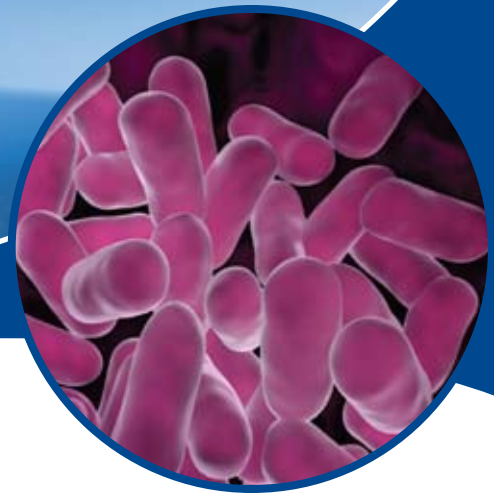


# MassARRAY® iSEQ™ – Comparative Sequence Analysis



Setting a New Standard in Molecular Typing.

Accurate. Sensitive. Rapid.

SEQUENOM®  
[www.sequenom.com](http://www.sequenom.com)

CCGATGATCGACCAGTATGCGCATGATGATCGAAGTATGCGCATTATGCGCAT  
GCGCATTATGCGCATGATGATCGAAGCCGATGATCGACCAGTATGCGCATGA  
GCGCATTATGCGCGCATGATGATCGAAGTATCATGATGATCGAAGCCGATGA



## 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

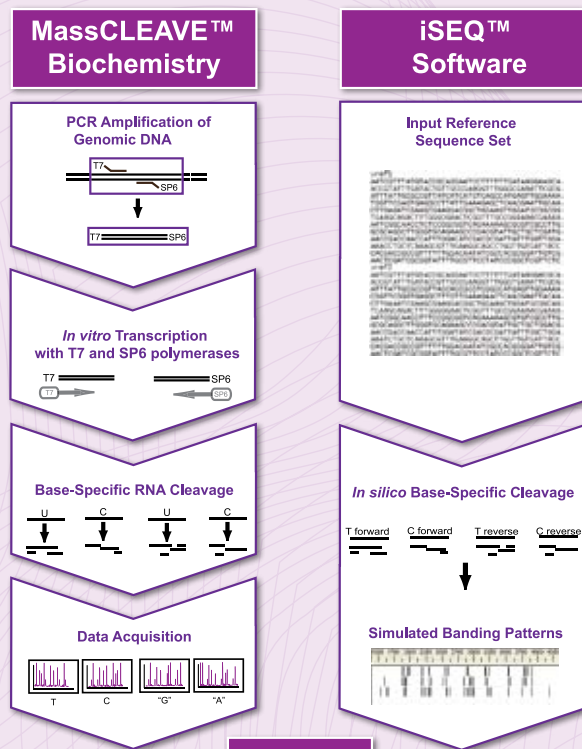
### Rapid

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

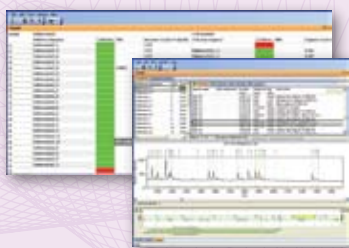
## ■ Accurate, Rapid Comparative Sequence Analysis

