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Doc. Type: Work Instruction

Status: Production

Doc. ID: PMI-RRP-WKI-111621

Version N°: 4.0.0

Effective date:
28-Feb-2018

NTDS GC×GC-TOFMS Volatile (RDNEU)



PHILIP MORRIS
INTERNATIONAL

NTDS GC×GC-TOFMS Volatile (RDNEU)

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1 Purpose

This method describes an assay for the detection of significant differences between two samples using comprehensive two-dimensional gas chromatography coupled to a time-of-flight mass spectrometer (GC×GC-TOFMS). The assay is based on a comprehensive chemical characterization of complex mixtures with no predefined target compounds.

To maximize the coverage of the chemical space in terms of polarity and volatility, the non-targeted differential screening (NTDS) GC×GC-TOFMS assay consists of three analytical methods, for nonpolar, polar and volatile compounds, respectively. The analytical methods compare two test items by comprehensive chemical screening and subsequent data evaluation to get summary tables with ranked chemical differences. This work instruction describes the method for volatile compounds, which is referred to as "Volatile method".

The high resolution power using comprehensive 2-dimensional gas chromatography, combined with spectral deconvolution, results in high quality electron ionization (EI) mass spectra, improving the search against commercial mass-spectral libraries.

Data acquisition is followed by advanced raw data processing using the ChromaTOF software for automatic peak finding, spectral deconvolution and peak alignment, resulting in an aligned peak table. The software tools CASI Pre-/Post-processor and CASI automate a sequence of important data evaluation steps, e.g. batch processing, data alignment, compound identification, semi-quantification, comparison and ranking.


Ranking of the compounds is done by applying a student's t-test to filter compounds with a significant difference followed by a ranking procedure that was developed empirically. The ranking procedure considers the relative differences in abundance of each compound as well as the absolute abundance. In addition flexible filtering (e.g. fold change, concentration cut-off) can be applied.

NTDS using GC×GC-TOFMS represents a key methodology to not only comprehensively characterize the chemical composition of aerosols derived from different test items, but also to determine significant differences of these complex matrices. Upon comparison of different reduced risk product (RRP) platforms, the detection of novel compounds or elevated levels of specific constituents provides an important basis for subsequent toxicological assessment.

2 Scope and Applicability

This document applies to the analytical laboratories of the Complex Matrix Analysis team, Testing Labs & Analytical Research (TL&AR), at PMI, RRP in Neuchâtel.

The methods were developed for smoke/aerosol-related samples (e.g. TPM, whole smoke) from conventional cigarettes and prototypes (e.g. RRP). Nevertheless, the described method can be taken as a universal approach for comparing samples of different matrices in an unbiased way.

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3 Responsibilities

Task/Activity	Responsible
Sample collection and sample preparation	Lab technician or equivalent trained
Setting up the instrument and verification of the quality control criteria according to <i>PMI-RRP-WKI-111668</i> - Operation of a LECO Pegasus 4D GC×GC-TOFMS system (<i>RDNEU</i>)	Lab technician or equivalent trained
Reporting of any procedural deviation to study director	Lab technician or equivalent trained
Selection of the detector voltage	Scientist or equivalent trained
Perform analysis	Lab technician or equivalent trained
Data processing and data export using the LECO ChromaTOF software	Lab technician or equivalent trained
Data evaluation using CASI Pre-processor, CASI and CASI Post-Processor	Lab technician or equivalent trained
Verification and finalization of the dataset	Scientist or equivalent trained
Preparation of a report	Scientist or equivalent trained
Release of results	Study director

Table 1. Tasks and responsible persons for the complete workflow of NTDS GC×GC-TOFMS Volatile.


4 Description of the Method

4.1 Principle

This method describes an assay for the detection of the most significant differences between two samples using comprehensive two-dimensional gas chromatography coupled to a time-of-flight mass spectrometer. The assay is based on a comprehensive chemical characterization of complex mixtures with no predefined target compounds.

4.2 Sample Requirements and Workload

An example for the workload is shown in **Table 2**. The time is calculated for one full-time equivalent (FTE) and under the assumption that two test items are compared using three replicates per test item.

