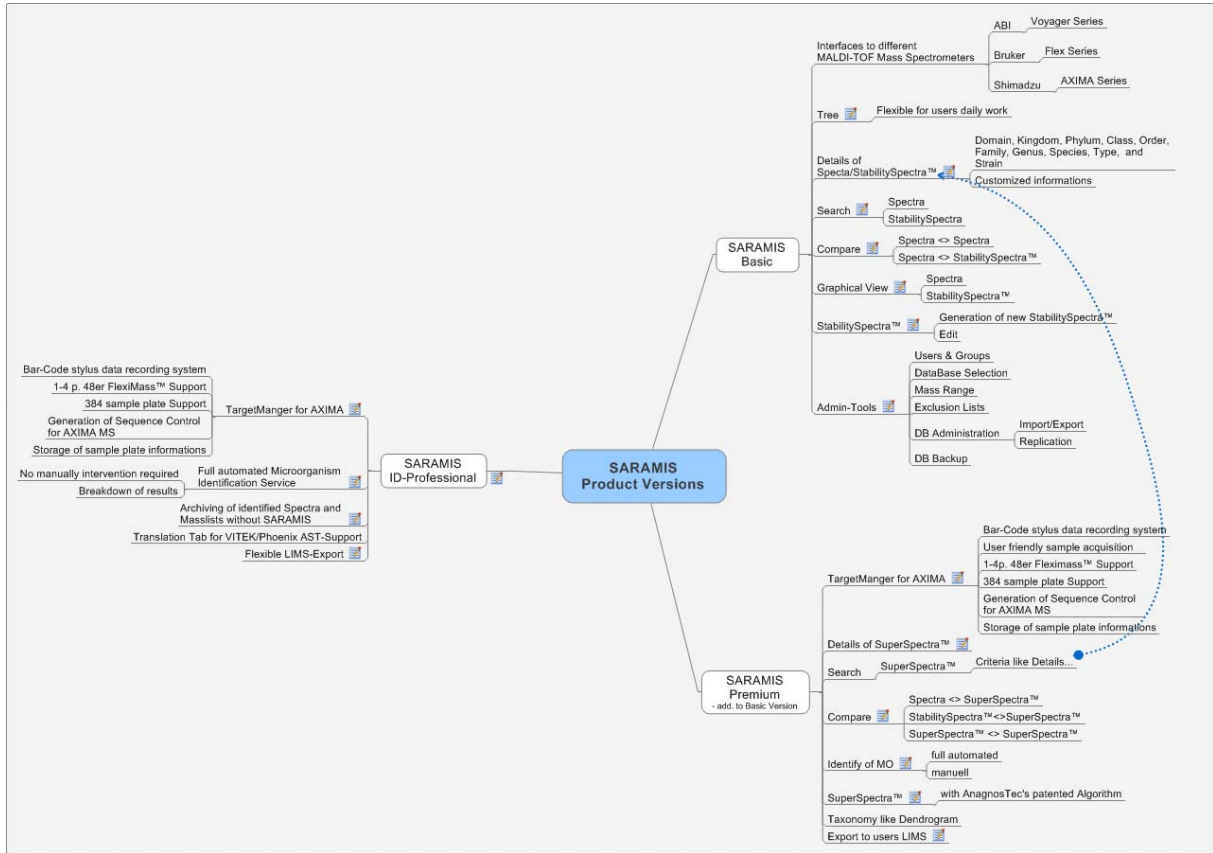


# SARAMIS Product Versions



# SARAMIS Basic

## 1.1 Interfaces to different MALDI-TOF Mass Spectrometers

### ABI

#### *Voyager Series*

### Bruker

#### *Flex Series*

### Shimadzu

#### *AXIMA Series*

## 1.2 Tree

Spectra and Superspectra of microorganisms are well ordered by the international nomenclature, e.g. bacteria by the International Code of Nomenclature of Bacteria or yeasts and fungi by the International Code of Botanical Nomenclature.

Beside, customized folders and internal sorting according to a special project or other criteria is available.

### **Flexible for users daily work**

## 1.3 Details of Spectra/StabilitySpectra™

Within the spectra file different parameters can be used in order to assign the spectra clearly to the corresponding sample. Beside identification information like Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species, Type, and Strain, customized data can be included, like the project no. or the customer name.

### **Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species, Type, and Strain**

### **Customized informations**

## 1.4 Search

My means of the search function, single Spectra, StabilitySpectra and Spectra & StabilitySpectra can be searched within the database. Either the name of the Spectra can be feed in or you can search for a Spectra via different parameters like Genus, Species, Strain, mass, file name and all other parameters which are stored in the file header.

### **Spectra**

### **StabilitySpectra**

## 1.5 Compare

Any single spectra within the database can be compared with any other fingerprint spectra stored in the database. Furthermore the single spectra can be checked against the StabilitySpectra and vice versa.

[Spectra <> Spectra](#)

[Spectra <> StabilitySpectra™](#)

## 1.6 Graphical View

Any Spectra or StabilitySpectra can be shown in two different ways:

- 1) Peak list with masses and intensities
- 2) Mass Spectrum

[Spectra](#)

[StabilitySpectra™](#)

## 1.7 StabilitySpectra™

A StabilitySpectra is a theoretical spectra calculated of at least 10 data reduced fingerprint mass spectra of a certain microorganism.

