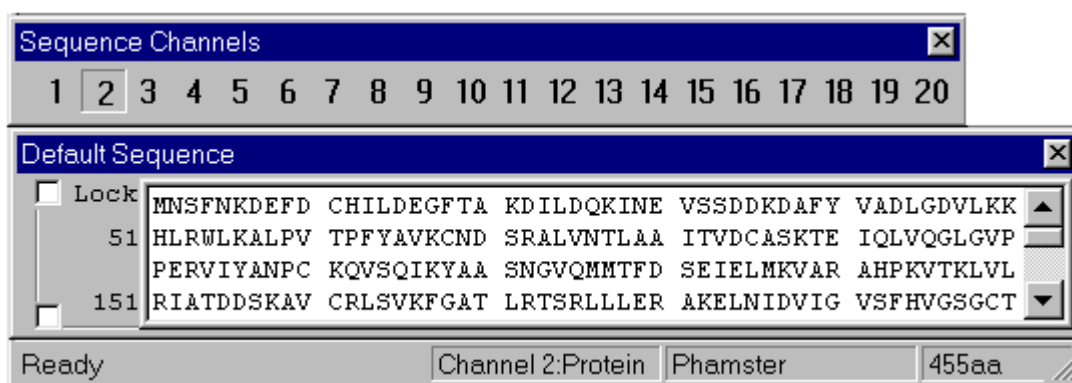
[Editing](#)

[Sequence composition and conversion](#)

[BLAST documents](#)

Sequence input

DNAMAN provides 20 sequence channels to keep active sequences in memory. These sequence channels simplify multiple functional analyses and substantially increase the efficiency of your works. A panel window shows the current working sequence. You may edit the sequence directly in the panel.



Information exchange

DNAMAN accepts sequence files in GenBank, GCG, CUSTAL, FASTA, PIR and GDE format. It can export multiple sequences in GCG, CUSTAL, PIR and GDE format.

DNAMAN provides a word processor for sequence editing. With this word processor, you can incorporate charts, images, graphics from any other Windows software into your documents.

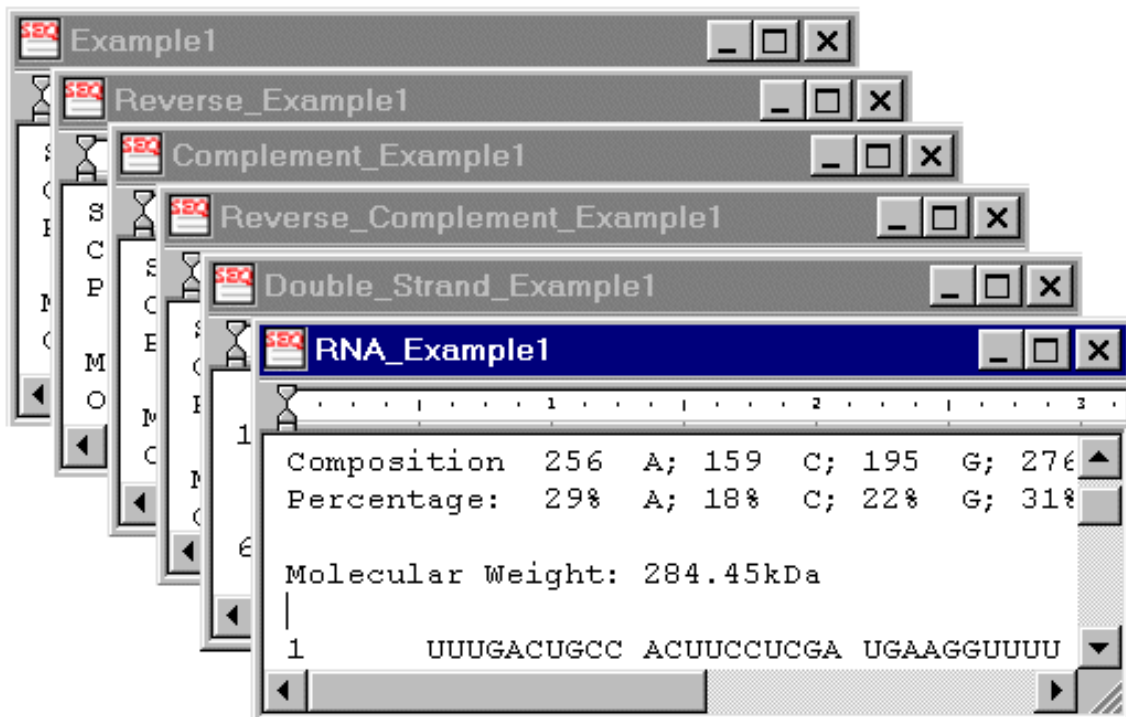
DNAMAN works as an object linking and embedding (OLE) server to exchange the information of restriction maps with other software. With OLE, you can incorporate your restriction maps into other Windows applications, and directly modify the maps within the applications.

Editing

Editing a text file with DNAMAN is as easy as working with your favorite word processor. With the word processor of DNAMAN, you can edit original sequence files, and the analysis results as well.

Sequence composition and conversion

DNAMAN reports the composition and molecular weight of a sequence. It performs the conversion of a sequence to its reverse, complementary, reverse complementary, double strand, and RNA sequences.



BLAST documents

In addition to accessing the Internet through Web browser, DNAMAN prepares a file in BLAST document formats with a query sequence for directly accessing BLAST E-mail Server. Five BLAST document formats are currently available: *Blastn*, *Blastx*, *Tblastx*, *Blastp* and *Tblastn*. Examples:

Blastn

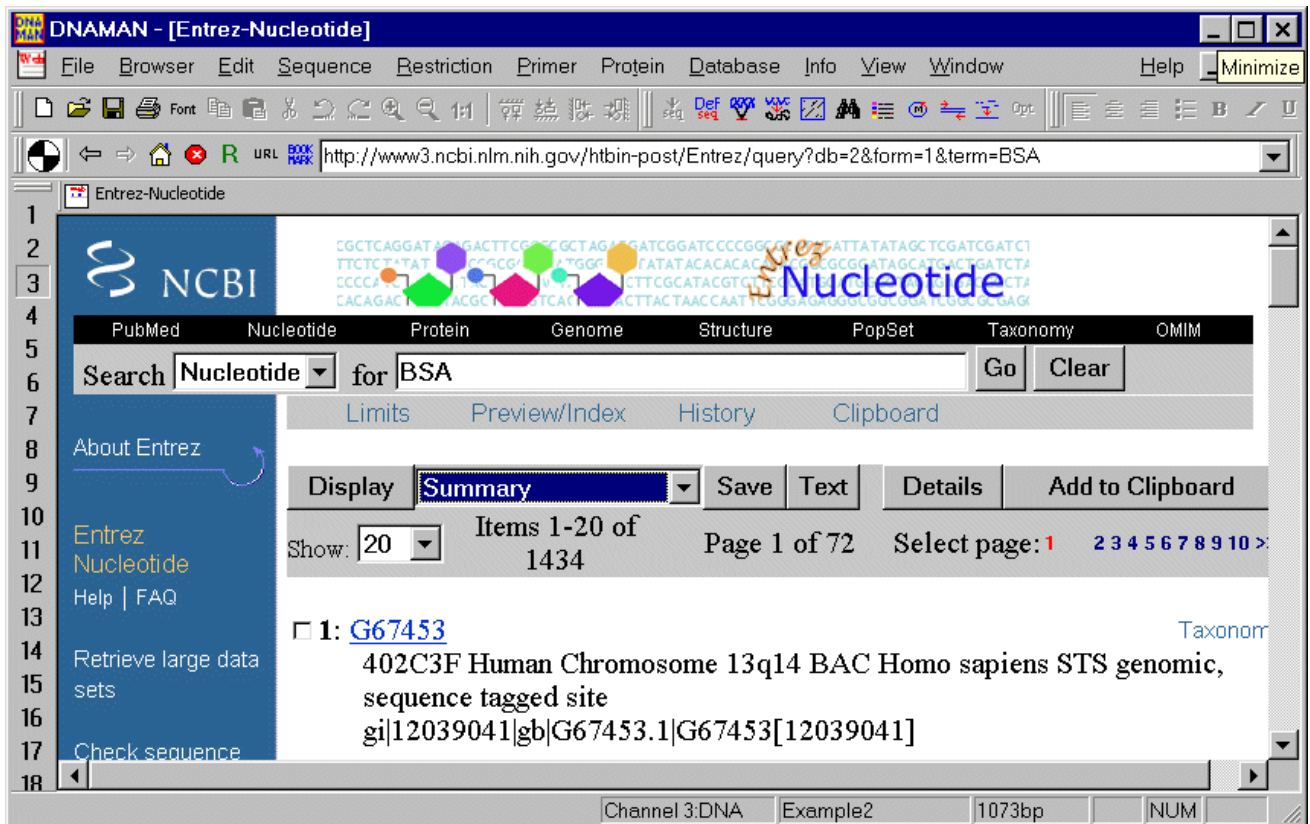
```
e-mail to: blast@ncbi.nlm.nih.gov
PROGRAM blastn
DATALIB nr
BEGIN
>Nt sequence of EXAMPLE1
TTTGACTGCCACTTCCTCGATGAAGGTTTACTGCCAAG
```

Blastp

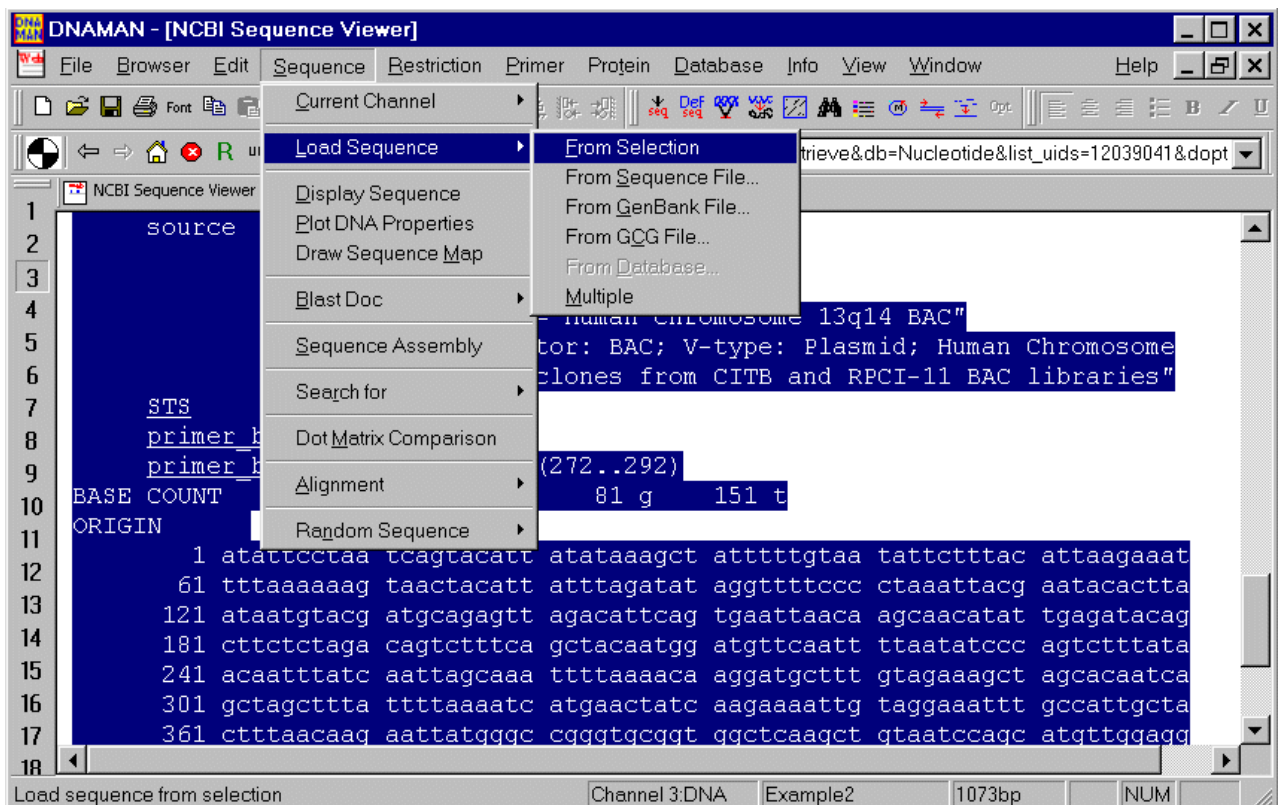
```
e-mail to: blast@ncbi.nlm.nih.gov
PROGRAM blastp
DATALIB nr
BEGIN
>Protein sequence translated from EXAMPLE1 in RF1
FDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVADLGDILK
```

Internet/Intranet Browser

DNAMAN provides an integrated Web browser to access to the Internet or your Intranet.



You may load sequence from the browser for direct analysis.



You may also work with the servers on the Internet.

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DNAMAN - [BLAST Search]

File Browser Edit Sequence Restriction Primer Protein Database Info View Window Help

http://www.ncbi.nlm.nih.gov/blast/blast.cgi?Jform=1

Computational Biology or ... BLAST Search Example2

Program **blastn** Database **nr**

NEW To search the **Human Genome** sequences, go to the [human genome blast page](#)

Perform ungapped alignment
 Perform CDD Search (proteins only)

The query sequence is **filtered** for low complexity regions by default.

