

DNAMAN

Sequence Analysis Software

Introduction

BIOINFORMATICS PLATFORM

DNAMAN Features

- ▶ Integrated Sequence Analysis System
- ▶ Sequence Editing
- ▶ Restriction Analysis – In Silico Cloning
- ▶ Multiple Sequence Alignment
- ▶ Phylogenetics Analysis
- ▶ Dot-Plot Analysis
- ▶ Sequence Assembly
- ▶ PCR Primer Selection
- ▶ Protein Sequence Analysis
- ▶ Database – Sequence Management

DNAMAN User Interface

The screenshot displays the DNAMAN software interface for the file 'abi_sample1.abi'. The interface is divided into several main sections:

- Menu Bar:** Includes 'File', 'Sequence', 'Protein & Database', and 'View'. The 'Sequence' menu is expanded, showing options like 'Cut', 'Copy', 'Paste', 'Delete', 'Font', 'Repeat', 'Replace', 'Zoom In', 'Zoom Off', 'Zoom Out', 'Paragraph', 'Align to Left', 'Output', 'Load Seq', 'Define Seq', 'Translation', 'Restriction Analysis', 'Align Pairwise', 'Align Multiple', 'Seq Assembly', 'PCR Primers', 'Seq Search', 'Custom Command', 'Convert Enzyme File', 'Amino Acid', 'Methylase', 'Nucleotide', 'Codon Table', and 'Settings'.
- File Explorer:** Located on the left, it shows a tree view of 'DNAMAN Files' with subfolders like 'assembly-ben', 'consens', 'dbase', 'input', 'malign', 'output', 'plugins', and 'seq'. A list of files is shown below, including '3seq-test.seq', 'abi_sample1.abi', and various '.seq' and '.dmp' files.
- Sequence Editor:** The central pane displays the sequence of 'EXAMPLE1.SEQ'. It includes 'COLOURS' (sequence = 1, features = 0), 'FEATURES' (intron at 31..161, cds at 163..601), and 'ORIGIN' with a multi-line DNA sequence. Below the editor is a 'DNAMAN' plasmid map showing 'Promoter A', 'Amp^r', 'Lac', 'MCS', 'Gene 1', and 'Deletion' regions, along with restriction enzyme sites like 'BamHI (600)', 'KpnI (750)', 'HindIII (1730)', and 'SacI (1740)'. A legend lists enzymes such as 'NotI (2574)', 'KpnI (2562)', 'HindIII (2550)', 'SmaI (2543)', 'BamHI (2531)', 'SacI (2513)', and 'EcoRI (2502)'.
- Chromatogram:** On the right, it shows a chromatogram for 'abi_sample1.abi' with 'ABI01.abi' selected. The plot displays four traces for A (red), G (blue), C (green), and T (black) over a sequence range from 40 to 100. A legend below the plot shows checked boxes for A, G, C, and T, and unchecked boxes for 'P. C. Strand' and 'Sync All Traces'. An 'Export Seq' button is also present.

DNAMAN User Interface

The screenshot shows the DNAMAN software interface with several components highlighted by red arrows and labels:

- Quick Tool Bar:** Located at the top left, below the ribbon, containing icons for File, Load Seq File, Define Seq, Translation, Restriction Analysis, Custom Command, and Information.
- Ribbon Tool Bar:** The top ribbon containing tabs for Home, Sequences, Protein & Database, and View, with various sub-panels for editing and analysis.
- Sequence Controls:** A panel on the left side of the main workspace, containing a file browser and a list of files.
- Document Bar:** A horizontal bar at the top of the main workspace showing open documents like EXAMPLE1.SEQ, EXAMPLE2.SEQ, etc.
- Browser Bar:** A panel at the bottom left showing a file tree structure under 'DNAMAN Files'.
- Documents:** A panel at the bottom right showing a list of files with columns for Name, Size, and Type.

Name	Size	Type
3seq-test.seq	34 KB	DNAMAN Docu
3seq-test2.seq	34 KB	DNAMAN Docu
65seqs.saf	57 KB	DNAMAN saf
abi_sample1.abi	132 KB	DNAMAN abi
AJ403983.seq	8 KB	DNAMAN Docu
AssemblySampl...	1,278 KB	DNAMAN Docu
EXAMPLE1.SEQ	2 KB	DNAMAN Docu
EXAMPLE2.SEQ	2 KB	DNAMAN Docu
EXAMPLE3.SEQ	2 KB	DNAMAN Docu
EXAMPLE22017...	2 KB	DNAMAN Docu
EXAMPLE32017...	2 KB	DNAMAN Docu
fasta_example.f...	4 KB	DNAMAN msd
FJ389172.seq	14 KB	DNAMAN Docu
FJ389178.seq	12 KB	DNAMAN Docu
FVE-dna.ptr	1 KB	DNAMAN ptr
FVE-protein.ptr	1 KB	DNAMAN ptr
genbank_puc18...	315 KB	DNAMAN Docu
GFF_seq.seq	3 KB	DNAMAN Docu

