# DNASIS® MAX Version 2.5

MiraiBio
A Group of Hitachi Software

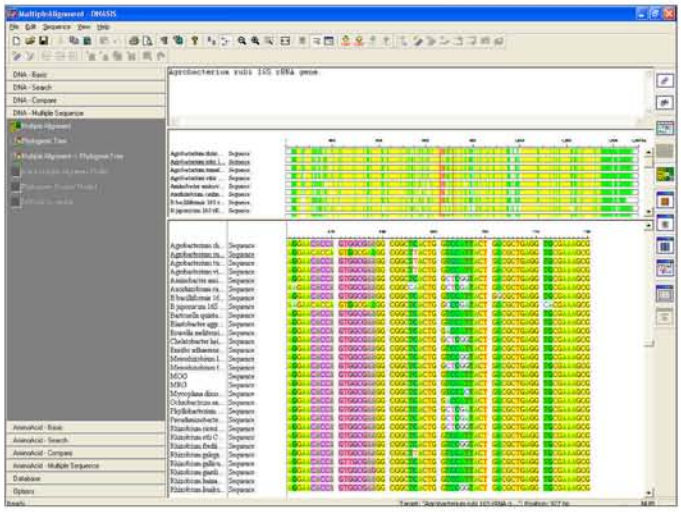
**Software for Advanced Data Management & Sequence Analysis**

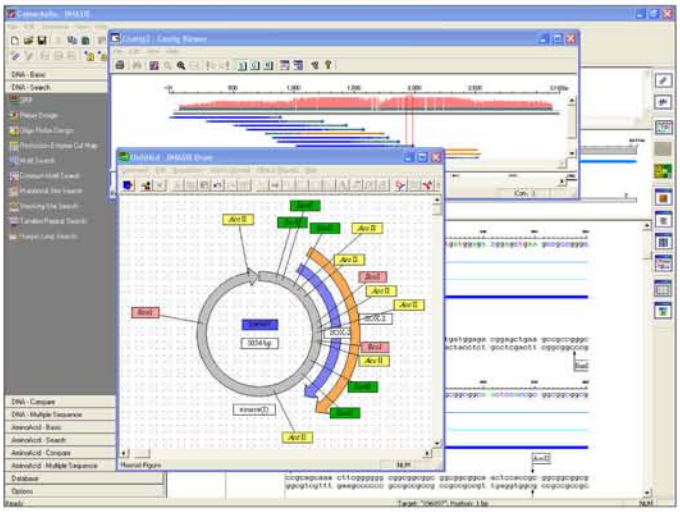
The revolution in molecular biology has been made possible by advances in computer technology and software design. Bioinformatics tools - once considered a luxury - are now a research requirement. By refining and accelerating components of the discovery process, these tools allows researchers to rapidly discern relationships that could not be easily detected by any other means and provide more time to focus on experimental design and results interpretation.

DNASIS® MAX is a fully integrated and complete desktop sequence analysis software package for DNA and amino acids that delivers everything expected from a state of the art bioinformatics tool - powerful molecular biology functions, multiple consensus calling methods, and quick BLAST searches - plus unique features that enhance common task performance and allow user-defined product customization.

## Features

- Sequence Editing/Annotation
- Primary and Secondary Structure Analyses
- Contig Management
- Plasmid Map Editing
- PCR/Oligo Probe Design
- Sequence Clustering
- Multiple Alignment
- Vector and Low Quality End Trimming
- Optional Phred/Phrap Capability





The release of DNASIS MAX 2.5 - the next generation of sequence analysis software in the line of DNASIS® MAX programs - will lead your research to the next level. This new version of DNASIS MAX offers additional advanced data management and analysis capabilities and enables state-of-the-art computing technology.

