Design Concept of msFineAnalysis

msFineAnalysis has fully automated the entire qualitative analysis process for data acquired by GC/EI and GC/soft ionization (CI, PI, FI).

The software compares molecular formula information acquired from the NIST library search with soft ionization exact mass data analysis to ensure accurate qualitative results. To do this, it examines the NIST library search results, reduces the possibility of false positive identifications, and selects the correct components from multiple candidates with similar scores. For unknown components not registered in the NIST libraries, it estimates molecular formulas by using the soft ionization data, acquires partial structure information and estimates structural formulas by using the EI data. msFineAnalysis is a powerful tool based on a new concept for supporting qualitative GC-MS analysis.

Specifications
- Automatic peak detection and automatic creation of mass spectrum
- Mass spectrum creation by manual peak detection
- Analysis of identical components in two measurement data
- Analysis of molecular ions from two mass spectra
- Display of NIST database search results
- Display of accurate mass analysis result
- Display of isotopic pattern analysis result

Applicable model
JMS-T2000GC Series
AccuTOFTM GCx, AccuTOFTM GCx-plus

Notes
- This product supports only MS-56210MP (main program) format data. It is necessary to save data in Profile format for measurement data.
- This product works on the Windows® 10 operating system (64 bit version).
- For operation of this product, PC performance equal to or higher than MS-57042PCE is recommended.

Microsoft, Windows, PowerPoint and Microsoft Office are registered trademarks of Microsoft Corporation in USA and other countries. Microsoft Word is a product name of Microsoft Corporation.

The product specification is subject to change without prior notice.

Design Concept of msFineAnalysis

msFineAnalysis has fully automated the entire qualitative analysis process for data acquired by GC/EI and GC/soft ionization (CI, PI, FI).

The software compares molecular formula information acquired from the NIST library search with soft ionization exact mass data analysis to ensure accurate qualitative results. To do this, it examines the NIST library search results, reduces the possibility of false positive identifications, and selects the correct components from multiple candidates with similar scores. For unknown components not registered in the NIST libraries, it estimates molecular formulas by using the soft ionization data, acquires partial structure information and estimates structural formulas by using the EI data. msFineAnalysis is a powerful tool based on a new concept for supporting qualitative GC-MS analysis.

Specifications
- Automatic peak detection and automatic creation of mass spectrum
- Mass spectrum creation by manual peak detection
- Analysis of identical components in two measurement data
- Analysis of molecular ions from two mass spectra
- Display of NIST database search results
- Display of accurate mass analysis result
- Display of isotopic pattern analysis result

Applicable model
JMS-T2000GC Series
AccuTOFTM GCx, AccuTOFTM GCx-plus

Notes
- This product supports only MS-56210MP (main program) format data. It is necessary to save data in Profile format for measurement data.
- This product works on the Windows® 10 operating system (64 bit version).
- For operation of this product, PC performance equal to or higher than MS-57042PCE is recommended.

Microsoft, Windows, PowerPoint and Microsoft Office are registered trademarks of Microsoft Corporation in USA and other countries. Microsoft Word is a product name of Microsoft Corporation.

The product specification is subject to change without prior notice.
New Auto Analysis combines 2 types of data acquired by GC/EI and GC/soft ionization

msFineAnalysis provides qualitative results by combining data acquired with GC/EI and GC/soft ionization (CI, PI, FI). Once the operator selects the GC/EI data and corresponding GC/soft ionization data, the software will automatically complete 5 analytical steps that identify the peaks detected in the chromatograms.

msFineAnalysis guarantees speedy data analysis, efficient operation, and enhanced quality of analytical results!

Conventional Manual Qualitative Analysis

Auto qualitative analysis that combines 5 qualitative techniques for the peaks detected

1. NIST Library Search
2. Molecular Ion Search
3. Exact Mass Analysis of Molecular Ions
4. Isotopic Pattern Analysis
5. EI Fragment Ion Analysis

Simple process produces accurate analytical results

The software displays analytical results, allowing the operator to review TIC, peak detection/assignment, and mass spectra. It also allows for re-analysis of the results.

Auto qualitative analysis that combines 5 qualitative techniques for the peaks detected

1. NIST Library Search
2. Molecular Ion Search
3. Exact Mass Analysis of Molecular Ions
4. Isotopic Pattern Analysis
5. EI Fragment Ion Analysis

Formula Candidate 1): CaHbOc
Degree of Similarity: Good

Formula Candidate 2): CaHbOc
Degree of Similarity: Poor

Formula Candidate 3): CxHyOz
Degree of Similarity: Poor

When the chemical formulas for the fragment ions were calculated using the elements present in the molecular ion, all ions produced a formula. When this happens, isotopic pattern analysis is effective for filtering the formula candidates.
**Specifications**
- Automatic peak detection and automatic creation of mass spectrum
- Mass spectrum creation by manual peak detection
- Analysis of identical components in two measurement data
- Analysis of molecular ions from two mass spectra
- Display of NIST database search results
- Display of accurate mass analysis result
- Display of isotopic pattern analysis result

**Applicable model**
JMS-T2000 GC Series
AccuTOF™ QCL, AccuTOF™ GCx-plus

**Notes**
- This product supports only MS-56210MP (main program) format data. It is necessary to save data in Profile format for measurement data.
- This product works on the Windows® 10 operating system (64 bit version).
- For operation of this product, PC performance equal to or higher than MS-57042PCE is recommended.

Microsoft, Windows, PowerPoint and Microsoft Office are registered trademarks of Microsoft Corporation in the USA and other countries. Microsoft Word is a product name of Microsoft Corporation.

The product specification is subject to change without prior notice.

---

**Design Concept of msFineAnalysis**

msFineAnalysis has fully automated the entire qualitative analysis process for data acquired by GC/EI and GC/soft ionization (CI, PI, FI).

The software compares molecular formula information acquired from the NIST library search with soft ionization exact mass data analysis to ensure accurate qualitative results. To do this, it examines the NIST library search results, reduces the possibility of false positive identifications, and selects the correct components from multiple candidates with similar scores. For unknown components not registered in the NIST libraries, it estimates molecular formulas by using the soft ionization data, acquires partial structure information and estimates structural formulas by using the EI data. msFineAnalysis is a powerful tool based on a new concept for supporting qualitative GC-MS analysis.

**msFineAnalysis**

Designed specifically for high resolution GC-TOFMS

Auto analysis software for data acquired by electron ionization/soft ionization

---

**CI, PI, FI**
(soft ionization techniques)

**EI**
(hard ionization techniques)