



Superior accuracy and speed—MicroSEQ Rapid Microbial Identification System

Featuring the 3500 Genetic Analyzer

Achieve right-the-first-time microbial identification

Next-generation, high-throughput comparative DNA sequencing system for identification of bacteria and fungi

The answer is in the DNA

Harmful bacteria and fungi can contaminate raw materials, production facilities, and even worse, branded products.

The Applied Biosystems™ MicroSEQ™ Rapid Microbial Identification System (Figure 1) uses a highly accurate phylogenetic approach for microbial identification based on the sequencing of the 16S rRNA gene for bacteria or the D2 region of the large subunit for fungi, and the comparison of the sequences to those in its validated libraries.

After sequencing the rRNA gene, the MicroSEQ Rapid system automatically compares the results to validated sequences in the Applied Biosystems™ MicroSEQ™ microbial libraries. The results are ranked according to genetic distance of the reference sequences to the sample and displayed on the system monitor along with a phylogenetic tree (Figure 2).

The system includes the largest fully validated bacterial and fungal libraries. The bacterial library includes over 2,000 species, including *Staphylococcus* spp., *Bacillus* spp., coryneforms, mycobacteria, and Gram-negative nonfermenters. The library for fungal species includes over 1,100 entries. Both are frequently updated and expanded with new entries.



Figure 1. The MicroSEQ Rapid Microbial Identification System with Applied Biosystems™ components. (A) 3500 and 3500xL DNA sequencing instruments; **(B)** MicroSEQ™ ID Analysis Software with 3 libraries; **(C)** Fast MicroSEQ™ Bacterial 500 16S ID Kit, Fast MicroSEQ™ Fungal D2 ID Kit, MicroSEQ™ Full Gene 16S ID Kit; **(D)** Veriti™ Thermal Cycler.

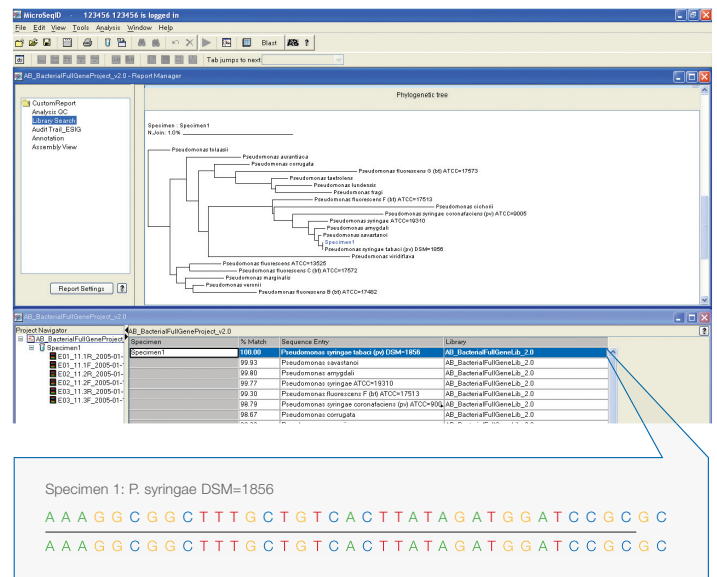


Figure 2. MicroSEQ report. Genetic distance from reference sample and phylogenetic tree.

“DNA-based amplification and sequencing results are faster, more sensitive, more accurate, and more reproducible than current microbiological methods.”

—Dr. Robert Johnson
Director, Dialogue (Switzerland)

Generate actionable results in less than 5 hours

With the MicroSEQ Rapid Microbial ID System, bacteria and fungi can be identified in under 5 hours, using a logical workflow that requires minimum hands-on time (Figure 3). A single, standardized procedure is used for identifying both bacterial and fungal isolates.

With the data collection analysis software (Figure 4), the system delivers a guided setup process and performs the analysis with limited interaction from the user.

No Gram staining or ancillary tests are required to achieve the highest level of accuracy in the minimum amount of time.

