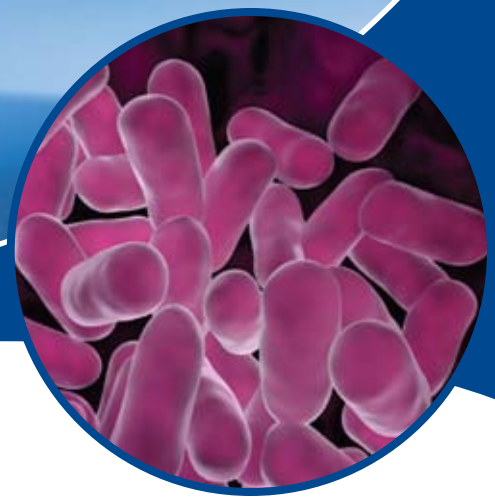
MassARRAY®
iSEQ™ – Comparative Sequence Analysis



Setting a New Standard in Molecular Typing.

Accurate. Sensitive. Rapid.

SEQUENOM®
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MassARRAY®
iSEQ™ – Comparative Sequence Analysis

Overview

Advancing Molecular Typing

iSEQ™ is a new MassARRAY® application for automated comparative sequence analysis that combines the sensitivity of PCR with the accuracy of mass spectrometry. The combination creates a highly accurate, reproducible method for identifying and typing microbes, viruses, and other haploid organisms. The iSEQ™ solution allows you to analyze one or multiple target regions on multiple samples in a convenient homogeneous assay format, and enables automatic sample identification or sample clustering. The software package delivers automatic data analysis, customizable plate setups, data portability and database management.

Testimonial

"In our laboratory, we use the MassARRAY identification system in several projects. This technology serves as a basis for developing new methods for rapid genotyping of hepatitis B and C viruses and quasispecies analysis of the hepatitis C virus. Currently, a new project is underway to adapt the MassARRAY system to sequencing of whole genomes of hepatitis A and B viruses."

Laboratory of Molecular Epidemiology and Bioinformatics, Division of Viral Hepatitis, Centers for Disease Control and Prevention (CDC).

The iSEQ™ Solution for Comparative Sequence Analysis

iSEQ™ offers a combination of automation, versatility and discriminatory power that is superior to any other comparative sequence analysis system. The versatility of the iSEQ™ software and open database access enables comparative sequencing with a wide range of global reference databases. Analysis results for 384 reactions are automatically achieved in less than an hour.

Flexible

- Scalable throughput
- Comparative sequence analysis with a wide range of reference databases
- Read length up to 800 bp

Sensitive and Accurate

- Two levels of amplification: PCR and *in vitro* transcription
- Discriminatory power down to a single nucleotide

Cost Effective

- 10 µl PCR reactions in 384 microplate format
- No product purification required

Efficient

- Automated data analysis
- Ideal for a few or several target regions
- Data portability

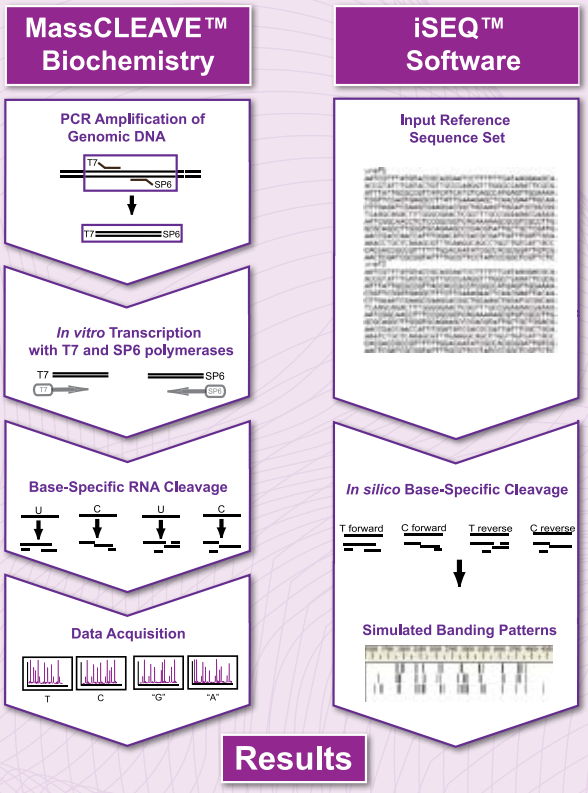
Rapid

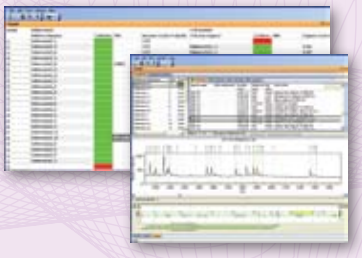
- Data acquisition for 384 reactions in < 1hr
- Analyze up to 3,072 reactions / day
- Throughput up to 614,400 bp / day

Accurate, Rapid Comparative Sequence Analysis

How It Works

iSEQ™ uses reference sequences as a comparative measure to identify microbes, viruses, or other haploid organisms. The starting point of the protocol is the amplification of a target region of interest. T7- and SP6- promoter tagged primers are used to amplify the template.





Sample Identification
Sequence Variation Detection
Cluster Analysis (Distance Matrix)

After SAP treatment, *in vitro* transcription provides RNA transcripts which are base-specifically cleaved. The resulting RNA cleavage products are analyzed by matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry. The iSEQ™ software automatically generates a report containing ID results by listing the best matching reference sequences and any sequence variations for each target region.

Instrumentation – Sequenom developed the MassARRAY system and SpectroCHIP® arrays to meet the requirements of moderate- to high-throughput comparative sequence analysis. Several system options are available depending on throughput and study requirements.