Enter here your input data as **Sequence in FASTA format** Search

```
CTTGCAGTTA ATATCATTGC CAAGAAAATT GTATTAAAGG AACAGACGGG
CTCTGATGAC GAAGATGAGT CGAGTGAGCA GACCTTTATG TATTATGTGA
ATGATGGCGT CTATGGATCA TTTAATTGCA TACTCTATGA CCACGCACAT
GTAAAGCCCC TTCTGCAAAA GAGACCTAAA CCAGATGAGA AGTATTATTC
ATCCAGCATA TGGGGACCAA CATGTGATGG CCTCGATCGG ATTGTTGAGC
```

Channel 3:DNA Example2 1073bp NUM

Sequence Search

[Search for nucleotide sequences](#)

[Search for consensus sequences](#)

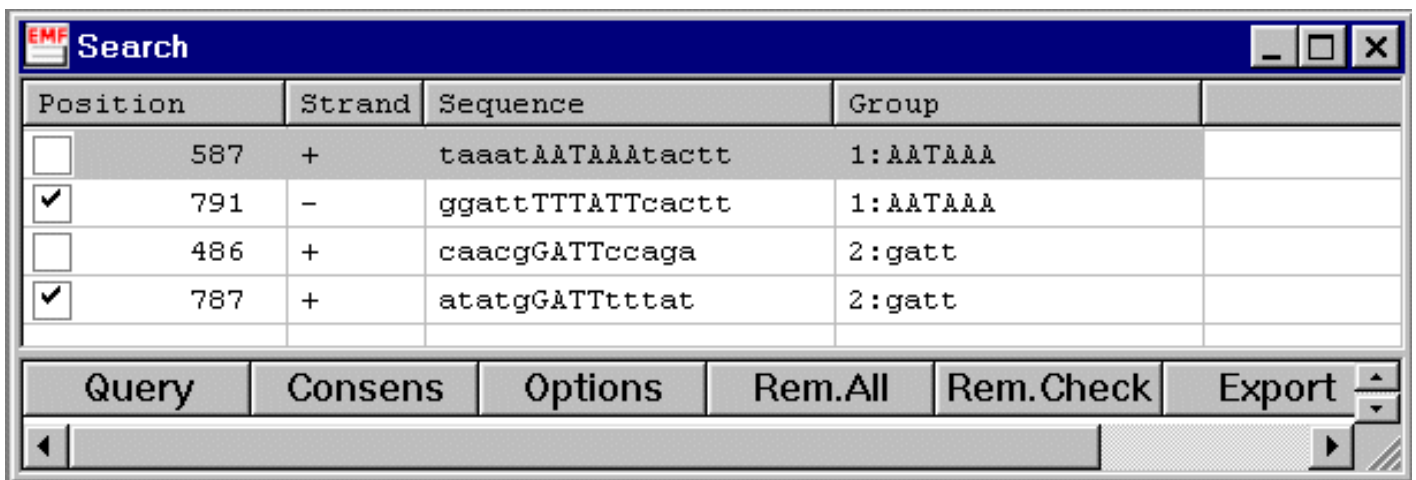
[Search for open reading frames](#)

[Search for repeat sequences](#)

[Search for amino acid sequences](#)

Search for nucleotide sequences

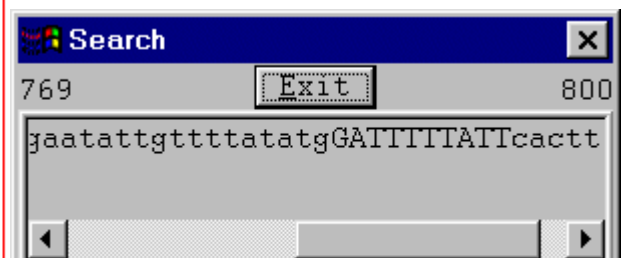
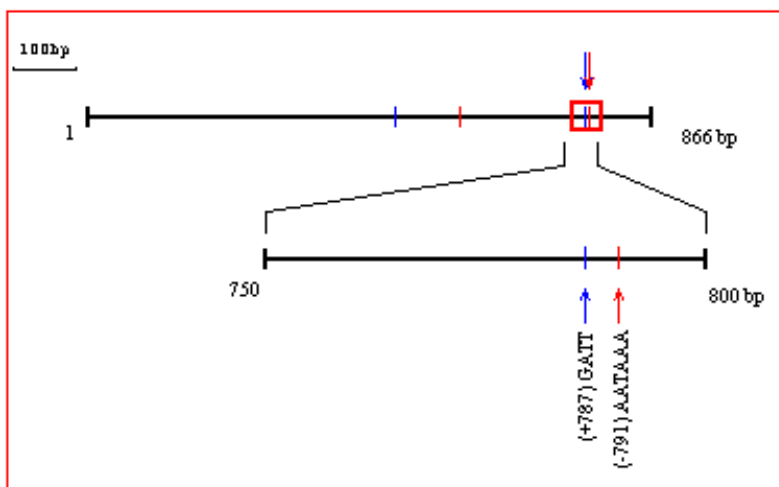
With DNAMAN, you can search for nucleotide sequences from one or both strands of a DNA sequence. Gaps and ambiguous nucleotides are allowed in the query sequences. You may search for a list of query sequences on the target sequence.



Position	Strand	Sequence	Group	
<input type="checkbox"/>	587	+	taaataATAAAtactt	1: AATAAA
<input checked="" type="checkbox"/>	791	-	ggattTTTATTcactt	1: AATAAA
<input type="checkbox"/>	486	+	caacgGATTccaga	2: gatt
<input checked="" type="checkbox"/>	787	+	atatgGATTtttat	2: gatt

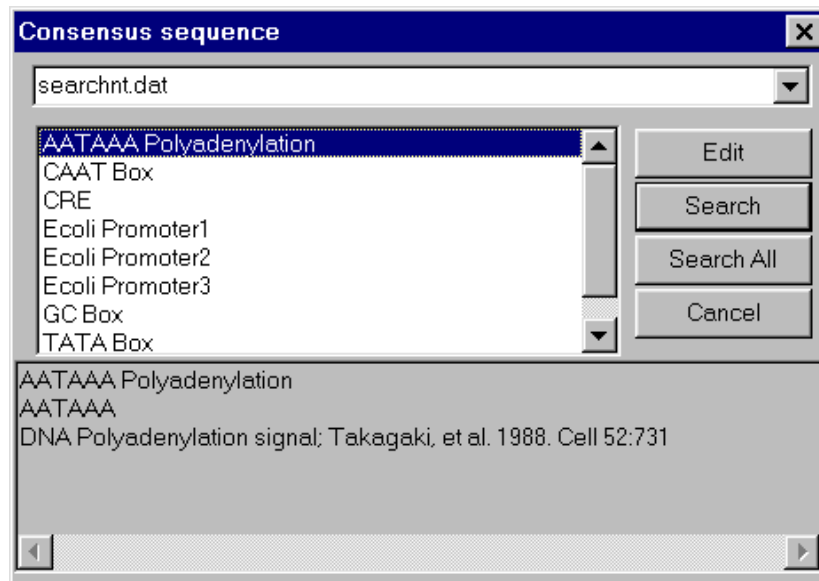
Query Consens Options Rem.All Rem.Check Export

DNAMAN instantly reports the searching results in graphics. Colors and arrowheads indicate different sequence groups and sites. You may magnify any region of the DNA fragment and display the regional sequence of by selection.



Search for consensus sequences

With DNAMAN, you can search for DNA or protein consensus sequences from both strands or six reading frames of DNA sequences. DNAMAN provides a database of DNA and protein consensus sequences. The database is expandable and editable. You can create custom consensus sequence databases.



Search for open reading frames

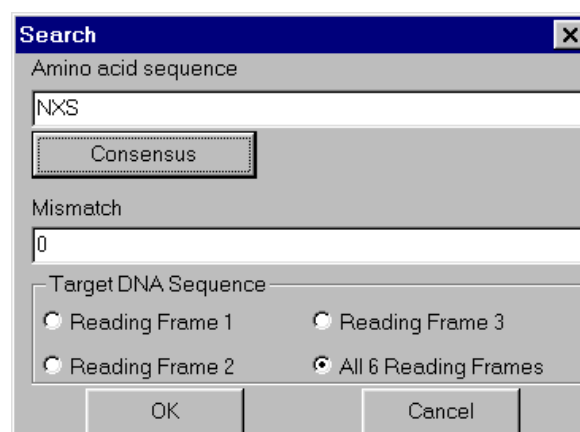
You may search for open reading frames from six reading frames of a DNA sequence. The searching results are shown in a text table. DNAMAN also provides a graphical view of the location of Start/Stop codons on a DNA sequence.

Search for repeat sequences

You may search for *direct repeat* and *reverse repeat* sequences from both stands of a DNA sequence. You can also search for *reverse complementary repeat* sequences that may form hairpin/stem-loop structures.

Search for amino acid sequences

You may search for an amino acid sequence and its variations from the six reading frames of a DNA sequence. DNAMAN allows ambiguous amino acids as well as a number of mismatches in a query sequence.



Restriction Analysis

[Restriction site analysis](#)

[Restriction map](#)

[Restriction pattern illustration](#)

[Electronic cloning](#)

[Constructing restriction maps](#)

[Silent mutation](#)

[Directed mismatch](#)

Restriction site analysis

You can search any restriction site on a DNA sequence. DNAMAN supplies two restriction enzyme files; the *restrict.enz* file with 180 most frequently used restriction enzymes, and the *dnamanre.enz* file with 1364 enzyme records. You can also create your own enzyme files. All the enzyme files are editable and expandable.

DNAMAN provides custom restriction enzyme filters on cutter, ends, frequency and methylation sensitivity. Users can define the DNA molecule as a linear or a circular type.

The screenshot shows a dialog box titled "Restriction Analysis" with a close button (X) in the top right corner. The dialog is divided into two main sections: "Results" and "Target DNA".

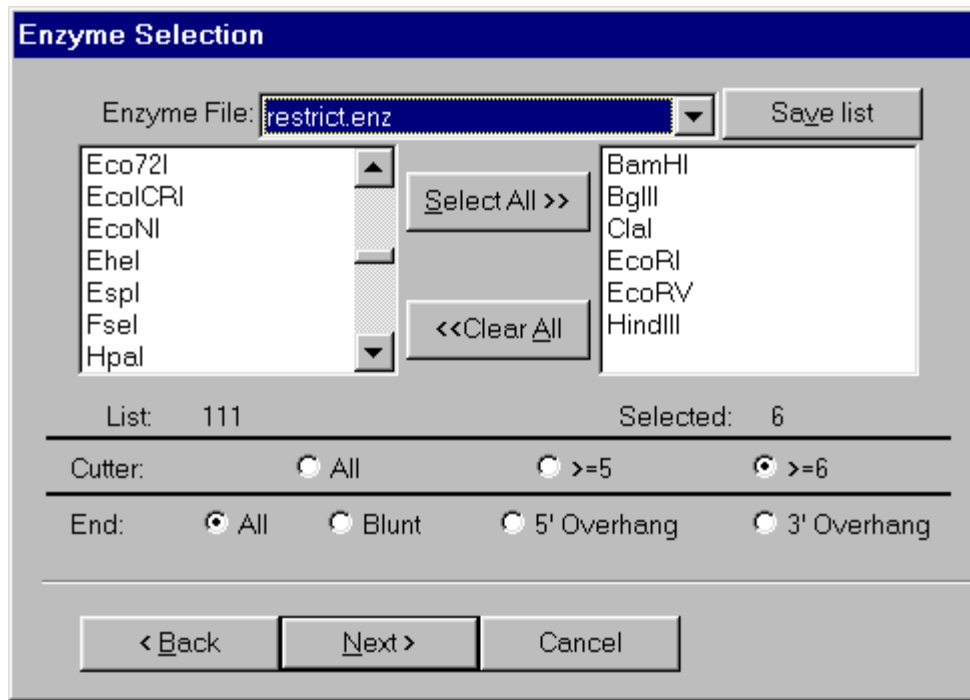
Results Section:

- Show summary (with a text box containing "10" and the label "sites per line")
- Show sites on sequence (with a text box containing "60" and the label "bases per line")
- Draw restriction map
- Draw restriction pattern
- Ignore enzymes with more than [0] sites
- Ignore enzymes with less than [0] sites
- With double-stranded sequence
- With enzyme position
- Including annotations

Target DNA Section:

- Circular
- dam methylation
- All DNA in sequence channels
- dcm methylation

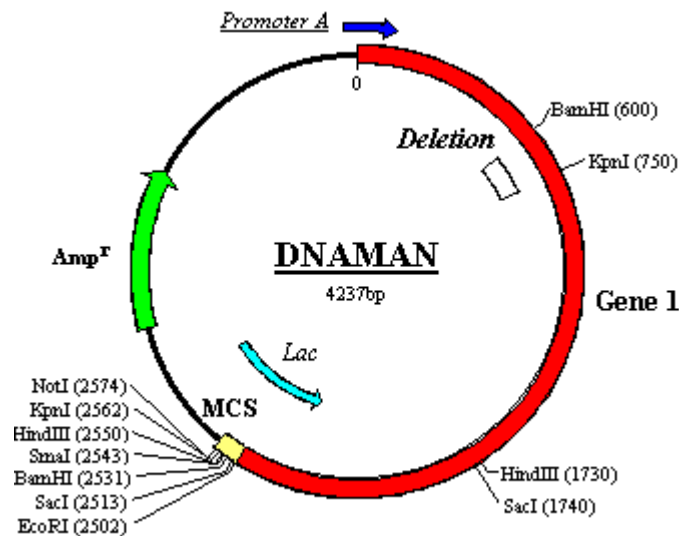
At the bottom of the dialog, there are four buttons: "< Back", "Next >", "Cancel", and "Help".