Quick Start

DNAMAN Uses Channels to Keep Active Sequences for Analysis

The screenshot shows the DNAMAN software interface. The 'File' menu is open, displaying a list of files in the 'DNAMAN Files' folder. The file 'EXAMPLE1.SEQ' is highlighted with a red circle and the number '2'. The 'File' menu item is also circled in red with the number '1'. The 'Channel' tab is selected in the bottom navigation bar, with a red circle and the number '3' next to it. An orange callout box on the right contains the following instructions:

Start DNAMAN Program

1. Click File tab in Sequence Controls
2. Double-Click Example1.seq
3. Click Channel tab in Sequence Controls

Example1 sequence loaded into Channel 1

Name	Size	Type
3seq-test.seq	34 KB	DNAMAN Docu
3seq-test2.seq	34 KB	DNAMAN Docu
65seqs.saf	57 KB	DNAMAN saf
abi_sample1.abi	132 KB	DNAMAN abi
AJ403983.seq	8 KB	DNAMAN Docu
AssemblySampl...	1 278 KB	DNAMAN Docu
EXAMPLE1.SEQ	2 KB	DNAMAN Docu
EXAMPLE2.SEQ	2 KB	DNAMAN Docu
EXAMPLE3.SEQ	2 KB	DNAMAN Docu
EXAMPLE22017...	2 KB	DNAMAN Docu
EXAMPLE32017...	2 KB	DNAMAN Docu
fasta_example.f...	4 KB	DNAMAN msd
FJ389172.seq	14 KB	DNAMAN Docu
FJ389178.seq	12 KB	DNAMAN Docu
FVE-dna.ptr	1 KB	DNAMAN ptr

Quick Start

DNAMAN - EXAMPLE1.SEQ

Home Sequence Protein & Database View

Clipboard Editing Quick Analysis Information

Channel EXAMPLE1.SEQ

All Channels

- Channel 1: example1 (DNA)
 - Len=886 From 1 to 886: 2 Annotations
 - 31..161 [intron] Unknown
 - 163..601 [cds] PBS
- Channel 2: Empty
- Channel 3: Empty
- Channel 4: Empty
- Channel 5: Empty
- Channel 6: Empty
- Channel 7: Empty
- Channel 8: Empty
- Channel 9: Empty
- Channel 10: Empty
- Channel 11: Empty
- Channel 12: Empty
- Channel 13: Empty
- Channel 14: Empty
- Channel 15: Empty
- Channel 16: Empty
- Channel 17: Empty
- Channel 18: Empty
- Channel 19: Empty
- Channel 20: Empty

EXAMPLE1.SEQ

```
SEQ example1.seq: 886 bp;
Composition 256 A; 159 C; 195 G; 276 T; 0 OTHER
Percentage: 28.9% A; 17.9% C; 22.0% G; 31.2% T; 0.0% OTHER
Molecular Weight (kDa): ssDNA: 274.14 dsDNA: 546.13
COLOURS
sequence = 1
features = 0
FEATURES
intron          31..161
                /name="Unknown"
cds             163..601
                /name="PBS"
ORIGIN
1      TTTGACTGCC ACTTCCTCGA TGAAGTTTT ACTGCCAAGG ACATTCTGGA CCAGAAAATT
61     AATGAAGTTT CTTCTTCTGA TGATAAGGAT GCCTTCTATG TGGCAGACCT GGGAGACATT
121    CTAAGAAAC  ATCTGAGGTG GTTAAAAGCT CTCCTCGTGG TCACCCCTTT TTATGCASTC
181    AATGTAAATG ATAGCAAAGC CARGACGAAG ACGAGAGAAT GACAAAACAC TCATGTATTA
241    CGGGAATGAT GGTGTCTATG GATCGTTCAA TTGCATCTTG TATGATCATG CACATGTTAA
301    ACCAGTTCTG CAAAAGCGGC CTAACCAGAG TGACGCGCTG TACTCCTGCA GCATATGGGG
361    ACCAACGTGT GATGGCCTGG ATCGTATTGT TGTGCGTGTG AACATGCCAG AGITGCAAGT
```