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Task	Man-hours FTE) (1
Sample collection	
ARMS request	2
Preparation of solvent and working solutions	16
Setting up the instrument	8
Analytical quality assurance	
Sensitivity test	6
System suitability test	16
Sample preparation	2
Data processing and evaluation	
Raw data processing	32
CASI Pre-Processor, CASI, CASI Post-Processor	24
Reporting	48
Archiving of study related data	16
TOTAL	170

Table 2. Workload in man-hours, one FTE, comparison of two test items.

4.3 Material, Equipment, Chemicals, Standards and References

4.3.1 Equipment

GC×GC-TOFMS system 1, PMI ID 7764:


Instrument	Instrument ID	PMI ID
Autosampler	Agilent 7683 Series	3484
Injector	Agilent 7683B Series	11650
Gas chromatograph	Agilent 7890A	7765
Mass spectrometer	LECO Pegasus 4D SN 3390	7766
Dewar	Cryotherm Apollo 350	6478

Table 3. GC×GC-TOFMS system 1.

GC×GC-TOFMS system 2, PMI ID 10606:

Instrument	Instrument-ID	PMI ID
Autosampler	Agilent 7683 Series	11651
Injector	Agilent 7683B Series	0896
Gas chromatograph	Agilent 6890N	2938
Mass spectrometer	LECO Pegasus 4D SN 3284	3103
Dewar	Cryotherm Apollo 200	7771

Table 4. GC×GC-TOFMS system 2.

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GC×GC-TOFMS system 3, PMI ID 6472:

Instrument	Instrument-ID	PMI ID
Autosampler	Agilent 7683 Series	3494
Injector	Agilent 7683B Series	12457
Gas chromatograph	Agilent 6890N	6474
Mass spectrometer	LECO Pegasus 4D SN 3242	6473
Dewar	Cryotherm Apollo 350	9878

Table 5. GC×GC-TOFMS system 3.

4.3.2 Chemicals/Reagents


Name	Specification (equivalent or higher)	Supplier (or equivalent)	Product No.
N,N-Dimethylformamide	puriss. p.a. ≥ 99.8%	Sigma-Aldrich	33120
Hexafluorobenzene	99%	Sigma-Aldrich	H8706

Table 6. List of chemicals/solvents used for the Volatile method.

4.3.3 Internal Standard Compounds

Name	Specification (equivalent or higher)	Supplier (or equivalent)	Product No.
Acetone-d6	≥ 99.5% purity/atom-%d	Sigma-Aldrich	151793
Benzene-d6	≥ 99.5% purity/atom-%d	Sigma-Aldrich	175870
2-Butanone-d5	≥ 98.0% purity/atom-%d	CDN Isotopes	D-293
Butyraldehyde-d8	≥ 98.0% purity/atom-%d	Sigma-Aldrich	755532
Cyclohexene-d10	≥ 98.0% purity/atom-%d	CDN Isotopes	D-173
Cyclopentane-d10	≥ 99.0% purity/atom-%d	CDN Isotopes	D-236
1,2-Dichloroethane-d4	≥ 99.0% purity/atom-%d	Sigma-Aldrich	396540
Dimethyl sulfide-d6	≥ 99.0% purity/atom-%d	Sigma-Aldrich	416452
Ethyl acetate-d8	≥ 99.0% purity/atom-%d	Sigma-Aldrich	522899
Furan-d4	≥ 98.0% purity/atom-%d	Sigma-Aldrich	338753
Methacrylonitrile-d5	≥ 97.0% purity/atom-%d	Sigma-Aldrich	693480
3-Methylhexane-d16	≥ 98.0% purity/atom-%d	Sigma-Aldrich	491470
Propylene oxide-d6	≥ 98.0% purity/atom-%d	CDN Isotopes	D-1915
Tetrahydrofuran-d8	≥ 99.0% purity/atom-%d	Sigma-Aldrich	184314

Table 7. List of deuterium labeled internal standard (ISTD) compounds used for the Volatile method.