DNAMAN reports the restriction analysis results in an easy-to-read table. The cutting sites are shown in alphabetical order of enzymes, and in site position order as well. The non-cutting enzymes are also listed. In addition, DNAMAN displays enzyme sites on the top of the DNA sequence.

Restriction map

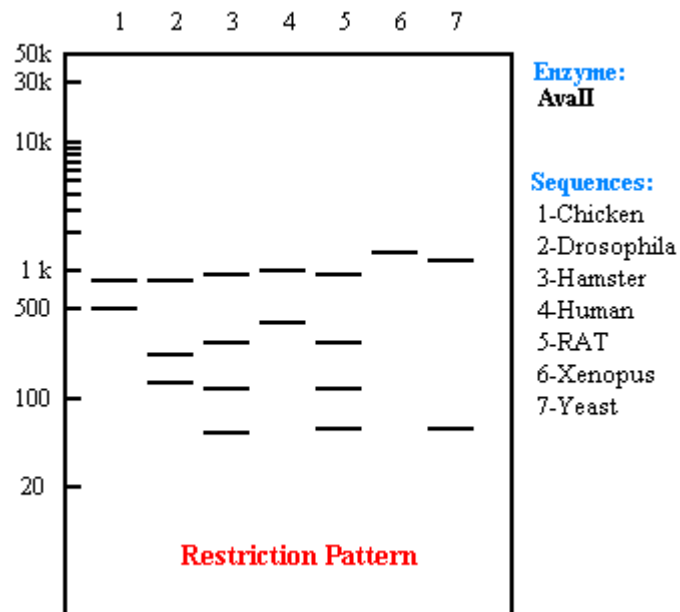
DNAMAN provides easy-to-use tools to produce publication-quality restriction maps. These tools can be used to draw linear or circular restriction maps with or without DNA sequence information. You can also draw maps for other projects, such as PCR strategy diagrams, gene structural maps, etc.



DNAMAN accompanies with a high quality drawing program, [LBDraw](#). Working with LBDraw, you can easily make sophisticated diagrams with many restriction maps.

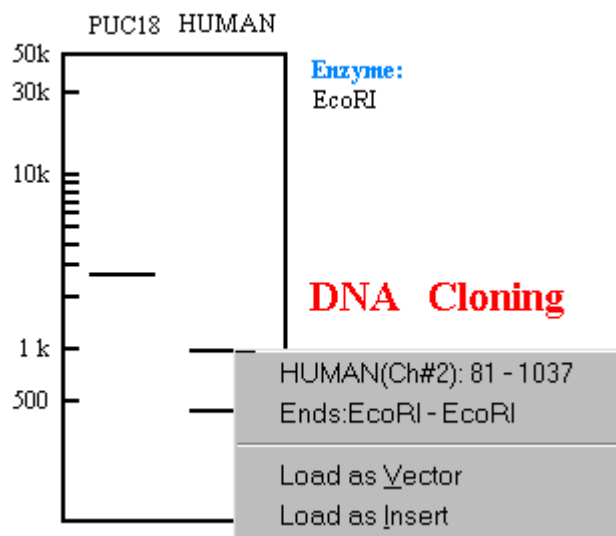
Restriction pattern illustration

DNAMAN predicts the patterns of restriction enzyme digested DNA fragments in a gel electrophoresis. You can perform single enzyme digestion on multiple sequences, and single or multiple digestion on a single sequence. DNAMAN shows the information of restriction fragments on their sizes and ends when you click on these fragments.



Electronic cloning

DNA cloning is a time consuming and expensive process. DNAMAN provides easy-to-use tools to design a cloning strategy and performs evaluation analyses on target sequences. This feature could improve the efficiency of your cloning work in laboratory.



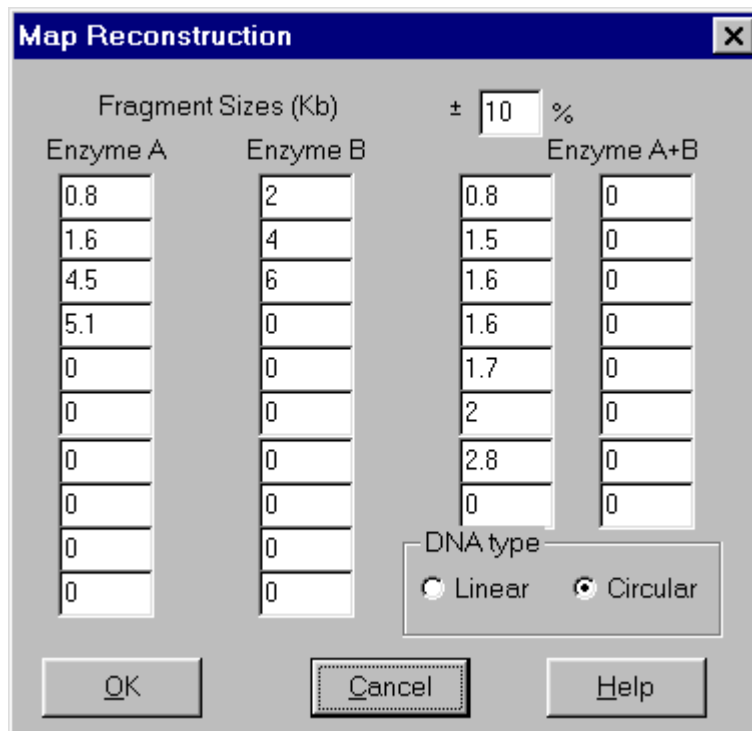
DNAMAN mimics basic steps of the actual cloning process:

- Restriction analysis on the original vector and insert sequences
- Selection of vector and insert fragments from restriction pattern
- Verification of the end compatibility of DNA fragments

- Modification of fragment ends if necessary
- Insertion of linkers if necessary
- Producing the final clone sequence

Constructing restriction maps

DNAMAN can help you reconstruct a restriction map in the absence of DNA sequence. You must provide all fragment sizes in single and double digestion. DNAMAN deduces the possible restriction map(s) from the information of restriction fragments.



Map Reconstruction

Fragment Sizes (Kb) ± 10 %

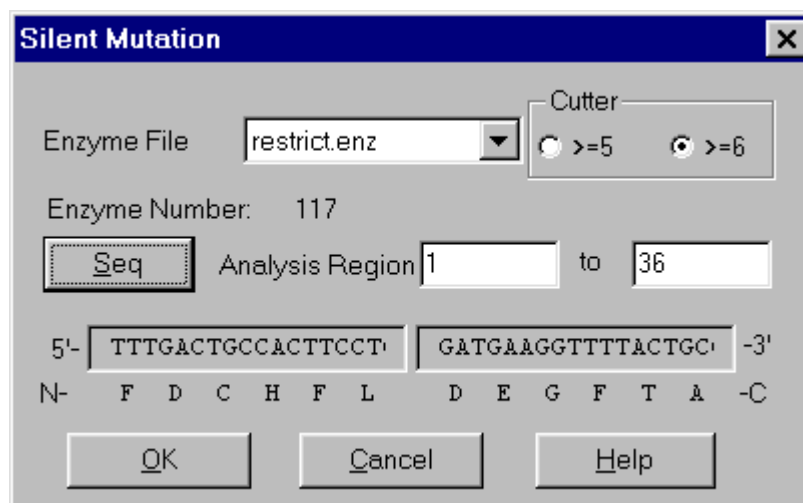
Enzyme A	Enzyme B	Enzyme A+B	
0.8	2	0.8	0
1.6	4	1.5	0
4.5	6	1.6	0
5.1	0	1.6	0
0	0	1.7	0
0	0	2	0
0	0	2.8	0
0	0	0	0
0	0		
0	0		
0	0		
0	0		

DNA type
 Linear Circular

OK Cancel Help

Silent mutation analysis

Silent mutation analysis allows you to design a desired mutation site on a DNA sequence. This mutation will result in the modification of restriction property without changing the coding amino acid sequence. This function searches for potential mutation positions to create or destroy restriction enzyme sites.



Silent Mutation

Enzyme File: restrict.enz Cutter: >=5 >=6

Enzyme Number: 117

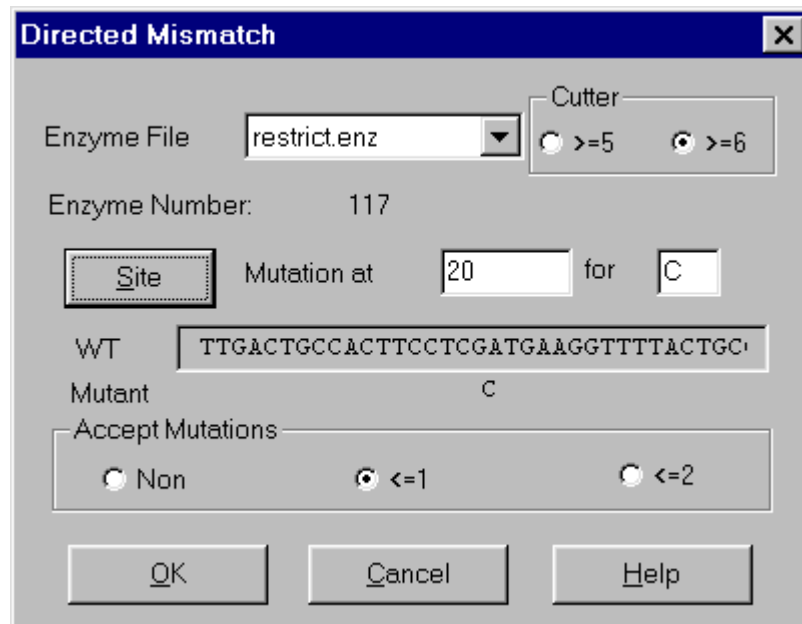
Seq Analysis Region: 1 to 36

5'- TTTGACTGCCACTTCCT GATGAAGGTTTACTGC -3'
 N- F D C H F L D E G F T A -C

OK Cancel Help

Directed mismatch analysis

Directed mismatch analysis allows you to create or remove restriction sites on a DNA sequence or its mutants (variants) by incorporating a single or double mismatch at a site near the mutation. Using this function you can create or destroy a restriction site in order to distinguish the wild type allele and a common mutant allele.



The image shows a dialog box titled "Directed Mismatch" with a close button (X) in the top right corner. The dialog contains the following fields and controls:

- Enzyme File:** A dropdown menu showing "restrict.enz".
- Cutter:** Two radio buttons: ">=5" (unselected) and ">=6" (selected).
- Enzyme Number:** A text field containing "117".
- Site:** A button labeled "Site" with a dotted border.
- Mutation at:** A text field containing "20".
- for:** A text field containing "C".
- WT:** A text field containing the sequence "TTGACTGCCACTTCCTCGATGAAGGTTTTACTGC".
- Mutant:** A text field containing the letter "C".
- Accept Mutations:** Three radio buttons: "Non" (unselected), "<=1" (selected), and "<=2" (unselected).
- Buttons:** "OK", "Cancel", and "Help" buttons at the bottom.

Sequence Assembly

[Sequence assembly method](#)

[Sequence assembly editor](#)

Sequence assembly method

DNAMAN uses fast alignment algorithms to assemble quickly and accurately a large number of overlapping sequences. DNAMAN can automatically adjust the orientation of each fragment and remove vector sequences as well. You can set sensitivity parameters to control gaps and ambiguous sequences in contigs.

The screenshot shows the 'Sequence Assembly' dialog box in DNAMAN. The title bar is blue with the text 'Sequence Assembly' and standard window controls. The main area is grey and contains the following elements:

- Sequence#:** 50
- File list:** A list of files from 'C:\dnaman\test\'. The first file, 'frg9.seq', is selected and highlighted. The list includes 'frg1.seq' through 'frg17.seq'.
- Actions:** A vertical stack of buttons on the right: 'Add file', 'Folder', 'Channel', 'Database', 'Remove', and 'Clear'.
- Options:**
 - Load entire file if format unknown
 - Remove flanking regions when ACGT% < 50 %
 - Remove vector sequence: EXAMPLE1
- Alignment Parameters:**
 - Minimum overlap: 40
 - Identity >=: 90 %
 - Overlap close to sequence ends
- Quick Alignment Section:** A box containing:
 - K-tuple: 4
 - Gap penalty: 6
 - Window size: 4
- End Comparison Section:** A box containing:
 - Maximum overlap: 300
- Assembly Method:** Radio buttons for 'Quick Alignment' (selected) and 'End Comparison'.
- Buttons:** 'Assemble' and 'No overlap'.
- Final Options:**
 - Minimize window while running
 - Allow base verification in trace files
 - Not necessarily compare all sequences prior to final assembly
 - Re-order sequences
 - Use less memory
- Bottom Buttons:** 'Show result' and 'Cancel'.