[Generation of new StabilitySpectra™](#)

[Edit](#)

## 1.8 Admin-Tools

SARAMIS is protected by a license key and other administration tools. Users and working groups can be defined with different read and write access to the fingerprint or PSD database. Furthermore all pre-settings for the automatic identification (mass range, mass accuracy) can be done. Import/Export routines incl. synchronisation and backup functions are included as well.

[Users & Groups](#)

[DataBase Selection](#)

[Mass Range](#)

[Exclusion Lists](#)

[DB Administration](#)

*[Import/Export](#)*

*[Replication](#)*

[DB Backup](#)

## 2 SARAMIS Premium - add. to Basic Version

### 2.1 TargetManger for AXIMA

The TargetManager generates the automatic measurement protocol for Shimadzu's Axima MS. By means of a Barcode interface the sample of each single target is clearly described incl. growth conditions like temperature, incubation time, medium, customized parameter and many others. The TargetManager supports the Feleximass target and the 384 sample plate of Shimadzu's Axima.

**Bar-Code stylus data recording system**

**User friendly sample acquisition**

**1-4p. 48er Fleximass™ Support**

**384 sample plate Support**

**Generation of Sequence Control for AXIMA MS**

**Storage of sample plate informations**

### 2.2 Details of SuperSpectra™

For the generation of one SuperSpectra™ at least 15 to 20 different representatives (isolates) of one species from different locations (hospitals, reference centers and strain culture collections) are needed. The isolates have to be in different growth phases on various growth media. The MALDI-TOF fingerprint mass spectra of each isolate will be treated by a patented weighting procedure of specific signals.

### 2.3 Search

**SuperSpectra™**

*Criteria like Details...*

quod vite: [Details of Spectra/StabilitySpectra™](#)

### 2.4 Compare

Any data set (spectra) can be compared with any other spectra stored in the database, with other Spectra, StabilitySpectra or SuperSpectra.

**Spectra <> SuperSpectra™**

**StabilitySpectra™<>SuperSpectra™**

**SuperSpectra™ <> SuperSpectra™**

### 2.5 Identify of MO

The identification of microorganisms can be carried out automatically or manually. All Fingerprint Mass Spectra which have no entry in Genus and Species are automatically compared against all SuperSpectra available in the database during the import process. The Spectra will be renamed and sorted in the tree.

A manually identification routine allows the verification of the automatic identification and is suitable for a subsequent identification.

**full automated**

**manuell**

## **2.6 SuperSpectra™**

AnagnosTec's SuperSpectra™ are generated based on Fingerprint Spectra of well known microorganisms and contain sets of genus, species and strain specific biomarkers which are characteristic for the respective group of microorganisms. The SuperSpectra were produced by a patented procedure for statistic evaluation and weighting of data.

**with AnagnosTec's patented Algorithm**

## **2.7 Taxonomy like Dendrogram**

## **2.8 Export to users LIMS**

Results of the microorganism identification with SARAMIS(TM) can be automatically submitted to the LIMS

## **SARAMIS ID-Professional**

SARAMIS™ ID-Professional allows the automatic identification of microorganisms by means of its MALDI-TOF fingerprint mass spectrum matched against SARAMIS™ SuperSpectra™.

FingerprintSpectra generated by MALDI-TOF instruments are transmitted to SARAMIS™ ID-Professional and directly compared with SARAMIS™ SuperSpectra™. The FingerprintSpectra are stored and the identification is automatically transferred to any LIMS in the users' clinical laboratory.

SARAMIS™ ID-Professional is an ideal tool for High Throughput Identification of microorganisms for commercial and non-commercial applications.

### **2.9 TargetManger for AXIMA**

The TargetManager generates the automatic measurement protocol for Shimadzu's Axima MS. By means of a Barcode interface the sample of each single target is clearly described incl. growth conditions like temperature, incubation time, medium, customized parameter and many others. The TargetManager supports the Feleximass target and the 384 sample plate of Shimadzu's Axima.

**Bar-Code stylus data recording system**

**1-4 p. 48er FlexiMass™ Support**

**384 sample plate Support**

**Generation of Sequence Control for AXIMA MS**

**Storage of sample plate informations**

### **2.10 Full automated Microorganism Identification Service**

FingerprintSpectra generated by MALDI-TOF instruments are automatically transmitted to SARAMIS™ ID-Professional and directly compared with SARAMIS™ SuperSpectra™.

It is an ideal tool for High Throughput Identification of microorganisms for commercial and non-commercial applications.

**No manually intervention required**

**Breakdown of results**

### **2.11 Archiving of identified Spectra and Masslists without SARAMIS**

The FingerprintSpectra and resultss are stored in an external archive outside SARAMIS.

### **2.12 Translation Tab for VITEK/Phoenix AST-Support**

### **2.13 Flexible LIMS-Export**

The identification is automatically transferred to any LIMS in the users' clinical laboratory.