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4.3.4 Retention Index Marker Compounds

Name	Specification (equivalent or higher)	Supplier (or equivalent)	Product No.
n-Pentane-d12	≥ 98.0% purity/atom-%d	CDN Isotopes	D-28
n-Hexane-d14	≥ 99.0% purity/atom-%d	Sigma-Aldrich	303003
n-Heptane-d16	≥ 99.0% purity/atom-%d	CDN Isotopes	D-1142

Table 8. List of retention index marker (RIM) compounds used for the Volatile method.

4.4 Procedure

No calibration for quantification is used in this assay. The assay uses a semi-quantification procedure described in **Section 4.5.2**.

4.4.1 Sample Collection

4.4.1.1 Generation of Smoke/aerosol-related Samples

Cigarette smoke/aerosol related samples are generated according to *PMI-RRP-WKI-111729*. All the necessary parameters for smoke/aerosol collection are described in the respective ARMS request.

Whole smoke is collected in two micro-impingers connected in series. The extraction solution is N,N-Dimethylformamide (N,N-DMF) containing internal standards and retention index markers (ISTDs/RIMs_{volatile}). The preparation of stock solutions, working solution (ISTD_{work}) and extraction solution (ISTD_{extract}) is described and has to be documented in *PMI-RRP-FOR-111487* - Chemicals, solvents, solutions and internal standard amount used for NTDS GCxGC-TOF (*RDNEU*). Stock solutions, ISTD_{work} and ISTD_{extract} have to be freshly prepared.

After generation of the smoke/aerosol samples the micro-impingers are sealed and kept in dry ice/isopropanol. The samples are analyzed as soon as possible after sample generation. In case samples need to be stored, storage of the impinger contents/crude extracts or e-liquids/e-liquid extracts has to be documented in *PMI-RRP-FOR-111488* - Storage of samples and study related materials for NTDS (*RDNEU*).


4.4.1.2 Generation of Other Samples

The described method can be used for comparing samples with different kinds of matrices. The samples will be analyzed as soon as possible after sample generation.

4.4.2 Sample Preparation

A step-by-step workflow for sample preparation is described and has to be documented in *PMI-RRP-FOR-111493* - Sample preparation NTDS GCxGC-TOF volatile (*RDNEU*). The workflow is briefly described here point by point:

- the content of the micro-impingers (twice 10mL N,N-DMF) containing a set of internal standard and retention index marker compounds is added to a Pyrex tube
- an aliquot is transferred into an autosampler vial and analyzed by GCxGC-TOFMS in full scan mode

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- pool sample(s) is/are created from equal volumes of aerosol/smoke replicates to represent the chemical space of all sample groups


Storage of the remaining extracts has to be documented in **PMI-RRP-FOR-111488** - Storage of samples and study related materials for NTDS (**RDNEU**). Remaining extracts are kept until the study is closed.