Sequence assembly editor

DNAMAN displays sequence assembly project in three windows:

- **Graphic window** provides an overview of the assembly construction. You can edit this graphical presentation to produce high quality diagrams for publications.
- **Name list window** contains all assembled sequence names. You can change the sequence order by moving the sequence names in this window.
- **Sequence window** shows all original sequences and a consensus sequence. You can edit any of the original sequences to improve the result of sequence assembly.

The screenshot displays the DNAMAN software interface with the following components:

- Consensus window:** Shows a consensus sequence and two original sequences (frg16 and frg41) aligned to it. The consensus sequence is: `GATGGGAATCGGGATCATTCAAAAAGGCGCATTTCGGTTACTCGCTAAACTACTGTACTCACTATTCTTCGGACCTGCGAAATCTACCCTTAGCCCTAGTAAGTTTTCCGCGTAAAGGCAATGAGCGATTTGATGACATGAGTGATAAGAAGCCTGGACGCTTTA`. frg16 and frg41 are shown with their respective alignments.
- Options window:** Contains two tabs: "Options" and "Export".
- Graphic window:** Shows a graphical representation of the assembly. A horizontal line represents the consensus sequence, with vertical red bars indicating gaps. Below it, a list of original sequences (frg7, frg16, frg41, frg2, frg33, frg40, frg35, frg49, frg29) is shown with blue arrows indicating their alignment to the consensus sequence.

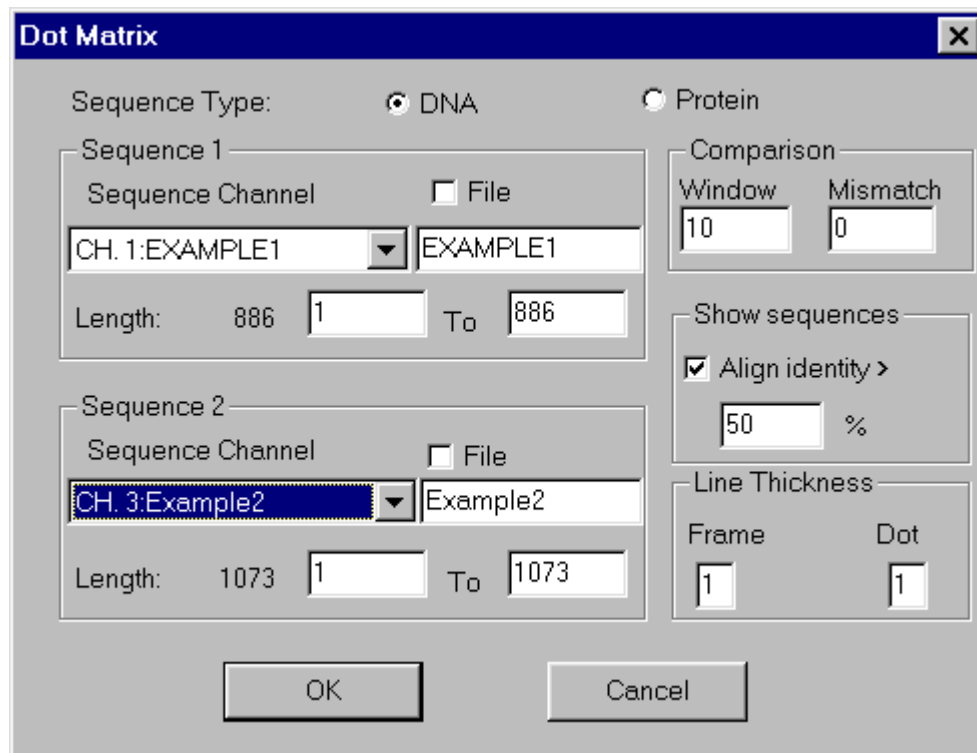
DNAMAN exports sequence the assembly result in a text window. You have options of reporting the consensus sequence only, or all sequences including the consensus sequence and original sequences.

Sequence Homology Analyses

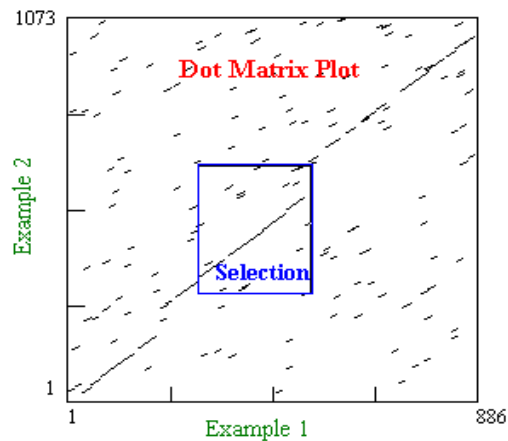
[Dot matrix plot](#)
[Two sequence alignment](#)

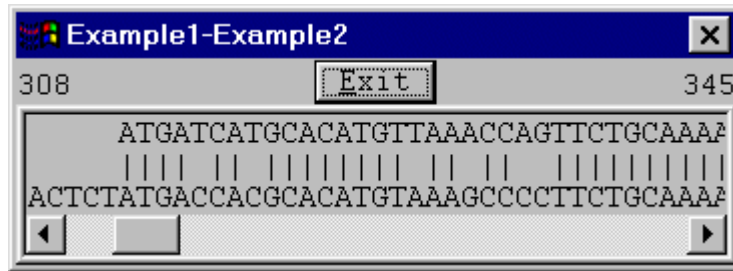
Dot matrix plot

With DNAMAN, you may compare two DNA sequences or two protein sequences in a dot matrix plot. A specific algorithm is developed to yield high quality dot matrix plot. With this method, long DNA sequences can be compared in short time with little background noise. You may efficiently compare genomic sequence with the dot-matrix plot function of DNAMAN.



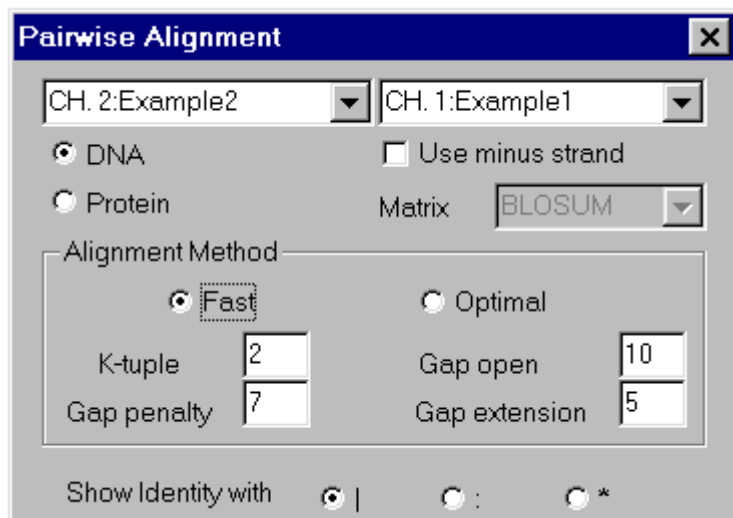
DNAMAN displays the actual sequences and their alignment on any selected region in a sequence window.



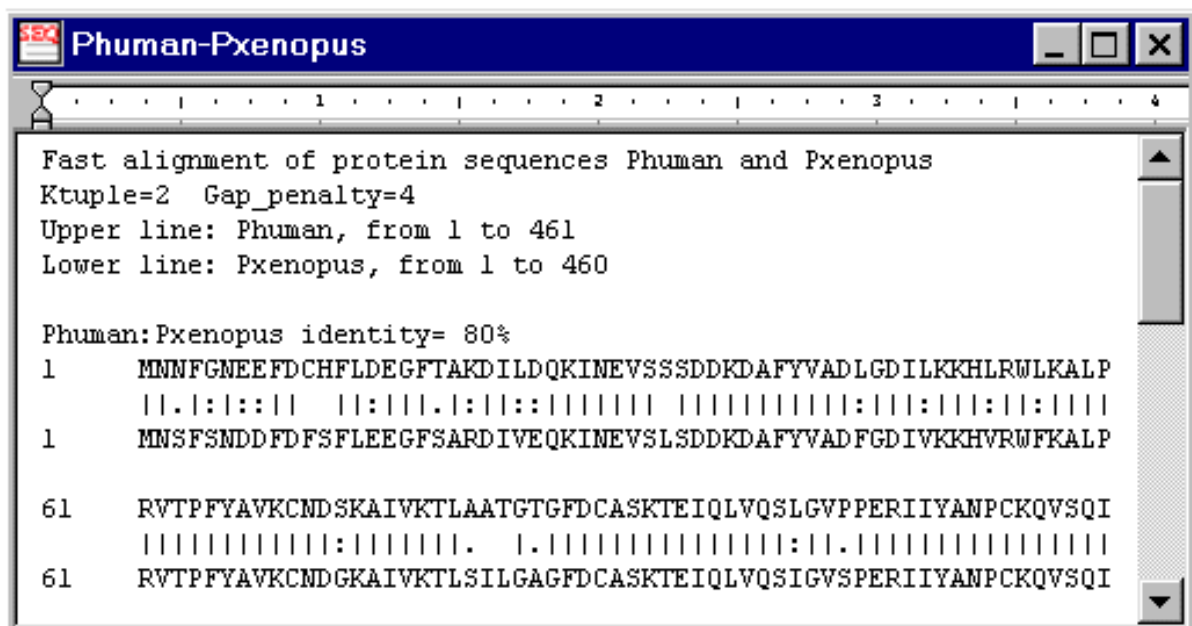


Two sequence alignment

DNAMAN uses fast or optimal algorithms to align two DNA or protein sequences. You have options to control the sensitivity of alignment. DNAMAN also allows you to select any region of target sequences for alignment.



For DNA sequence alignment, you have an option to use the minus strand for comparison. For protein sequence alignment, DNAMAN can report the amino acid similarity of two protein sequences in a text window. The amino acid similarity matrix is editable by users.



Multiple Sequence Alignment

[Multiple sequence alignment methods](#)

[Multiple sequence alignment editor](#)

[Multiple sequence input and output](#)

[Phylogenetic trees](#)

[Restriction analysis](#)

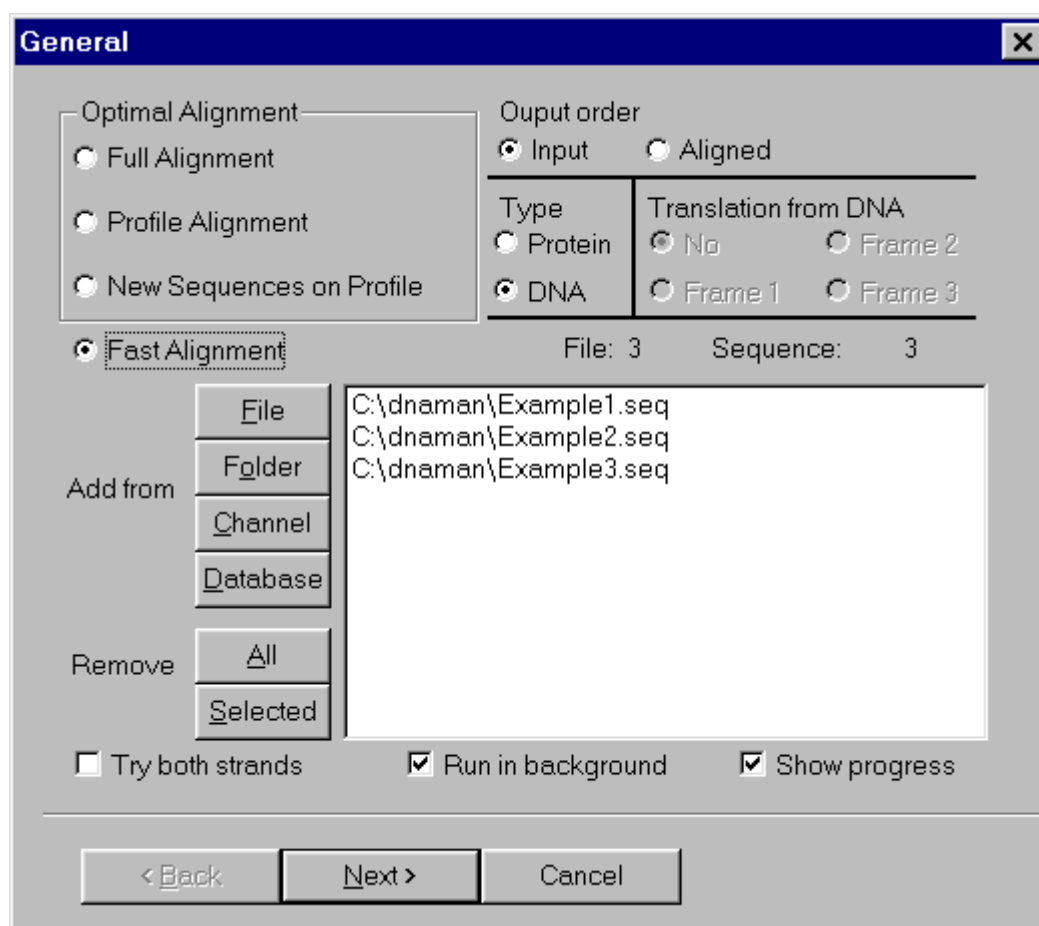
[Hydrophobic / hydrophilic profile](#)

[Secondary structure prediction](#)

Multiple sequence alignment methods

Algorithms

DNAMAN uses ClustalW algorithm (Feng-Doolittle and Thompson) for Optimal Alignment, and the global alignment algorithm (Wilbur and Lipman) for fast alignment. The three types of Optimal Alignment in DNAMAN provide high quality alignment results. With the Fast Alignment method, you may quickly align a large number of DNA or protein sequences.