Qualify with ease, use with success

To help ensure seamless integration into your laboratory from installation to routine operation, we offer comprehensive installation and operational qualification (IQ/OQ) and validation support services.

The program includes:

- Consultation with client to determine needs for training, system installation, and validation timelines and plans
- System software installation, operation, and security verification
- Installation Qualification (IQ) protocol and service
- Operational (OQ) Qualification protocol and service
- Detailed data analysis and review
- Consultation on laboratory workflow
- Performance qualification (PQ)—recommended guidelines

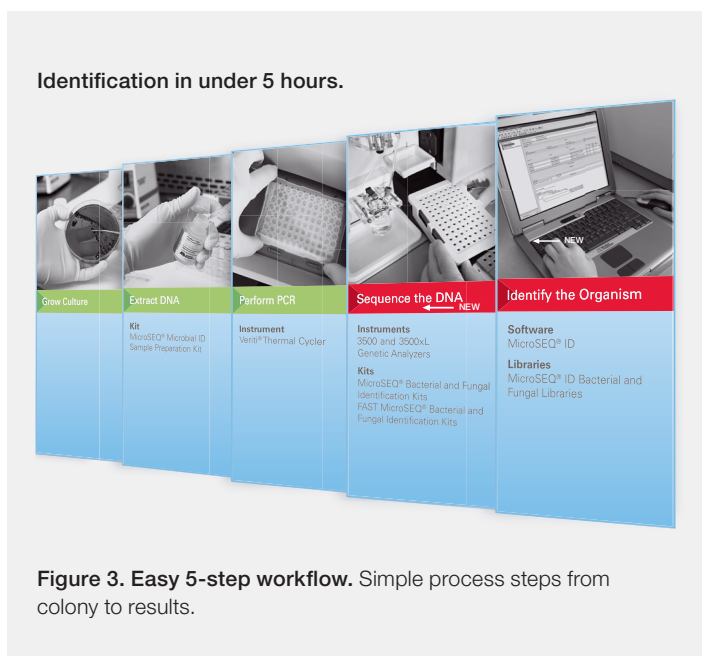


Figure 4. Data analysis. Easy-to-use sample input screens with automated data analysis.

| Well | Sample Name | Library | Creation Date | Modification Date | Comments |
|------|-------------|---------|---------------|-------------------|----------|
| 1 | A01 | Sample1 | | | |
| 2 | B01 | Sample1 | | | |
| 3 | C01 | Sample2 | | | |
| 4 | D01 | Sample2 | | | |
| 5 | E01 | Sample3 | | | |
| 6 | F01 | Sample3 | | | |
| 7 | G01 | Sample4 | | | |
| 8 | H01 | Sample4 | | | |
| 9 | A02 | | | | |
| 10 | B02 | | | | |
| 11 | C02 | | | | |
| 12 | D02 | | | | |
| 13 | E02 | | | | |
| 14 | F02 | | | | |
| 15 | G02 | | | | |
| 16 | H02 | | | | |
| 17 | A03 | | | | |
| 18 | B03 | | | | |

| Specimen | Library | Library Entry Name | % Match | Consensus Length | Library Entry Length | Total Mismatches |
|----------|----------------------|--------------------------------------|---------|------------------|----------------------|------------------|
| Sample-1 | AB_Bacteria000LB_2.2 | Ralstonia solanaceae (ATCC-27911) | 100.0 | 404 | 400 | 0 |
| Sample-1 | AB_Bacteria000LB_2.2 | Ralstonia medusae (DSMZ-17714) | 97.28 | 404 | 400 | 13 |
| Sample-1 | AB_Bacteria000LB_2.2 | Ralstonia mannohelica (ATCC-BAA-710) | 96.30 | 404 | 400 | 18 |
| Sample-1 | AB_Bacteria000LB_2.2 | Ralstonia solanaceae (ATCC-11956) | 95.29 | 404 | 400 | 23 |
| Sample-1 | AB_Bacteria000LB_2.2 | Ralstonia snyderi (ATCC-4954) | 95.05 | 404 | 400 | 24 |

Increased throughput with greater ease of use

The MicroSEQ Rapid Microbial ID System powered by the 3500 Series Genetic Analyzer simplifies the user experience and enables faster identifications for the laboratory.