4.4.3 Setting-up of Instruments

Instrument	Parameter	Settings																	
Injector	injector	cool-on-column, track-oven mode																	
	injection	on-column																	
	injection volume	0.1 µL																	
Gas chromatograph	carrier gas	helium																	
	flow	2.2 ml/min (68min), 1.2 ml/min (12min) (ramped flow)																	
	column 1 (1 st dimension)	30 m DB-624UI, 0.25 mm ID, 1.4 µm df																	
	column 2 (2 nd dimension)	2.4 m DB-FFAP, 0.10 mm ID, 0.1 µm df																	
	primary oven temperature program	<table> <tr> <th>rate (°C/min)</th><th>target temp. (°C)</th><th>duration (min)</th></tr> <tr> <td>initial</td><td>-20.0</td><td>1.0</td></tr> <tr> <td>5.0</td><td>-5.0</td><td>0.0</td></tr> <tr> <td>1.0</td><td>50.0</td><td>0.0</td></tr> <tr> <td>5.0</td><td>95.0</td><td>0.0</td></tr> <tr> <td>45.0</td><td>230.0</td><td>9.0</td></tr> </table>	rate (°C/min)	target temp. (°C)	duration (min)	initial	-20.0	1.0	5.0	-5.0	0.0	1.0	50.0	0.0	5.0	95.0	0.0	45.0	230.0
rate (°C/min)	target temp. (°C)	duration (min)																	
initial	-20.0	1.0																	
5.0	-5.0	0.0																	
1.0	50.0	0.0																	
5.0	95.0	0.0																	
45.0	230.0	9.0																	
	secondary oven temperature program	<table> <tr> <th>rate (°C/min)</th><th>target temp. (°C)</th><th>duration (min)</th></tr> <tr> <td>initial</td><td>0.0</td><td>4.0</td></tr> <tr> <td>1.0</td><td>55.0</td><td>0.0</td></tr> <tr> <td>5.0</td><td>100.0</td><td>0.0</td></tr> <tr> <td>45.0</td><td>235.0</td><td>9.0</td></tr> </table>	rate (°C/min)	target temp. (°C)	duration (min)	initial	0.0	4.0	1.0	55.0	0.0	5.0	100.0	0.0	45.0	235.0	9.0		
rate (°C/min)	target temp. (°C)	duration (min)																	
initial	0.0	4.0																	
1.0	55.0	0.0																	
5.0	100.0	0.0																	
45.0	235.0	9.0																	
Transfer line	temperature	250 °C																	
Modulator	modulator	enabled																	
	modulator temperature offset to secondary oven	15 °C																	
	2-dimension separation time	6 s																	
	hot pulse time	1.00 s																	
	cool time between stages	2.00 s																	
Mass spectrometer	acquisition delay	0 s																	
	mass range	29-500 u																	
	data acquisition rate	200 spectra/s																	
	detector voltage	1450 – 2000 V																	
	electron energy	-70 V																	
	temperature ion source	230 °C																	

Table 9. Setup of the instrument for the Volatile method.

Before the main sequence is started, the sensitivity and the chromatographic resolution of the system is tested. In the case of failure of at least one system suitability parameter, a troubleshooting will be initiated (e.g., new analytical column, increase of multiplier voltage, etc.).

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Prior to every analysis the instrument has to be checked and the changes documented in *PMI-RRP-FOR-111496* - Preparation of LECO PEGASUS 4D SYSTEM for NTDS GCxGC-TOFMS (*RDNEU*).

4.4.3.1 Sensitivity Test

The operating procedure of the LECO Pegasus 4D GCxGC-TOFMS system is given in *PMI-RRP-WKI-111668* - Operation of a LECO Pegasus 4D GCxGC-TOFMS system (*RDNEU*). The preparation of a hexafluorobenzene (HFB) stock solution/sensitivity test solution and the correct procedure to conduct a sensitivity test is described in the WKI and has to be documented *PMI-RRP-FOR-111495* - Sensitivity test and system suitability test NTDS GCxGC-TOF volatile (*RDNEU*). The final detector voltage chosen for the subsequent analysis has to be indicated in the form *PMI-RRP-FOR-111495* and a LECO ChromaTOF report (template name "Detector Sensitivity") has to be generated, saved electronically in the study folder and printed, signed and stored in the study binder.


Sensitivity testing of the system is done by measuring the sensitivity test solution prior to the analytical series. A sequence with an increasing multiplier voltage in steps of 50-V-increments is prepared. The maximum detector voltage is given in **Section 4.4.3**. The analysis will be performed in 1-dimensional mode. The main criterion for the sensitivity is the **quant signal to noise ratio (quant S/N)** of the m/z 186 ion of HFB. Additionally the correct name has to be assigned (Benzene, hexafluoro-) when matching the EI spectrum to the HFB library. In general an increase of the detector voltage leads to an improvement in S/N, yet at some point the improvements are less pronounced as the noise increases along with the signal. Typically the acceptance criterion is a **quant S/N ≥ 180**, however the final detector voltage has to be selected by the scientist. The decision has to be commented in the form *PMI-RRP-FOR-111495*.