Parameters and Methods

You may set different parameters to make adequate alignment for your DNA or protein sequences.

The multiple alignment function of DNAMAN is threaded. You may run up to 16 sets of multiple alignment simultaneously. You may also perform other sequence analysis while doing the multiple alignment.

Pairwise Alignment

Quick Alignment Dynamic Alignment

Quick Alignment

Gap Penalty	<input type="text" value="7"/>
K-tuple	<input type="text" value="3"/>
No. of Top Diagonals	<input type="text" value="4"/>
Window Size	<input type="text" value="4"/>

Default Parameters

Dynamic Alignment

Gap Open Penalty	<input type="text" value="10"/>
Gap Extension Penalty	<input type="text" value="5"/>
DNA transition weight	<input type="text" value="0.5"/>
Protein Weight Matrix	<input type="text" value="BLOSUM"/>

< Back

Next >

Cancel

Multiple Alignment

Gap Open Penalty	<input type="text" value="10"/>
Gap Extension Penalty	<input type="text" value="5"/>
%Delay Divergent Sequences	<input type="text" value="40"/>
Protein Weight Matrix	<input type="text" value="BLOSUM"/>

Use negative matrix

Default Parameters

Protein Gap Parameters

Use Residue-Specific Penalties

Use Hydrophilic Penalties

Hydrophilic Residues

Gap Separation Distance

Use End Gap Separation

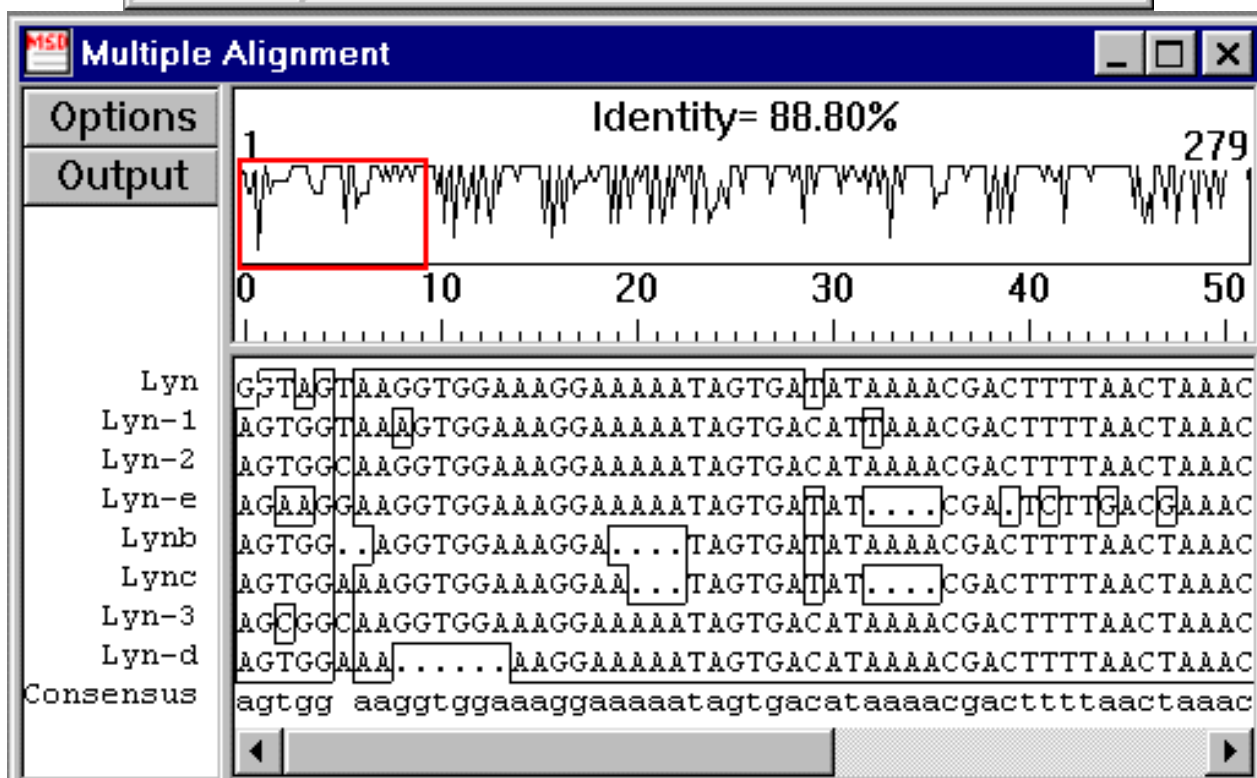
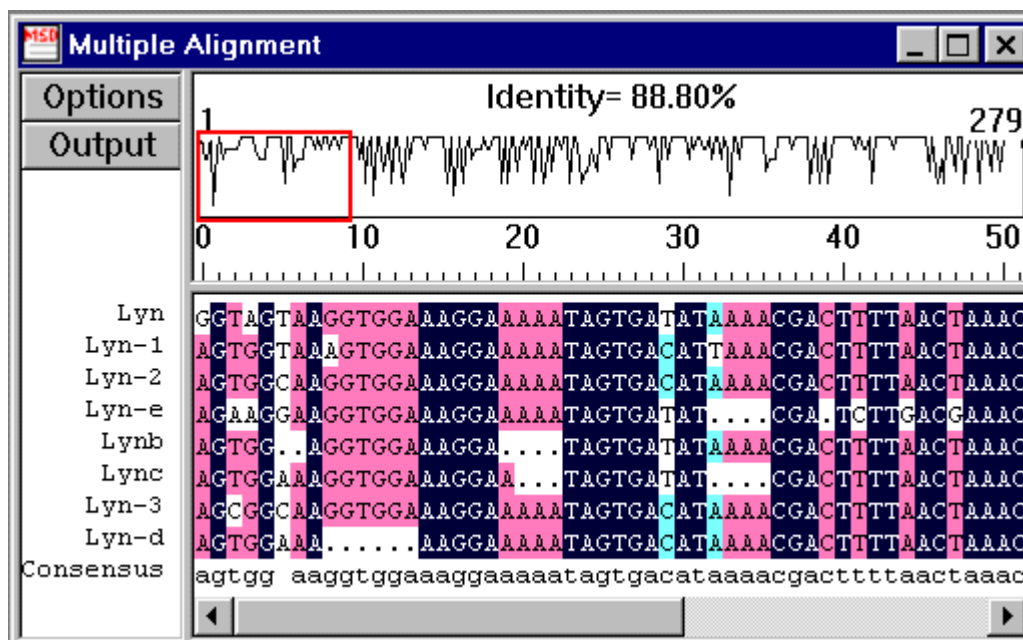
< Back

Finish

Cancel

Multiple sequence alignment editor

DNAMAN provides a high performance alignment editor. A graphical view of the alignment allows you to quickly move to an interesting region. You can change the alignment list order by drag and drop sequence names. You are also able to add or delete gap insertions, move a fragment within a gap and truncate aligned sequences.



You can modify the appearance of multiple alignment sequences:

- displaying identical residues in *colors* or *blocks*
- displaying consensus sequence
- changing text font

Multiple alignment input and output

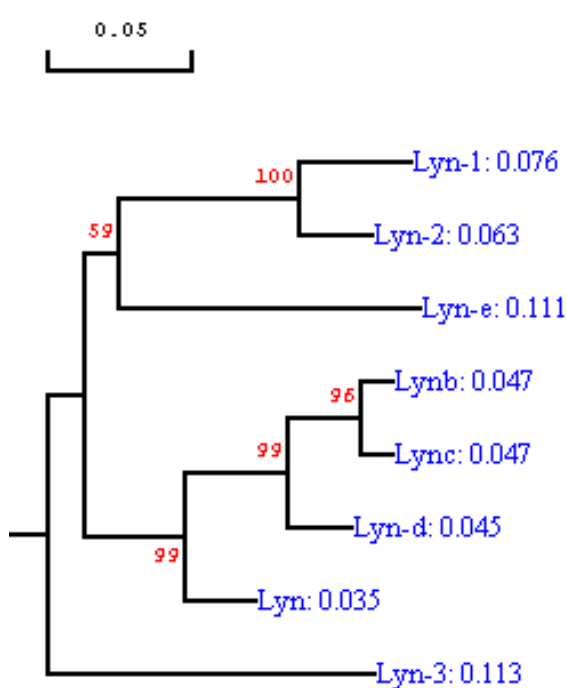
You can directly input sequences or multiple alignment profiles for alignment from the following sources:

- *GenBank*,
- *EMBL/Swiss Prot*,
- *GCG/MSF*,
- *CLUSTAL*,
- *FASTA*,
- *NBRF/PIR*
- *GDE*

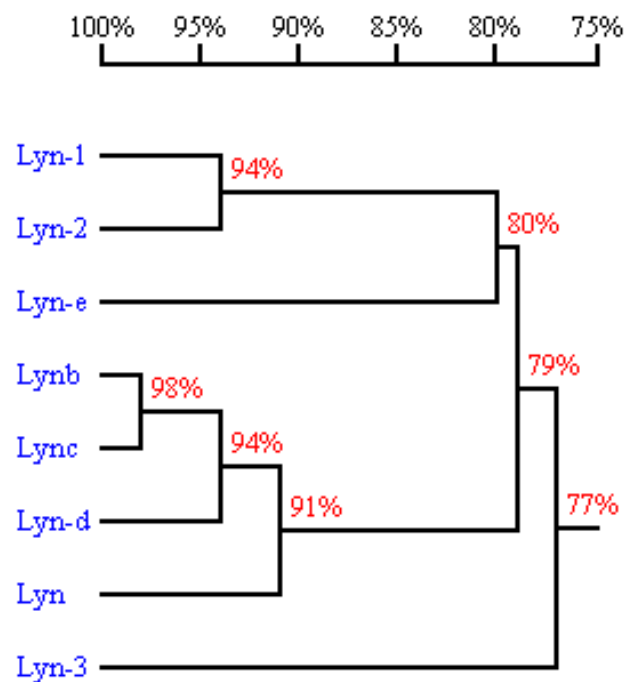
The multiple alignment editor can output an alignment in different formats: *GCG/MSF*, *CLUSTAL*, *NBRF/PIR*, and *GDE*. The multiple input and out put capacity of DNAMAN makes it compatible with major sequence analysis software.

Phylogenetic trees

DNAMAN calculates the homology matrix and establishes related distances between all pairs of sequences. Consequently, DNAMAN can output a **distance matrix** of multiple alignment, and draw **phylogenetic trees** or **homology trees**. You can carry out **bootstrapping** tests for the confidence value of a phylogenetic tree.



Phylogenetic tree



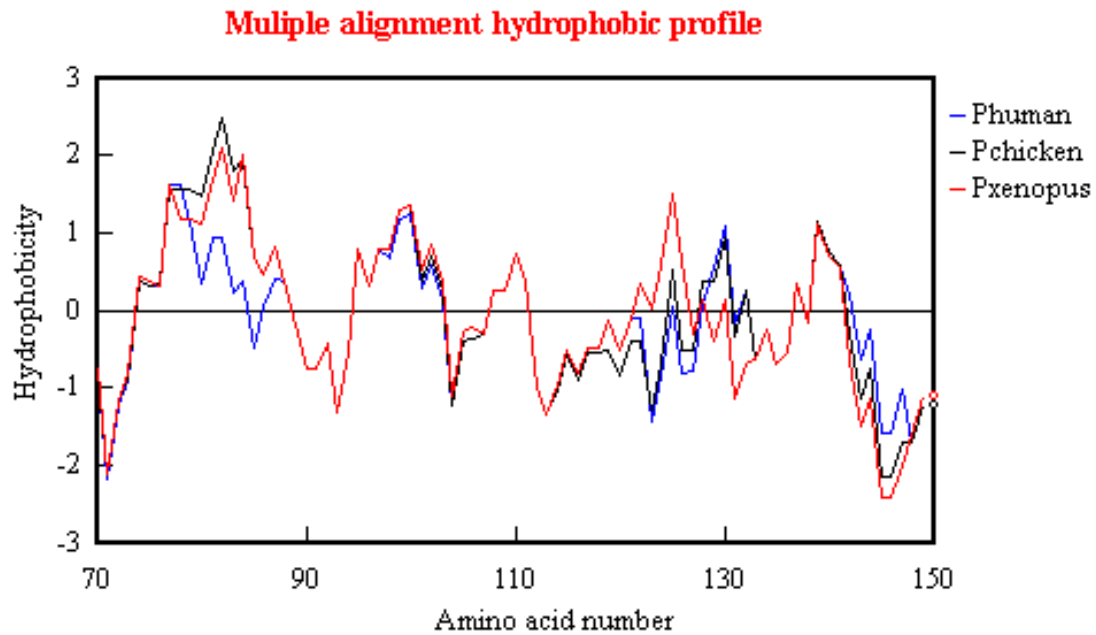
Homology tree

Restriction analysis

If the sequences in multiple alignment editor are DNA, you can perform a restriction analysis on these sequences. This analysis is useful in restriction site comparison of aligned DNA sequences.

