charles river

MICROBIAL SOLUTIONS

Click to learn more

Accugenix® AccuBLAST®

Services

- Affordable access to the Accugenix® proprietary library
- Expert data analysis and interpretation methods
- Improved confidence and accuracy in Identification Reports
- A higher reportable rate to the species level

AccuBLAST® is a semi-automated data analysis service designed exclusively for clients who have purchased a MicroSeq® identification system but are not always confident with the identifications the system provides. AccuBLAST® is a cost-effective solution for those spending too much time trying to make sense of microbial sequence data or who are puzzled by the data generated by their automated system.

The AccuBLAST® service utilizes the robust, validated Accugenix® bacterial sequence library and Charles River expert data analysis and report generation capabilities, allowing us to deliver IDs more quickly, confidently and accurately.

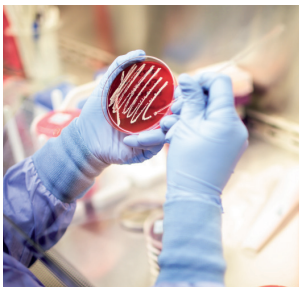
The AccuBLAST® Process

Clients submit their raw sample data files (*.ab1 extension) from bacterial (16S) reactions, as generated by the MicroSeq system, and Charles River utilizes the Accugenix® library and our manual data analysis methods to achieve an identification and produce a cGMP-validated report. The identification report will include the sample identification, confidence level information and neighborjoining tree, as well as the sequence data file names associated with the submitted sample request.

AccuBLAST® Sequencing Methods Versus MicroSeq v2.0

The fully automated MicroSeq v2.0 handles all sequence files in the same manner, regardless of the data quality. It weighs polymorphic positions differently than single-copy sequences and provides the top matches, relying on the end user to determine the true identity of the organism. At Charles River, our proprietary methods compare sample sequences against our full-coverage Accugenix® proprietary library, resulting in conclusive data interpretation and an identification with assigned confidence levels based on phylogenetic analysis. Utilizing a method that includes manually-assisted automated assembly and a continuously curated and validated proprietary library allows higher confidence in the interpretation of the results and the accurate trending and tracking of isolates.

EVERY STEP OF THE WAY



Advantages

- Library relevance and state of validation
- Analysis of the quality of the data generated
- Data assembly analysis and accurate and consistent

Comprehensive Library

Our cGMP-compliant proprietary library is the most comprehensive in the industry, providing twice the coverage of other commercially available libraries for bacteria encountered in manufacturing environments.* We currently have over 7,000 validated species entries in our bacterial library.

Expert Data Review and Analysis

Our staff phylogeneticists have extensive experience garnered from generating over 500,000 sequence-based reports to date. Our manual data review process provides you with six-times improved consensus sequence repeatability[1] over the MicroSeq automated processes.

For detailed technical information about the advantages offered by our manual reference method, please read our technical sheet, "Manual Reference Method Versus Commercial Automated Software for Data Analysis and Result Interpretation of 16S Bacterial Sequences." To learn more about the specific differences between Charles River Accugenix® and MicroSeq processes, please read our technical sheet, "A Comparison of the Attributes of the AccuGENX-ID® Microbial Sequencing Methods versus MicroSeq v2.0."

Service	Turnaround Time	Code
AccuBLAST® analysis of 16S raw data sequence files	Same day	AccuBLAST-0
	1 day	AccuBLAST-1
	2 day	AccuBLAST-2

* For a full listing of all entries in the Accugenix® bacterial database and to see how our library compares to other commercially available databases, please read our technical sheet, "Bacterial Library Comparison."

1. Smith, D. 2010 PDA Berlin Oral Presentation.

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