4.4.3.2 System Suitability Test

The chromatographic system is tested by injection of aliquots of the extraction solution (ISTD_extract). The samples are called SST (system suitability test) and are distributed equally across the analytical series (SST_1, SST_2, ...). The concentration is the same as in the measured samples. The sample preparation procedures are described in *PMI-RRP-FOR-111487* - Chemicals, solvents, solutions and internal standard amount used for NTDS GCxGC-TOF (*RDNEU*) and briefly in **Section 4.4.4**.

Test parameters are:

- **retention time** of selected compounds to test the flow and temperature programs of the analytical system
→ stability of the retention times is monitored
- **peak shape** to test the inertness of the analytical system, especially of the analytical columns
→ tailing factor is monitored

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Compound	1st Dimension RT (s)		2nd Dimension RT (s)		Tailing Factor 2nd Dimension
Acetone-d6	1212	±80 s	1.935	±0.4 s	<5
2-Butanone-d5	2208	±90 s	1.960	±0.5 s	<5
1,2-Dichloroethane-d4	2640	±120 s	3.380	±0.6 s	<5

Table 10. Acceptance criteria for the system suitability test using the Volatile method.

ChromaTOF processing and data evaluation of the system suitability test is described in *PMI-RRP-FOR-111495* - Sensitivity test and system suitability test NTDS GCxGC-TOF volatile (*RDNEU*). A LECO ChromaTOF (template name “System Suitability Test”) report has to be generated for each SST sample, saved electronically in the study folder and printed, signed and stored in the study binder. The results of the SST have to be documented in *PMI-RRP-FOR-111495*, saved electronically in the study folder and printed and stored in the study binder.


4.4.4 Preparation of Solutions and Media

Preparation of stock solutions, working and extraction solution is described and has to be documented in *PMI-RRP-FOR-111487* - Chemicals, solvents, solutions and internal standard amount used for NTDS GCxGC-TOF (*RDNEU*). All solutions are labeled with solution name, concentration, type of solvent, preparation date, storage condition and the initials of the person who prepared the solution (in accordance with *PMI-RRP-WKI-111814*). The solutions are stored at -10 to -80 °C. The stock solutions are prepared by adding the standard compound with a microliter syringe to the required volume of solvent using a piston pipette. Working and extraction solutions are only prepared by using piston pipettes according to work instruction *PMI-RRP-WKI-111700*.

Calculation of concentrations:

For liquid compounds:

$$\text{Concentration (mg/mL)} = \frac{\text{Compound volume (mL)} \cdot \text{density (g/mL)} \cdot (\text{purity atom-\%d} (\geq\%) / 100) \cdot (\text{purity content} (\geq\%) / 100)}{\text{Total volume (mL)}}$$

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4.4.4.1 Stock Solutions of Internal Standards and Retention Index Markers

Solution Name	Volume (µL)	Density (g/mL)	Volume (mL)	Solvent
Acetone-d6	12.5	0.872	10	DMF
Benzene-d6	10.0	0.950	10	DMF
2-Butanone-d5	12.5	0.860	10	DMF
Butyraldehyde-d8	12.5	0.887	10	DMF
Cyclohexene-d10	12.5	0.908	10	DMF
Cyclopentane-d10	12.5	0.858	10	DMF
1,2-Dichloroethane-d4	7.5	1.307	10	DMF
Dimethyl sulfide-d6	12.5	0.928	10	DMF
Ethyl acetate-d8	10.0	0.984	10	DMF
Furan-d4	10.0	0.991	10	DMF
Methacrylonitrile-d5	12.5	0.858	10	DMF
3-Methylhexane-d16	12.5	0.798	10	DMF
Propylene oxide-d6	12.5	0.916	10	DMF
Tetrahydrofuran-d8	10.0	0.985	10	DMF
n-Pentane-d12	15.0	0.731	10	DMF
n-Hexane-d14	15.0	0.767	10	DMF
n-Heptane-d16	15.0	0.794	10	DMF

Table 11. Target volumes for the ISTD and RIM stock solutions.


The appropriate volumes that need to be pipetted for the ISTD and RIM stock solutions are described in *PMI-RRP-FOR-111487* - Chemicals, solvents, solutions and internal standard amount used for NTDS GC×GC-TOF (RDNEU).