Example1 sequence loaded into Channel 1

1. Click Restriction Analysis Tool, or
2. Click Translation Tool, or
3. Click Search Tool

Ready Channel Database File

Channel 1:DNA example1 886bp CAP NUM SCRL

Restriction Analysis

Restriction Analysis



1

Results

Show summary

Show sites on sequence

2

Draw restriction map

Draw restriction pattern

Ignore enzymes with more than 0 sites

Ignore enzymes with less than 0 sites

List site order and non-cutting enzymes

60 bases per line

With double-stranded sequence

With enzyme position

Including annotations

Target DNA

Circular

dam methylation

All DNA in sequence channels

dcm methylation

Click Restriction Analysis Tool

1. Check Show Summary

2. Check Draw Restriction Map

3. Click Next

3

< Back

Next >

Cancel

Restriction Analysis

Enzyme Selection

Enzyme File: RESTRICT.ENZ Save list

AatI
AlwNI
ApaBI
ApaI
BbeI
BglI
BsmI
BstXI
DraIII
DrdI
Eam1105I
Eco57I
FseI
I-PpoI
KpnI
NsiI
PacI

2 Select All >>

<<Clear

Restriction Analysis

1. Click 3' Overhang
2. Press Select All Button
3. Click Finish

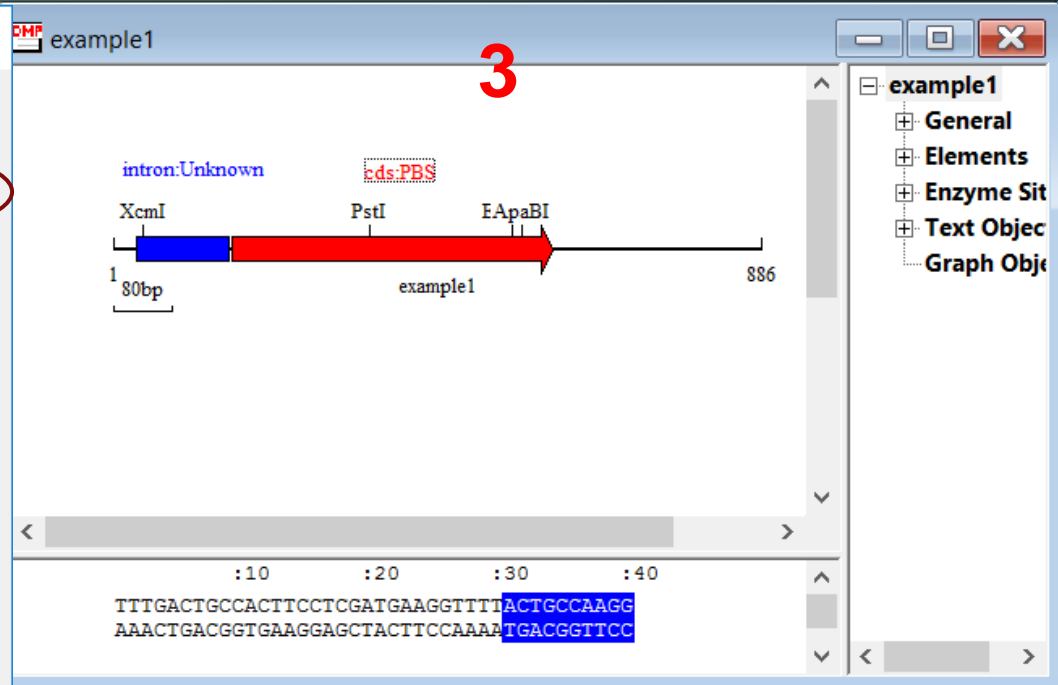
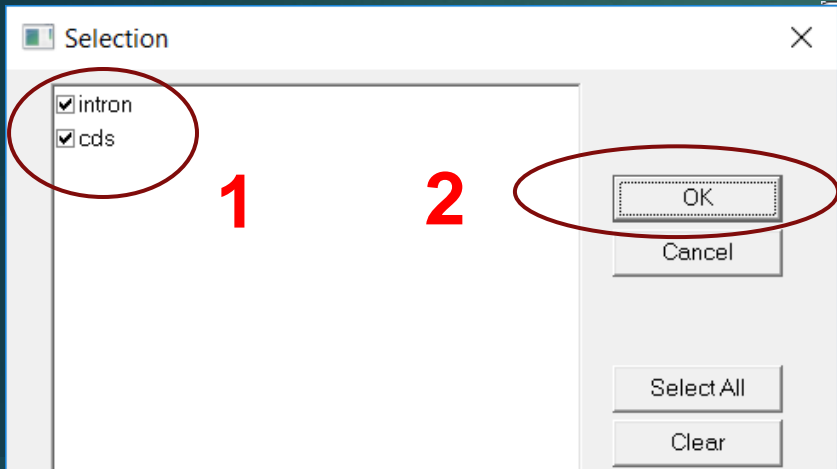
List: 29 Selected: 0

Cutter: All >=5 >=6 >=8

End: All Blunt 5' Overhang 3' Overhang **1**

3 < Back Finish Cancel

Restriction Analysis



- Restriction Analysis
1. Select Annotations
 2. Click OK Button
 3. Analysis Results