- Plug-and-play capillary array and consumables (Figure 5)
- Consumables dashboard monitor (Figure 6)
- Automated consumable usage tracking
- Simple on-screen navigation with automated maintenance tracking



Figure 5. 3500 Series Genetic Analyzer. (A) Prepacked consumables, and (B) expanded capillary array.

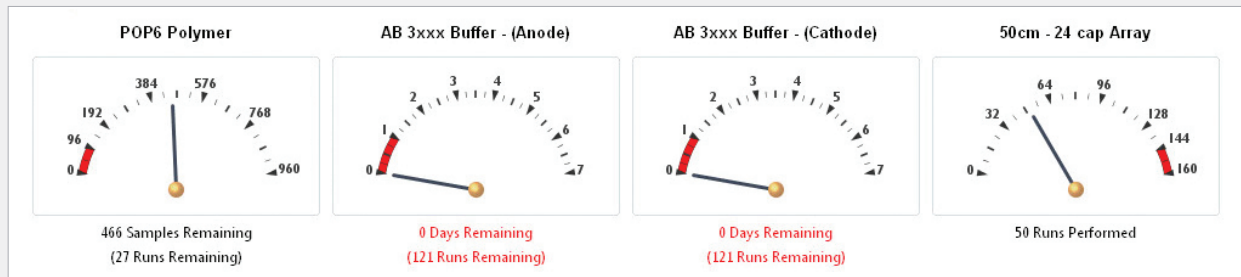


Figure 6. Consumables dashboard. Easy-to-understand, real-time information on consumable status.

Benefit from worldwide implementation and support

Our distribution and service network, composed of highly trained support and application personnel, reaches 150 countries on six continents. In addition to basic service and support, the following additional services are offered for the MicroSEQ Rapid Microbial ID System:

- On-site workflow and data analysis training
- Validation guidance



Top researchers worldwide use the MicroSEQ Rapid Microbial Identification System

Ideal for:

- Environmental monitoring
- Contamination investigation
- Root cause analysis
- Raw material testing

Drain-line_3

Pseudomonas aeruginosa ATCC = 10145

Pseudomonas aeruginosa ATCC = 25619

Pseudomonas citronellolis

Pseudomonas stutzeri

Pseudomonas nitroreducens

Pseudomonas monteilii

Pseudomonas oleovorans

Pseudomonas pseudoalcaligenes



Ordering information

| Description | Cat. No. |
|---|-----------------|
| System | |
| MicroSEQ Rapid Microbial ID System with 3500 Genetic Analyzer | 4462991 |
| MicroSEQ Rapid Microbial ID System with 3500xL Genetic Analyzer | 4462990 |
| Software | |
| MicroSEQ ID Analysis Software Bundle | 4448336 |
| MicroSEQ ID v2.2 | 4371431 |
| Installation and IQ/OQ | |
| IQ/OQ, 3500 MSID Service | 4468672 |
| IQ/OQ, 3500xL MSID Service | 4468673 |
| Kits | |
| Fast MicroSEQ 500 16S rDNA PCR Kit, with protocol and quick reference card | 4370653 |
| MicroSEQ 500 16S rDNA Sequencing Kit, with protocol and quick reference card | 4346479 |
| MicroSEQ Full Gene 16S rDNA PCR Kit, with protocol and quick reference card | 4349161 |
| MicroSEQ Full Gene 16S rDNA Sequencing Kit, with protocol and quick reference card | 4347483 |
| Fast MicroSEQ D2 rDNA Fungal Identification Kit, with protocol and quick reference card | 4382395 |
| MicroSEQ D2 rDNA Fungal Sequencing Kit, with protocol and quick reference card | 4347482 |

Find out more at thermofisher.com/microseq