Concentrations depend on the purity (content and atom-%d) of the used compounds. The exact values are documented in *PMI-RRP-FOR-111487*.

4.4.4.2 Working and Extraction Solution of ISTDs and RIMs

The ISTD and RIM working solution (ISTD_work) is prepared in a 10 mL headspace vial.

Concentrations depend on the purity of the used compounds. The exact values are documented in *PMI-RRP-FOR-111487*.

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Used Stock Solution	Volume Stock Solution (µL)	Concentration (µg/mL)
Acetone-d6	250	85
Benzene-d6	300	90
2-Butanone-d5	250	80
Butyraldehyde-d8	200	70
Cyclohexene-d10	130	45
Cyclopentane-d10	120	40
1,2-Dichloroethane-d4	250	75
Dimethyl sulfide-d6	60	20
Ethyl acetate-d8	100	30
Furan-d4	300	90
Methacrylonitrile-d5	250	80
3-Methylhexane-d16	170	50
Propylene oxide-d6	200	70
Tetrahydrofuran-d8	150	45
n-Pentane-d12	200	65
n-Hexane-d14	170	60
n-Heptane-d16	120	45

Table 12. Target volumes for the working solution of ISTDs and RIMs.

The extraction solution (ISTD_extract) is prepared by diluting the working solution (300µL ISTD_work filled up to 10mL with N,N-DMF). Calculation of concentrations is given in *PMI-RRP-FOR-111487*.

4.4.5 Number of Determinations


Each sample will be generated minimum in triplicate and analyzed. Blanks, SST samples, pool sample(s) and one technical replicate of each matrix will be evenly distributed across the sequence. The term technical replicate describes the process of injecting the same sample extract multiple times across a sequence to assess the instrumental variability.

4.4.6 Daily Verification or According to Use

Prior to each study the LECO Pegasus 4D system is verified according to *PMI-RRP-FOR-111496* - Preparation of LECO PEGASUS 4D SYSTEM for NTDS GCxGC-TOFMS (*RDNEU*) and tested in terms of sensitivity and system suitability according to *PMI-RRP-FOR-111495* - Sensitivity test and system suitability test NTDS GCxGC-TOF volatile (*RDNEU*).

4.4.7 Testing Procedure

This method describes an assay for detection of significant differences between two samples by GCxGC-TOFMS. The composition of different complex mixtures, like cigarette smoke or RRP aerosol, is compared in a hypothesis-free unbiased way (non-targeted). Compounds found to be different between samples are ranked according to relevance considering the relative difference in abundance of each compound as well as the absolute abundance. Focus of the approach is the comprehensive chemical characterization of a complex mixture using three GCxGC-TOFMS methods, which are allocated to different polarities and volatilities of the

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constituents. The methods are not intended to assess absolute quantitative amounts of the detected compounds, the concept is rather based on a semi-quantitative assessment.