## NEW in v2.5

- Customizable analyses and workflow with open API and SDK
- Drag and Drop Analysis
- New Analysis Wizard
- Improved Tandem Repeat, Hairpin Loop, and Stacking Site search capability
- Easier Multiple Alignment from trace files
- Improved BLAST search options
- Redesigned Analysis List View
- Increased User Database functionality with new text searching and editing options
- Direct sequence retrieval and export to DNASIS MAX editor window
- Automatic import of EMBL and PIR annotations
- Easy return to original parameter set
- Efficient interface with DNASIS GeneIndex multiple database query and knowledge mining service

## Call +49 (0) 6221/82 78 0 To Order

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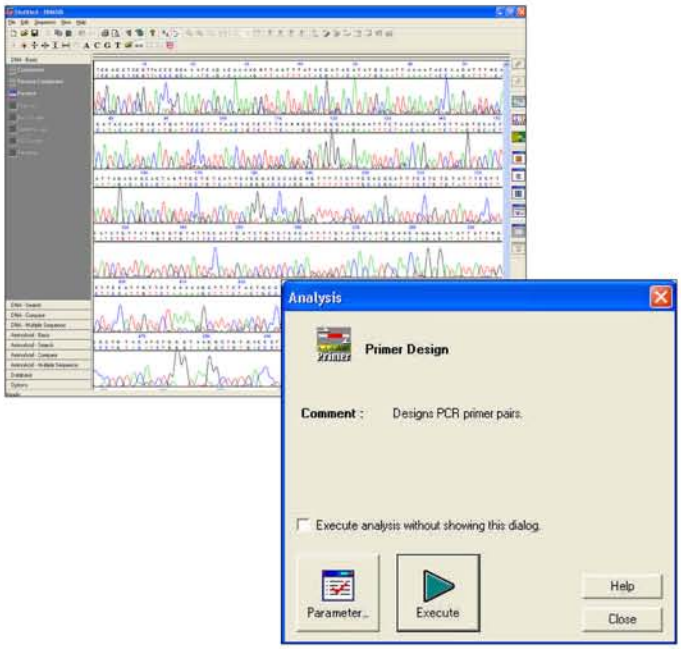
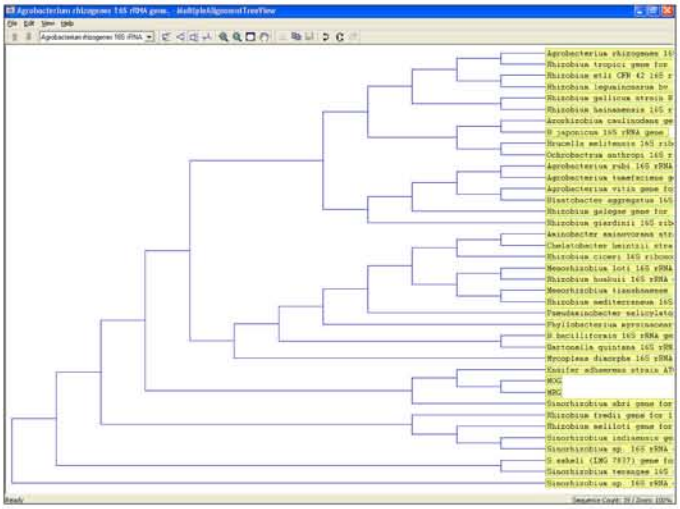



## DNASpace®

The DNASpace® module delivers the robust analysis environment found in DNASIS® MAX. With this program, thousands of data points can be automatically analyzed and work flows created by linking diverse functions.

- Customizable Interface
- Batch Processing
- Automated Analysis
- Personal Workflows



## Database Search

- BLAST
- Restriction Enzyme Site
- Mutation Site
- Tandem Repeat
- Smith-Waterman
- Motif
- Hairpin Loop
- Stacking Site

## Analysis

- Motif
- Phylogenic Tree
- ORF Analysis
- Hydrophobicity & Hydrophilicity
- Proteolytic Enzyme
- Amino Acid Translation
- Mutation Site

## Sequencing

- Sequence Import Wizard
- Multiple Trace Views
- Automated Display and Edit
- Multiple Alignment
- Sequence Editor
- Compatibility with most automated sequences

## Ordering Information

| Product | Cat. No. |
|---|---|
| DNASIS MAX V 2.5 Standalone | 51125-000-00 |
| DNASIS MAX V 2.5 Network (3 licenses) | 51125-000-01 |

## System Requirements

Windows 98, NT4.0 (SP6 or later), 2000, XP, 128MB Ram or higher recommended, 100MB disk space for program installation.

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