Hydrophobic / hydrophilic profiles

If the sequences in multiple alignment editor are protein, you can plot the hydrophobic or hydrophilic profile of all sequences for comparison.



Protein secondary structure prediction

DNAMAN predicts the secondary structure of multiple protein sequences using the DSC method developed by King and Sternberg.

Primer Analysis

[Primer design](#)

[Melting temperature prediction](#)

[Complementarity of primers](#)

[Mispriming analysis](#)

[Silent mutation primers](#)

[Directed mismatch primers](#)

Primer design

The function of primer design includes not only primer filtration by T_m , but also mispriming and restriction analyses on the primers. DNAMAN can help you to find optimal primers that satisfy your requirements.

- DNAMAN allows you to set numerous control criteria for optimal primer filtration, such as the regions of target DNA, size of PCR products, primer characteristics, reaction conditions and primer configurations.

Step 1 of 3: Primer filtration

Primer locations on target sequence		Primer characters <input checked="" type="checkbox"/> Shortest primers only				
Product size (bp) from	400	to	600			
Sense primer from	1	to	886			
Antisense primer from	1	to	886			
Discard primers when		Concentrations				
3' Dimers (bp) >	3	Primer (nM)	50			
Hairpin Stem (bp) >	3	Salt (mM)	50			
PloyN (base) >	3	3' Unique (base) <	6			
<input type="checkbox"/> Product for hybridization	T_m (°C) from	70	to	90	[Salt] (mM)	200
	GC (%) from	40	to	70	PloyN (base) <	8

< Back Next > Cancel Help

- You can carry out a restriction analysis on the primers in order to select those with or without restriction site(s).
- You can discard the primers that are easy to anneal to secondary sites of target DNA using mispriming analysis.

Step 2 of 3: Refinement and pair selection

22 Sense primers Export List 16 Antisense primers

1	TTTGACTGCCACTTCCTCGAT	62.1°C	409	TGGCATGTTACAACGCACAAC	62.9°C
3	TGACTGCCACTTCCTCGATG	62.4°C	411	TCTGGCATGTTACAACGCACA	63.6°C
4	GACTGCCACTTCCTCGATGAA	62.7°C	424	ACCAACTTGCAACTCTGGCAT	62.0°C
33	TGCCAAGGACATTCTGGACC	63.4°C	425	CACCAACTTGCAACTCTGGCA	64.6°C
94	TTCTATGTGGCAGACCTGGGA	62.9°C	426	TCACCAACTTGCAACTCTGGC	63.7°C
195	CAAAGCCAAGACGAAGACGAG	62.3°C	497	GCCTCTGGAATCCGTTGAAA	62.4°C
314	AAGCGGCCTAAACCAGATGA	62.0°C	498	GGCCTCTGGAATCCGTTGAA	64.6°C
367	GTGTGATGGCCTGGATCGTAT	62.1°C	500	TTGGCCTCTGGAATCCGTT	62.9°C
368	TGTGATGGCCTGGATCGTATT	62.6°C	526	GCACAGGAGCATCGCATAATG	63.9°C

Discard primers when :

Primer-Primer (bp) >

Primer Tm difference (°C) >

Mispriming analysis on target sequence Cut off >=

No restriction Keep primers with restriction site

Keep primers without restriction site

< Back Next > Cancel Help

Melting temperature prediction

DNAMAN calculates and reports the thermodynamic T_m, hybridization T_m, and GC+AT T_m of *DNA-DNA* hybridization. You can also have the T_m information on the hybridization of *DNA-RNA* and *RNA-RNA*. These T_ms can be used for PCR primers as well as hybridization probes.

Melting Temperature

Oligo sequence

Length GC% MW(kD)

Melting Temperature (°C):

Thermo Hybrid GC+AT

[DNA] (nM) DNA/RNA

[Na⁺](mM) Formamide(%)

Mismatch(bp)

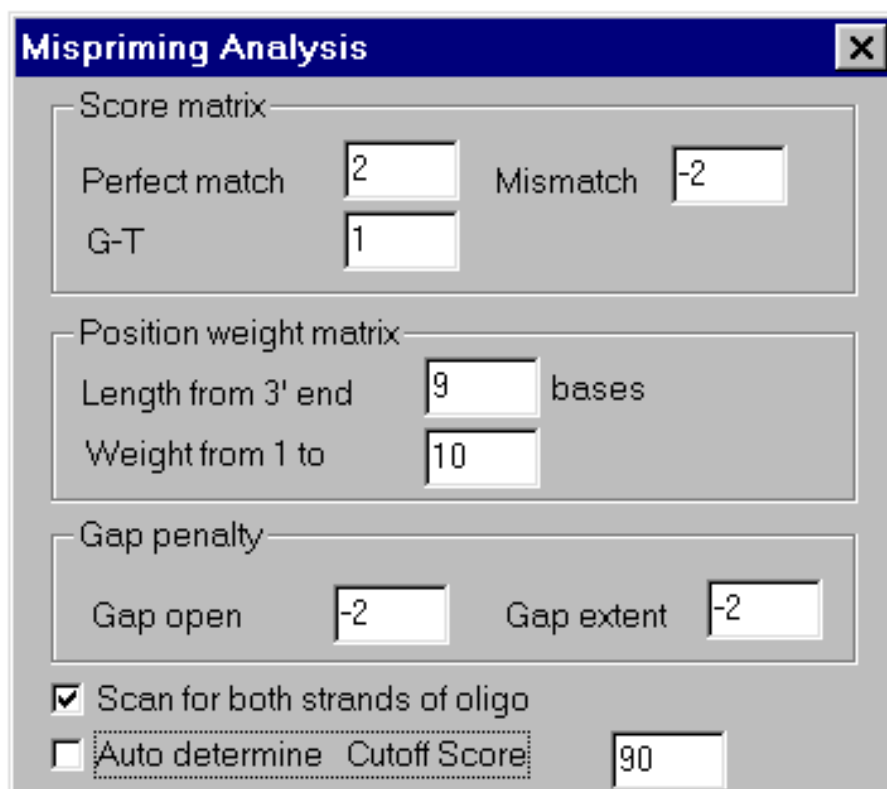
Complementarity of primers

Primer complementarity may affect the performance of PCR primers or hybridization probes. DNAMAN analyzes the following three kinds of primer complementarity.

- Self-complementary
DNAMAN searches for the most possible self-complementary configuration of primers with the lowest free energy.
- Complementarity with target DNA
DNAMAN searches for the complementary sequences between the primer and both stands of target DNA.
- Two primer complementarity
DNAMAN searches for complementary sequences between two primers. It reports the continuous and discontinuous complementary sequences.

Mispriming analysis

With mispriming analysis you can search for all possible annealing sites of a primer on target DNA sequence. DNAMAN allows you to set up **Score matrix**: perfect match, mismatch and G-T match; **Position weight matrix**, **Gap penalty** and **Cut-off score**. This analysis can eliminate PCR primers that are easy to anneal to secondary sites.



The image shows a screenshot of the 'Mispriming Analysis' dialog box. The dialog has a title bar with the text 'Mispriming Analysis' and a close button (X). The main area is divided into several sections with input fields:

- Score matrix:**
 - Perfect match: 2
 - Mismatch: -2
 - G-T: 1
- Position weight matrix:**
 - Length from 3' end: 9 bases
 - Weight from 1 to: 10
- Gap penalty:**
 - Gap open: -2
 - Gap extent: -2
- Scan for both strands of oligo
- Auto determine Cutoff Score: 90

Silent mutation primers

Silent mutation analysis allows you to design a desired mutation site on a DNA sequence. This mutation will result in the modification of restriction property without changing the coding amino acid sequence. This function searches for potential mutation positions to create or destroy restriction enzyme sites. You can use this function to design primers to create a silent mutation on target DNA sequence.

The 'Silent Mutation' dialog box features a title bar with a close button. It includes an 'Enzyme File' dropdown menu set to 'restrict.enz' and a 'Cutter' section with radio buttons for '>=5' and '>=6', with '>=6' selected. Below this, the 'Enzyme Number' is set to '117'. A 'Seq' button is followed by 'Analysis Region' input fields containing '1' and '36'. The DNA sequence is shown as '5'-TTGACTGCCACTTCCTGATGAAGGTTTACTGC-3'' with amino acid translations 'N- F D C H F L D E G F T A -C' below it. At the bottom are 'OK', 'Cancel', and 'Help' buttons.

Directed mismatch primers

Directed mismatch analysis allows you to create or remove restriction sites on a DNA sequence or its mutants (variants) by incorporating mismatch at a site near the mutation. Using this function you can design PCR primers to create or destroy a restriction site in order to distinguish the wild type allele and a common mutant allele.

The 'Directed Mismatch' dialog box has a title bar with a close button. It includes an 'Enzyme File' dropdown menu set to 'restrict.enz' and a 'Cutter' section with radio buttons for '>=5' and '>=6', with '>=6' selected. Below this, the 'Enzyme Number' is set to '117'. A 'Site' button is followed by 'Mutation at' input fields containing '20' and 'C'. The DNA sequence is shown as 'WT TTGACTGCCACTTCCTCGATGAAGGTTTACTGC' with a 'Mutant' label and a 'C' below it. An 'Accept Mutations' section has radio buttons for 'Non', '<=1', and '<=2', with '<=1' selected. At the bottom are 'OK', 'Cancel', and 'Help' buttons.

Translation and Protein Analysis

[Translation](#)

[Genetic code table](#)

[Reading frame overview](#)

[Codon usage analysis](#)

[Amino acid composition](#)

[Protein hydrophobic and hydrophilic profile](#)

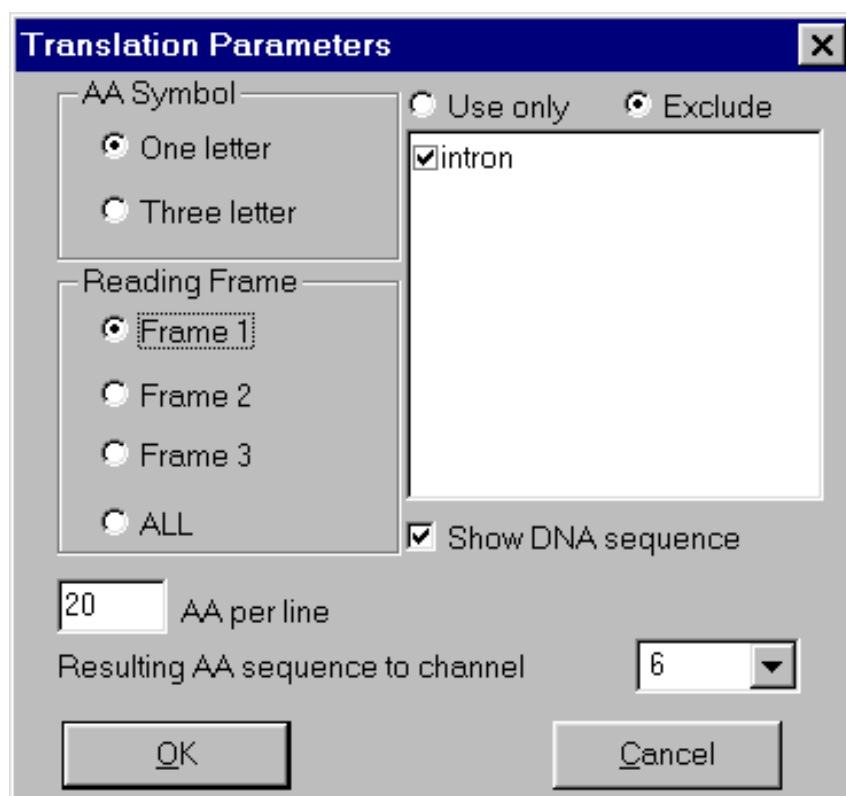
[Protein charge and pI analysis](#)

[Protein secondary structure prediction](#)

[Reverse translation](#)

Translation

DNAMAN deduces protein sequences from three reading frames of a DNA sequence and displays results with many options. By setting the number of amino acid per one line, you can change the layout of the translation file.