### 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.



### Results



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**

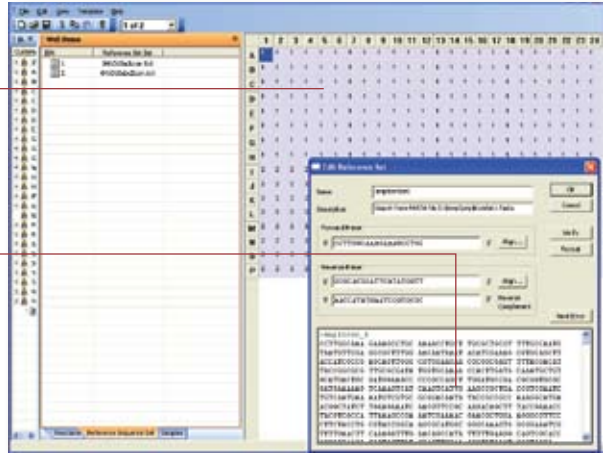
**Plate Editor**

**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**

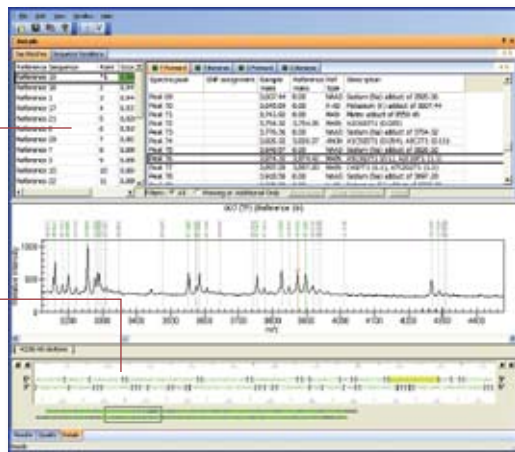
**TABULATED COMPARATIVE SEQUENCE ANALYSIS**

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

Sample	Reference Sequence	Confidence	SNPs	Reference Sequence	Confidence	SNPs
01	ReferenceSeq_1	0.999	0.000	ReferenceSeq_11	0.999	0.000
02	ReferenceSeq_2	0.999	0.000	ReferenceSeq_12	0.999	0.000
03	ReferenceSeq_3	0.999	0.000	ReferenceSeq_13	0.999	0.000
04	ReferenceSeq_4	0.999	0.000	ReferenceSeq_14	0.999	0.000
05	ReferenceSeq_5	0.999	0.000	ReferenceSeq_15	0.999	0.000
06	ReferenceSeq_6	0.999	0.000	ReferenceSeq_16	0.999	0.000
07	ReferenceSeq_7	0.999	0.000	ReferenceSeq_17	0.999	0.000
08	ReferenceSeq_8	0.999	0.000	ReferenceSeq_18	0.999	0.000
09	ReferenceSeq_9	0.999	0.000	ReferenceSeq_19	0.999	0.000
10	ReferenceSeq_10	0.999	0.000	ReferenceSeq_20	0.999	0.000
11	ReferenceSeq_11	0.999	0.000	ReferenceSeq_21	0.999	0.000
12	ReferenceSeq_12	0.999	0.000	ReferenceSeq_22	0.999	0.000
13	ReferenceSeq_13	0.999	0.000	ReferenceSeq_23	0.999	0.000
14	ReferenceSeq_14	0.999	0.000	ReferenceSeq_24	0.999	0.000
15	ReferenceSeq_15	0.999	0.000	ReferenceSeq_25	0.999	0.000
16	ReferenceSeq_16	0.999	0.000	ReferenceSeq_26	0.999	0.000
17	ReferenceSeq_17	0.999	0.000	ReferenceSeq_27	0.999	0.000
18	ReferenceSeq_18	0.999	0.000	ReferenceSeq_28	0.999	0.000
19	ReferenceSeq_19	0.999	0.000	ReferenceSeq_29	0.999	0.000
20	ReferenceSeq_20	0.999	0.000	ReferenceSeq_30	0.999	0.000
21	ReferenceSeq_21	0.999	0.000	ReferenceSeq_31	0.999	0.000
22	ReferenceSeq_22	0.999	0.000	ReferenceSeq_32	0.999	0.000
23	ReferenceSeq_23	0.999	0.000	ReferenceSeq_33	0.999	0.000
24	ReferenceSeq_24	0.999	0.000	ReferenceSeq_34	0.999	0.000
25	ReferenceSeq_25	0.999	0.000	ReferenceSeq_35	0.999	0.000
26	ReferenceSeq_26	0.999	0.000	ReferenceSeq_36	0.999	0.000
27	ReferenceSeq_27	0.999	0.000	ReferenceSeq_37	0.999	0.000
28	ReferenceSeq_28	0.999	0.000	ReferenceSeq_38	0.999	0.000
29	ReferenceSeq_29	0.999	0.000	ReferenceSeq_39	0.999	0.000
30	ReferenceSeq_30	0.999	0.000	ReferenceSeq_40	0.999	0.000

**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.

## ■ 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

## ■ 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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The products described in the brochure are for Research Use Only, and not for use in diagnostic procedures or for other purposes.