



FREE
1-MONTH TRIAL



Next Generation Sequencing

Bruker MBioSEQ™ Ridom Typer

Empower your bacterial genomics analysis for smarter decisions

Innovation with Integrity

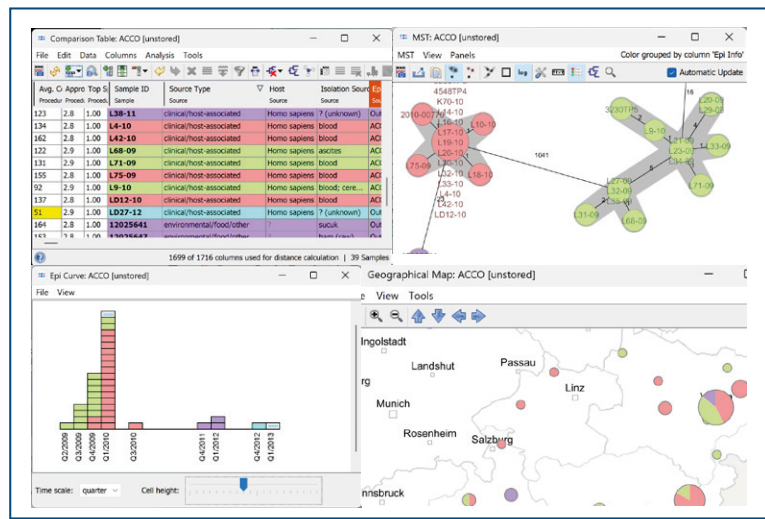
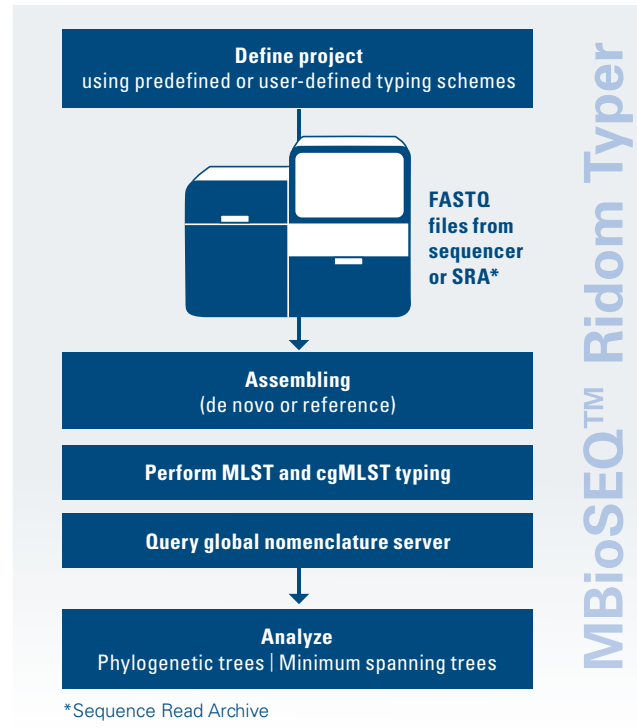
RUO

A software solution empowering epidemiology and hygiene management

State of the art comprehensive analysis of WGS data – fast and easy

Bruker MBioSEQ Ridom Typer (formerly known as SeqSphere) offers a streamlined, all-in-one solution for bacterial whole genome sequencing (WGS) data and amplicon data analysis. Compatible with most common NGS systems including Illumina, Pacific Biosciences, Oxford Nanopore Technologies (ONT), and Sanger data, it automates every step - from trimming, assembly to core genome MLST (cgMLST) or SNP typing, detection of antimicrobial resistance (AMR) genes, and/or geno-serotyping. All accompanied by public and globally shared typing nomenclature and documented by thousands of publications in peer-reviewed journals.

- No bioinformatic skills needed – runs on MS Windows
 - Built your own database, with all data stored locally and secure
 - Fully automated data processing
 - Regularly maintained databases – always up-to-date
 - Flexible licensing options that grow with your lab
 - Integrated Long Read Assembly to even enable plasmid transmission analysis
- New main features:**
- TB-Profiler AMR
 - CheckM2 Intra-species Contamination Check
 - GAMBIT Bacterial Species ID



Smart 4-dimensional surveillance for big NGS data

Bruker MBioSEQ Ridom Typer simplifies complex NGS genomic data analysis with intuitive 4D visualization - by person, place, time, and type. Designed for ease of use, it runs on a Windows interface, making it accessible to non-specialists. All views are interconnected, exportable in publication-ready formats, and backed by a robust SQL-database. Real-time alerts support clonal and plasmid transmission studies comparing new sequence entries against stored data.

User-friendly visualization of results with Bruker MBioSEQ Ridom Typer.

MBioSEQ Ridom Typer supports the fight against *M. tuberculosis* drug resistance - TB Profiler AMR as main feature

- Analyzing *M. tuberculosis* whole genome sequencing data to predict lineage and drug resistance
- MS Windows Graphical Interface instead of the command line Interface of TB Profiler
- User-friendly integration of the tool to make results searchable and filterable for users
- We care for you - feature is always evaluated, maintained and updated

Bruker epidemiology solution expands with MBioSEQ™ Ridom Typer

Bacterial typing generates isolate-specific genotypic or phenotypic characteristics that help trace the sources and transmission routes of bacterial infections. Typing also plays a key role in identifying emerging pathogenic strains or clones within a species.

