

SARAMIS a new way of data management of MALDI-TOF Ms for microorganism-identification

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Matrix-Assisted Laser Desorption/Ionisation Time-Of-Flight Mass Spectrometry (MALDI-TOF MS) for classification and identification of microorganisms became more and more popular during the last years. Our company has developed a new software in order to handle the enormous volumes of data and to make the analysis of the results fast and easy: **SARAMIS** (Spectral Archiving And Microbial Identification System)

MALDI-TOF MS data are reduced to easy-to handle mass lists and imported to the database. The Comparison of MS-data followed by a patented procedure that generates theoretical spectra (superspectra) enables the identification of various classes of microorganisms. Having recorded specific MS-signals of family, genus, species and strain, these signals are then ranked according to their specificity.

High quality superspectra can be used for automatic identification of family, genus, species or even strain level. In case of unknown organisms the superspectra allow grouping and dereplication of samples.

As in sequence and RNA analyses dendrograms are also calculated, here basing on the specific characteristics of MALDI-TOF MS data. This is done twofold: First method is based on the acquired absolute mass matches and second taking in account the percentage identity of spectra.

By using a special export routine and file format all MALDI-TOF MS-data can be imported into SARAMIS, regardless to the manufacturer of the MALDI-TOF hardware.