Software – The iSEQ™ software provides an advanced and versatile solution for automated data analysis:

- **Identification** – compares unknown samples to a set of reference sequences and identifies a best match
- **Sequence Variation Detection** – detects single base pair deviations and identifies new sequences
- **Clustering** – produces distance matrices that facilitate sample clustering based on homologous mass spectrometric patterns

Numerical and graphical interpretation tools are available for easy visualization and analysis. Data quality control and confidence ratings are provided for accurate identification.

iSEQ™ Software

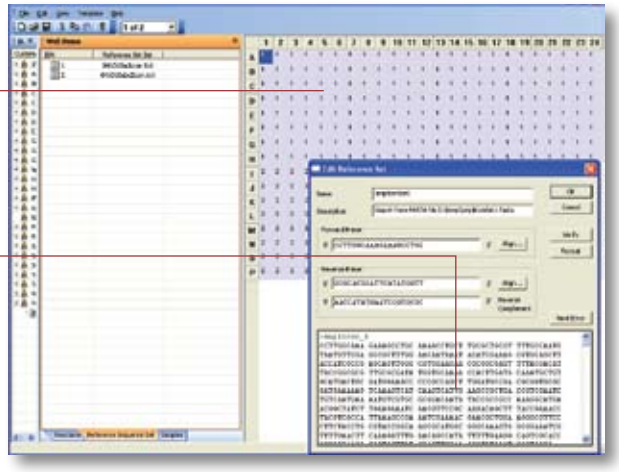
Plate Editor

FLEXIBLE PLATE FORMAT DESIGN

Customize your experiments with flexible plate formatting options for reference sequence sets, samples, and reactions.

IMPORT FUNCTIONALITY

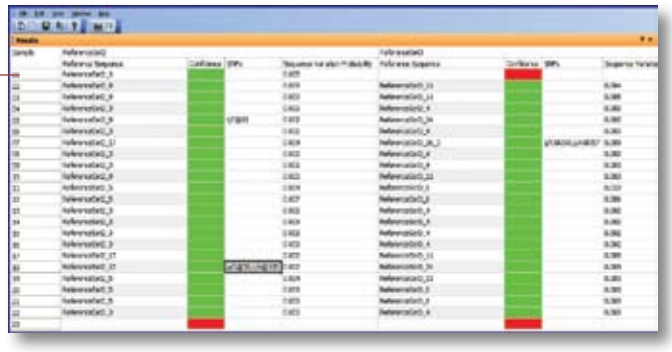
Upload your reference sequences rapidly in FASTA format.



Automated Data Analysis

TABULATED COMPARATIVE SEQUENCE ANALYSIS

The iSEQ™ analysis tool views sample identification results automatically listing the best matching reference sequences, sequence variations, and confidence scores.

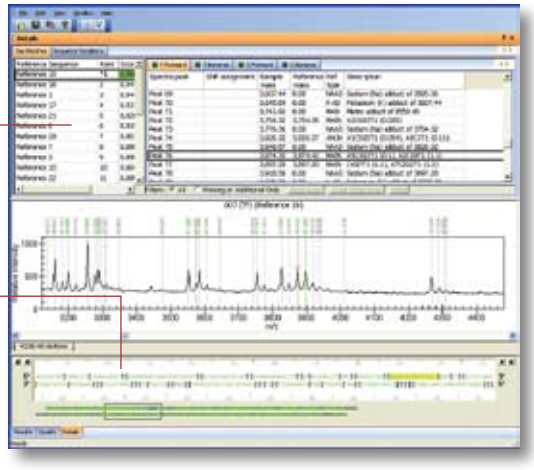


DETAILS OF SAMPLE RESULTS

Details on mass spectra, top matching reference sequences, sequence variations, and peak lists are available.

REFERENCE SEQUENCE VIEW PANE

View the entire forward and reverse nucleotide sequence for the selected reference sequence and navigate through the spectra.



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MassARRAY® System

MassARRAY® Compact System

The MassARRAY technology is trusted by the leading genetics institutions worldwide. The bench top MassARRAY Compact System is a multi-application platform that addresses the following applications:

- Comparative Sequence Analysis
- SNP Genotyping
- Quantitative Gene Expression
- Methylation Analysis

MassARRAY® Advantage

The iSEQ™ software for the MassARRAY System addresses the need for rapid and accurate comparative sequence analysis.

The combination of the iSEQ™ comparative sequence analysis and SNP genotyping capabilities enable automated identification and detection of microbes and viruses for research applications, including clinical microbiology, epidemiological and surveillance monitoring, biodefense, agricultural and food science applications, as well as forensics.

Flexibility of Scale with Versatility of Application

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Publications

Applebee, M. K. et al. (2008)
"Impact of individual mutations on increased fitness in adaptively evolved strains of *Escherichia coli*."
J Bact 190 (14) 5087-5094.

Honisch, C. et al. (2007)
"Automate comparative sequence analysis by base-specific cleavage and mass spectrometry for nucleic acid-based microbial typing."
Proc Natl Acad Sci USA 104 (25): 10649-54.

Herring, C. D. et al. (2006)
"Comparative genome sequencing of *Escherichia coli* allows observation of bacterial evolution on a laboratory timescale."
Nat Genet 38 (12): 1406-12.

Honisch, C. et al. (2004)
"High-throughput mutation detection underlying adaptive evolution of *Escherichia coli*-K12."
Genome Res 14 (12): 2495-502.

Lefmann, M. et al. (2004)
"Novel mass spectrometry-based tool for genotypic identification of mycobacteria."
J Clin Microbiol 42 (1): 339-46.

Stanssens, P. et al. (2004)
"High-throughput MALDI-TOF discovery of genomic sequence polymorphisms."
Genome Res 14 (1): 126-33.

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