DNAMAN allows you to select any region from a sequence file, and perform translation analysis. In the report file DNAMAN shows both translated and untranslated regions.

```
Example2_Translation
1 CACCTTCCTTTCCGAGGGCTTTACTGCCAaggatatcctcgaccaaaaaataaacgaagt
1 H L P F R G L Y C H
61 gtcacatcttctgatgataaagatgccttctatggtgctgacctcgggggatattgtaaagaa
121 gcacatgcggtggcataaagcccttctctcgagtaacccccTTCTACGCTGTCAAATGGTA
11 S T L S N G
181 ATCGACAGTCAGCTTTCACGCTTGCAGTTAATATCATTGCCAAGAAAAATTGTATTAAAGG
17 N R Q S A F T L A V N I I A K K I V L K
241 AACAGACGGGCTCTGATGACGAAGATGAGTCGAGTGAGCAGACCTTTATGTATTATGTGA
37 E Q T G S D D E D E S S E Q T F M Y Y V
301 ATGATGGCGTCTATGGATCATTTAATTGCATACTCTATGACCACGCACATGTAAAGCCCC
57 N D G V Y G S F N C I L Y D H A H V K P
361 TTCTGCAAAAAGAGACCTAAACCAGATGAGAAGTATTATTTCATCCAGCATATGGGGACCAA
77 L L Q K R P K P D E K Y Y S S S I W G P
```

Genetic code table

DNAMAN provides seven genetic code tables with the options of adding new code tables or editing any existing one. You may select any genetic code table for translation and protein analysis.

Reading frame overview

DNAMAN presents a graphical overview on six reading frames of a DNA sequence. It is a useful feature to locate the ORFs on a large DNA sequence.

Codon usage analysis

DNAMAN provides a codon usage table for any reading frame of a DNA sequence. The table indicates the number and frequency of each codon used in a reading frame.

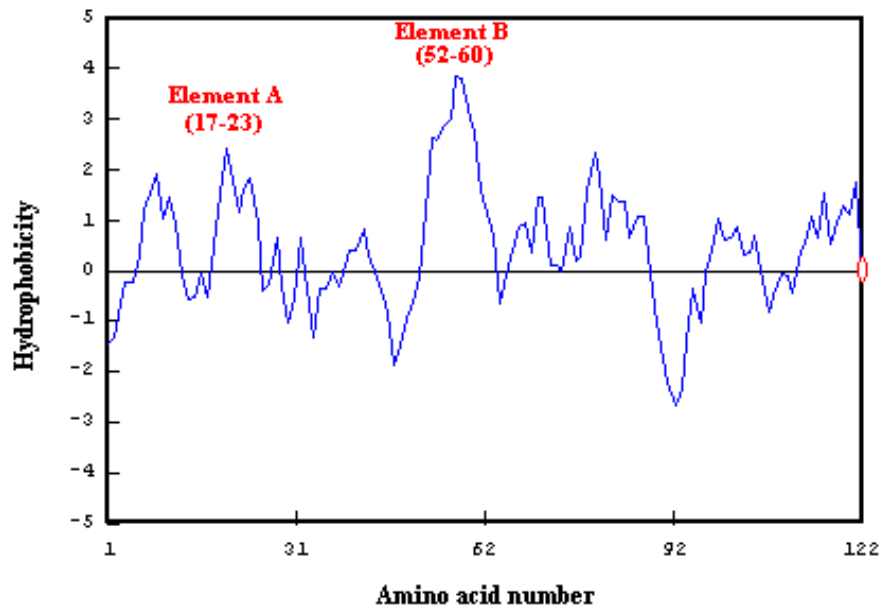
Amino acid composition

DNAMAN reports the amino acid composition, pI and molecular weight of a protein sequence.

Protein hydrophobic and hydrophilic profile

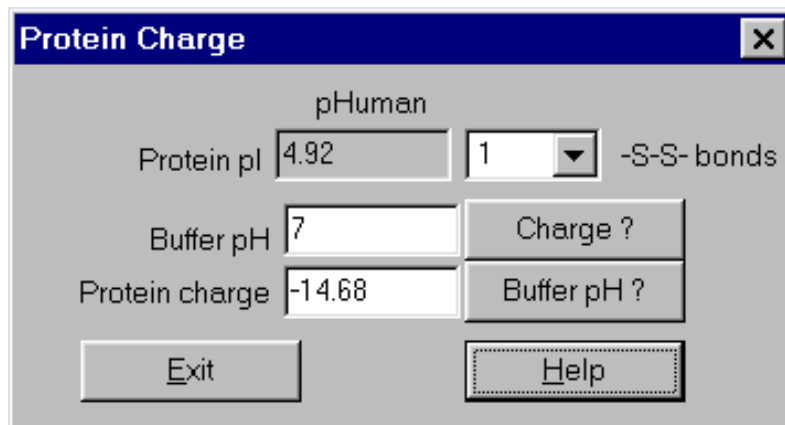
DNAMAN shows protein hydrophobic and hydrophilic profiles in a graphic window that may help you to predict *hydrophobic clusters* or *antigen regions* in a protein sequence. The graphical profiles are editable to produce high quality illustrations for publications.

EXAMPLE1:Reading frame 1:Hydrophobic profile



Protein charge and pI analysis

DNAMAN calculates protein charge at a given pH. It shows also the predicted isoelectric point of the protein. In addition, DNAMAN can deduce the suitable buffer pH for a desired charge.



Protein secondary structure prediction

DNAMAN predicts the secondary structure of a protein sequence using the DSC method developed by King and Sternberg.

Reverse translation

DNAMAN provides the reverse translation of a protein sequence. It reports the reverse translated DNA sequence with ambiguous nucleotides at variant positions. This feature can be used to degenerate primers from peptide sequences.

Database Management

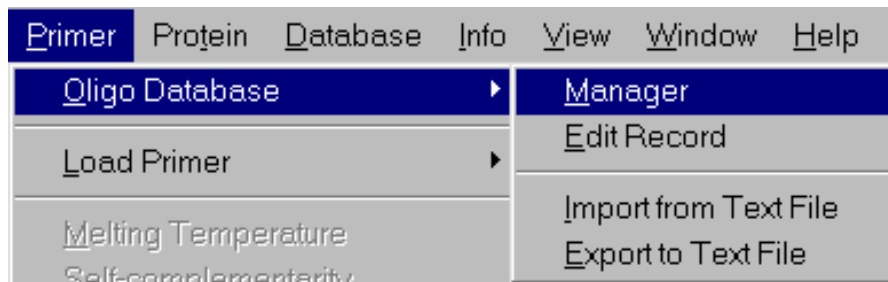
[Oligo database](#)

[DNA and protein database](#)

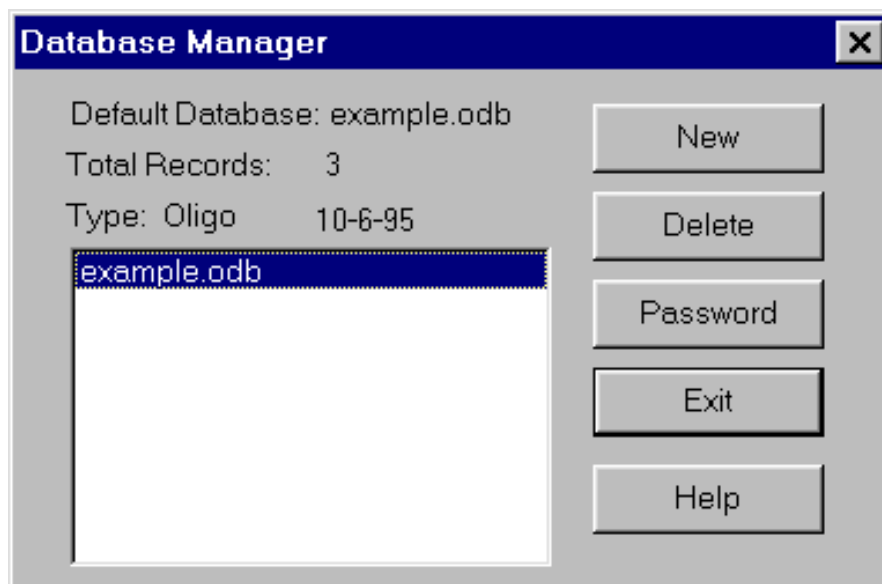
[Searching in DNA or protein database](#)

Oligo database

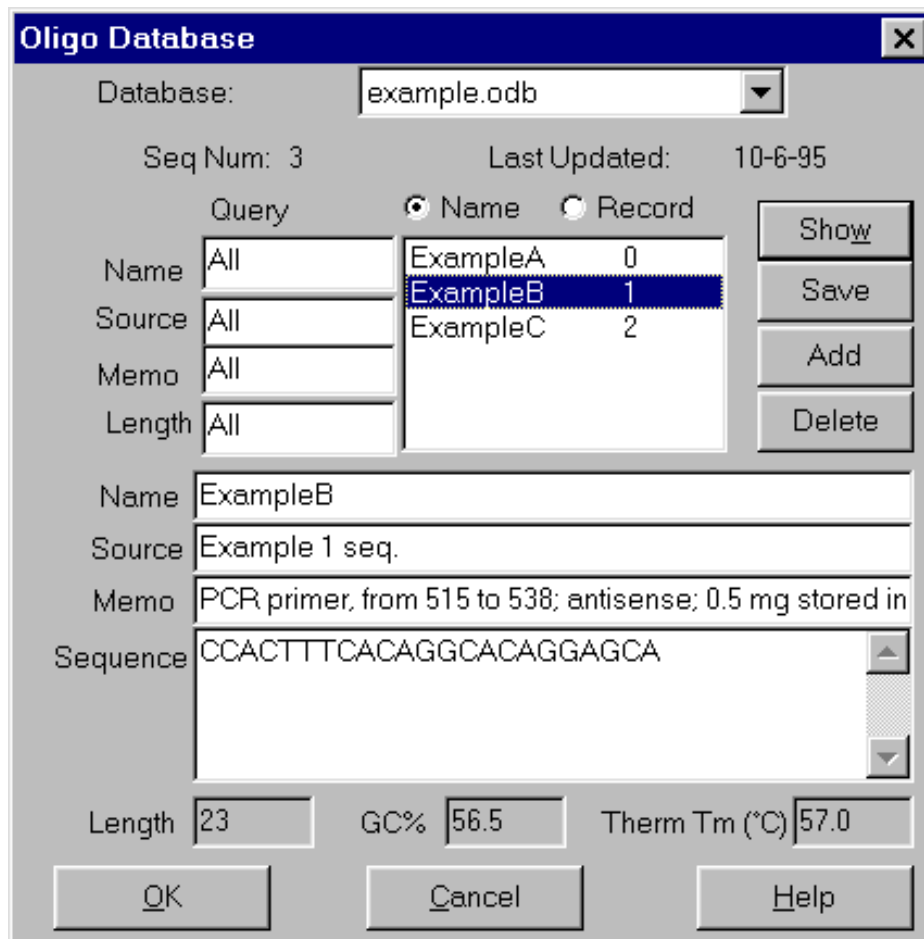
You may have a large number of oligo nucleotides for experiments of sequencing, blotting, PCR, etc....DNAMAN provides an oligo database manager that can help you to effectively organize and use these oligoes.



When you create oligo databases for different projects. DNAMAN allows you to attach a password for the security of the database.

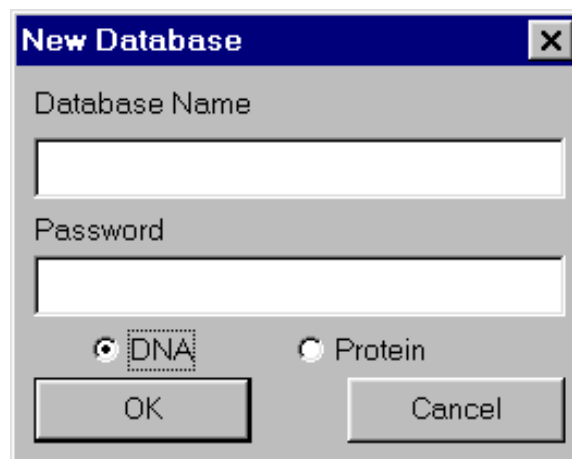


- Any oligo database is expandable and all records are editable.
- You can provide information for each record in seven fields: name, source, memo, length, GC content, melting temperature and sequence.
- The name, source, memo, length can be used as sorting keys.
- You can import a large number of oligo records from a text file, or export any record to a text file.



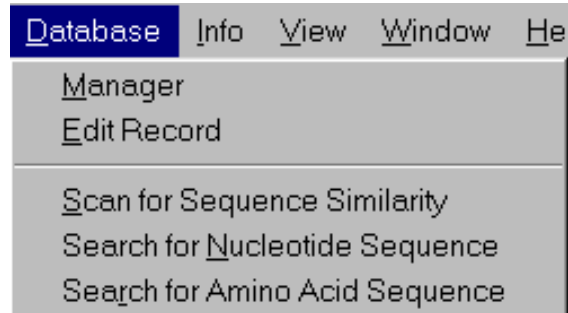
DNA and protein database

DNAMAN database manager is used to collect and store DNA and protein sequences. You can create or delete a DNA or protein database and set security to protect the database.



DNAMAN has an easy-to-use database manager. All databases are expandable and all records are editable. You can directly import records from text files, GCG and GenBank files. The information related to any record is shown in seven fields: sequence name, definition, keywords, source, reference, memo, coding region. The first four fields can be used as sorting keys.