Today, microbiologists can experience the genomic revolution that benchtop next generation sequencing (NGS) provides. With fast and cost-effective microbial WGS and Bruker's automated user-friendly analysis software MBioSEQ™ Ridom Typer, microbiologists can use genome-wide gene-by-gene allele calling of hundreds to thousands of genes (cgMLST) for genotyping.

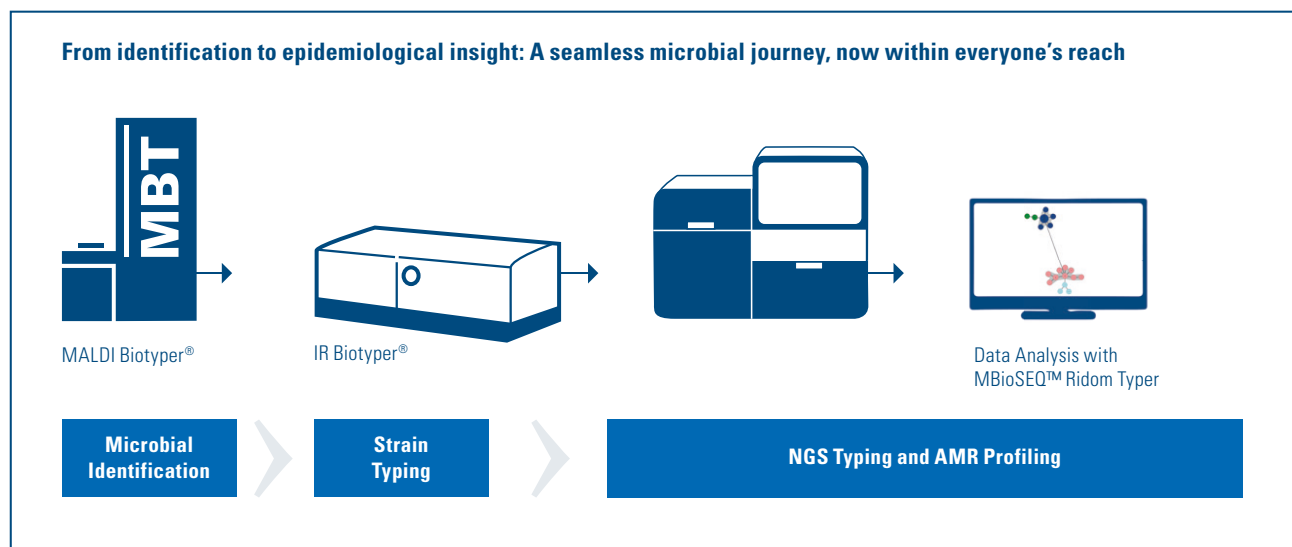


From identification to in-depth genotyping - all in one workflow

The market-leading MALDI Biotyper® identifies microorganisms to the species level with unequaled speed and accuracy. Following identification, the IR Biotyper® enables real-time strain typing, and fast outbreak detection, thanks to the new IR Tracker™ software. Bruker's MALDI Biotyper and IR Biotyper can be combined into a single seamless, high-throughput workflow for rapid microbial identification and typing.

To deepen your analysis, MALDI Biotyper identifications or IR Biotyper-identified outbreak suspects can be reflexed to WGS for the detection of resistance genes, specific mutations, and confirmation of strain identity. Recent integration of the main feature GAMBIT MBioSEQ Ridom Typer software makes a valuable contribution to identification of species unresolved by MALDI-TOF MS. Here, Bruker's automated and user-friendly MBioSEQ™ Ridom Typer software, takes your epidemiological approaches and microbial monitoring to a new level, enabling quick and smart decisions.

Bruker MBioSEQ Ridom Typer software running under Windows and Linux integrates easily into existing lab routines.



Computer Specifications

For detailed information on system requirements please visit our website



Flexible licensing options that grow with your lab

Bruker MBioSEQ™ Ridom Typer			
License period	Named users	Part number	
1 year	2 named users maximum number of concurrent pipelines in total 5	1921470 Academic, govt.	
		1921471 Commercial	
	5 named users maximum number of concurrent pipelines in total 12	1921472 Academic, govt.	
		1921473 Commercial	
	30 named users maximum number of concurrent pipelines in total 75	1921474 Academic, govt.	
		1921475 Commercial	
	3 years	2 named users maximum number of concurrent pipelines in total 5	1921476 Academic, govt.
			1921477 Commercial
		5 named users maximum number of concurrent pipelines in total 12	1921478 Academic, govt.
1921479 Commercial			
30 named users maximum number of concurrent pipelines in total 75		1921480 Academic, govt.	
		1921481 Commercial	
5 years	2 named users maximum number of concurrent pipelines in total 5	1921482 Academic, govt.	
		1921483 Commercial	
	5 named users maximum number of concurrent pipelines in total 12	1921484 Academic, govt.	
		1921485 Commercial	
	30 named users maximum number of concurrent pipelines in total 75	1921486 Academic, govt.	
		1921487 Commercial	

NEW: Including additional main features. The Long Read Module (LRM) functionality is now part of the regular license!

For ordering, please contact your local Bruker representative.

For Research Use Only. Not for use in clinical diagnostic procedures.
Please contact your local representative for availability in your country.



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For detailed product information and training materials please see
www.ridom.de

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