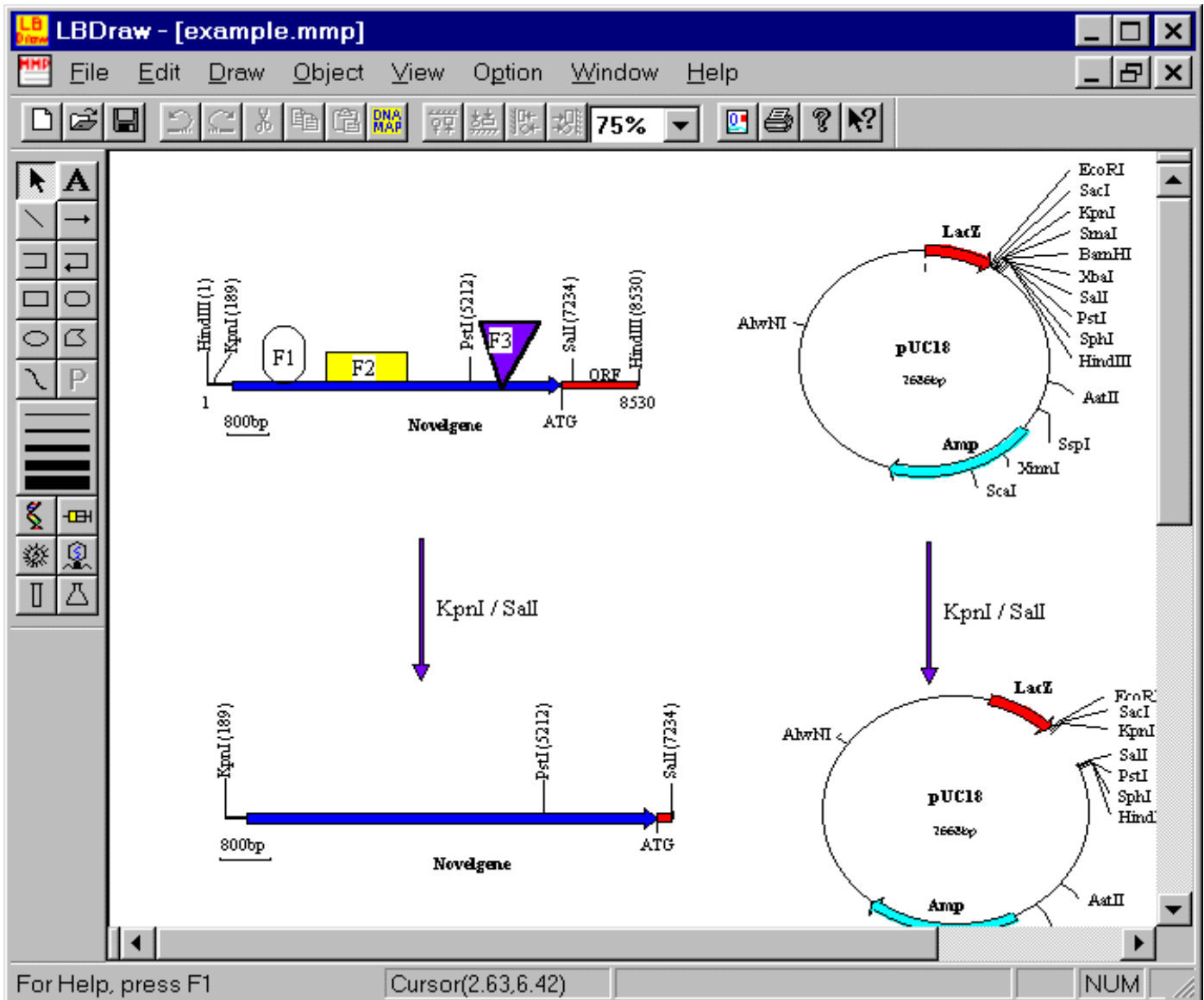
Searching in DNA or protein database



- You may search for homology sequences of a target DNA by scanning all records in a DNA database. The algorithm for the comparison is fast alignment method.
- You may search for a nucleotide sequence from both strands of all records in a DNA database.
- You may search for a peptide sequence from all records of a protein database as well as the six reading frames of all records in a DNA database.



LBdraw: Designed for Molecular Biologists



Features of LBDraw

[What LBDraw does](#)

[Communication with DNAMAN](#)

[Standard drawing tools](#)

[Drawing tools for molecular biologists](#)

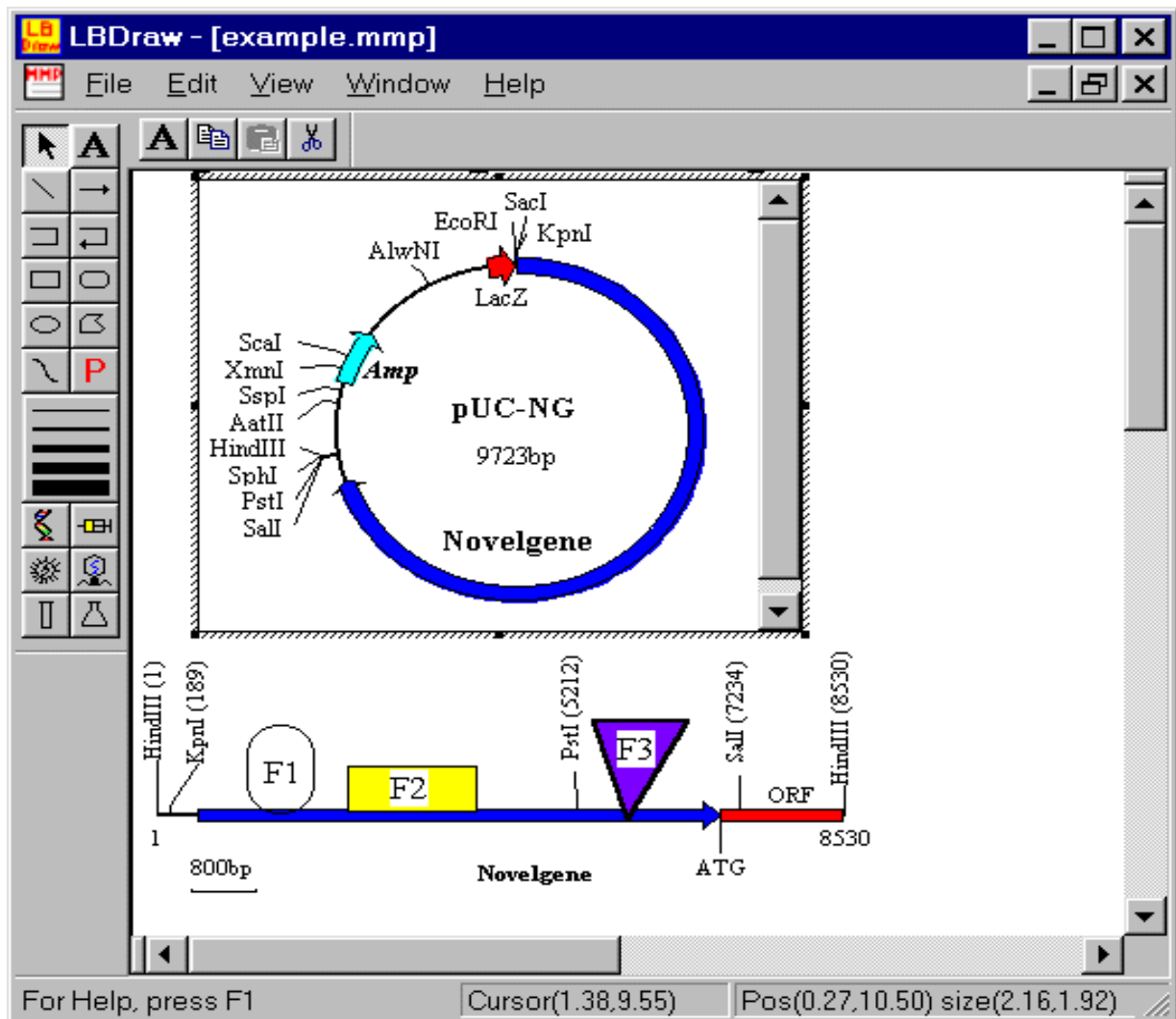
What LBDraw does

LBDraw is a Windows drawing program. It is designed to draw and assemble drawing objects. It provides not only standard drawing tools, such as rectangle and ellipse tools, but also the tools designed for molecular biologists, such as double strand DNA structure and virus tools. LBDraw is an OLE server and client application, which means you can incorporate objects of any other OLE server programs into LBDraw and

deliver LBDraw objects to other OLE client applications. This is especially useful to draw diagrams in molecular biology.

Communication with DNAMAN

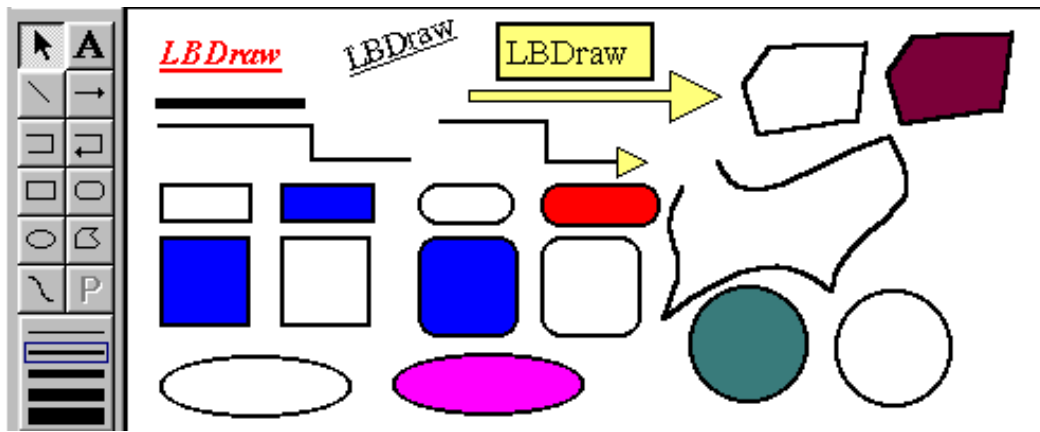
DNAMAN is an OLE server of the restriction map object. When you insert a restriction map of DNAMAN into a LBDraw document, you can edit the map directly in the document with the DNAMAN editing tools.



The word processor (Text Editor) of DNAMAN is an OLE client. You can insert the drawings of LBDraw into the word processor. You are also able to edit the drawings in DNAMAN with the drawing tools of LBDraw.

Standard drawing tools

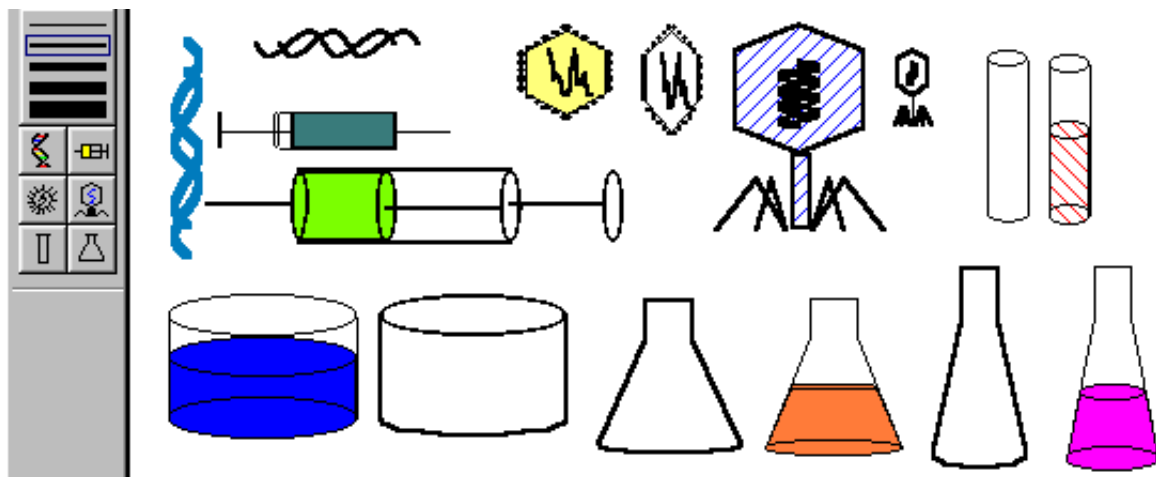
LBDraw provides the following standard drawing tools: Text, Straight Line, Arrow Straight Line, Multiple Line, Arrow Multiple Line, Rectangle and Square, Rounded Rectangle and Square, Ellipse and Circle, Polygon and Curves. You can select any color for drawing lines and filling into objects.



All objects in LBDraw can be aligned to top, bottom, left or right. You can also move them forward or back in the third dimension.

Drawing tools for molecular biologists

In addition to above standard drawing tools, LBDraw provides tools specifically for molecular biologists: Double Strand DNA Structure, Needle, Virus, Bacteriophage, Test Tube/Beaker and Flask.



You can fill with liquid (color) into Needle, Test Tube/Beaker and Flask. You can also regulate the levels of liquid in these containers.