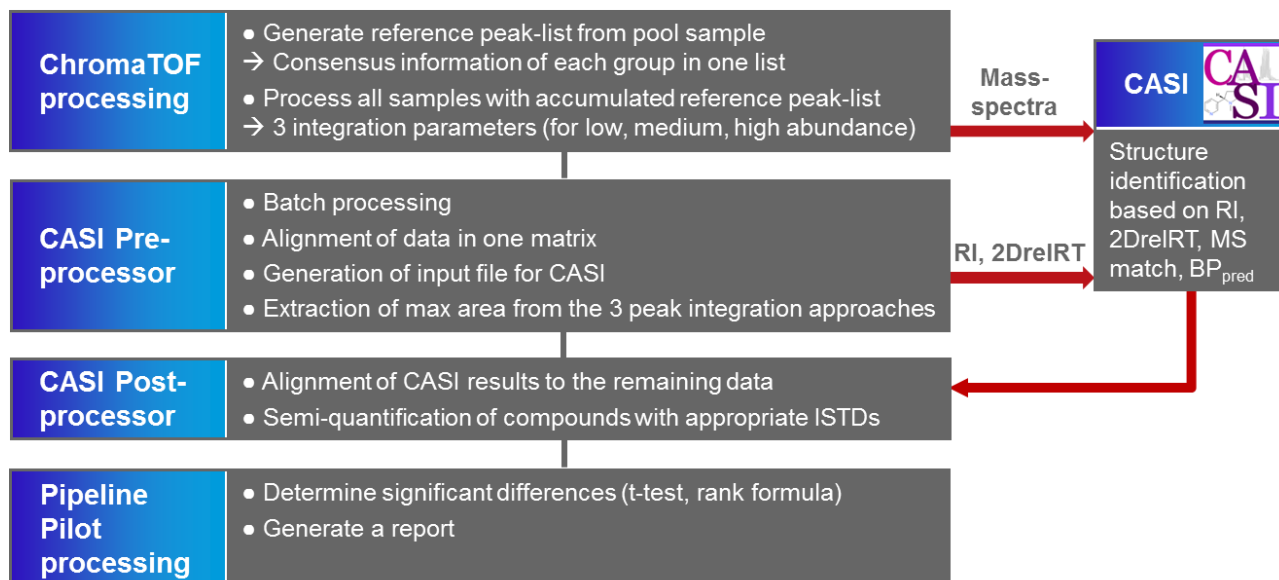


Figure 1. Overview of the data processing steps.

Data processing is divided into multiple steps, (1) ChromaTOF processing, (2) CASI Pre-processor, (3) CASI, (4) CASI Post-processor, and (5) Pipeline Pilot processing (see **Figure 1**).

First the raw data has to be processed by the LECO ChromaTOF software. After assembling all the relevant information each sample is processed with three different parameter settings to optimally assess the peak area of minor, medium and major peaks. Files are exported in .csv format.


The data is further processed using CASI Pre-processor, which processes the batches and aligns the data in one matrix. The maximum area of each peak is determined and an input file for CASI is created. The CASI input file contains the mean of retention indices (RI) and 2nd dimension relative retention times (2DreIRT) for all compounds. Together with the cas_i_input file the associated EI mass spectral library (converted with lib2nist) is submitted to CASI.

The CASI platform increases the accuracy for analytical identification of compound structures and accelerates and standardizes the identification process. It assures reproducibility and enables scientists to have higher confidence in the correct assignment of mass spectra to the right compounds. CASI automatically identifies, on-the-fly and with highest confidence, possible relevant structures from mass spectra associated with chromatographic values, including models for retention index, 2-dimensional relative retention time and boiling point.

CASI Post-Processor combines the high confidence identifications of CASI to the existing data matrix. Subsequently, semi-quantification is performed according to predefined rules.

In the final step, a Pipeline Pilot script is used to determine the significant differences and to transform the data to a suitable reporting format.

Alternatively, a manual Microsoft Excel process can be used instead of CASI Pre- and Post-processor. This procedure was employed before the automated CASI Pre- and Post-processor procedure, but became

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obsolete due the enormous time-consumption and the error-proneness. However it will be briefly described in **Section 4.4.7.2.3.**

4.4.7.1 Data Processing using the LECO ChromaTOF Software


A step-by-step description for the ChromaTOF processing is given in *PMI-RRP-FOR-111494* - Data processing in ChromaTOF NTDS GCxGC-TOF volatile (*RDNEU*). All the steps have to be documented. Different type of sheets can be selected according to the number of items that need to be compared. In the following an example for two items (e.g. 3R4F versus P1) is shown.

4.4.7.1.1 Generation of the Reference Peak Matrix from the Pool Sample

- **Processing of the pool sample**
 - computing of the baseline
 - finding peaks above the baseline
 - identifying peaks by library search (select only “ISTDs_RIMs” library)
 - integration of the peaks (area, height)

<input checked="" type="checkbox"/>	Baseline - computes baseline
<input checked="" type="checkbox"/>	Peak Find - finds peaks above the baseline
<input checked="" type="checkbox"/>	Library Search - identifies all peaks found
<input checked="" type="checkbox"/>	Calculate Area / Height - computes the area and height of peaks without a calibration

Figure 2. Processing steps that need to be activated in the Data Processing Method (DPM).

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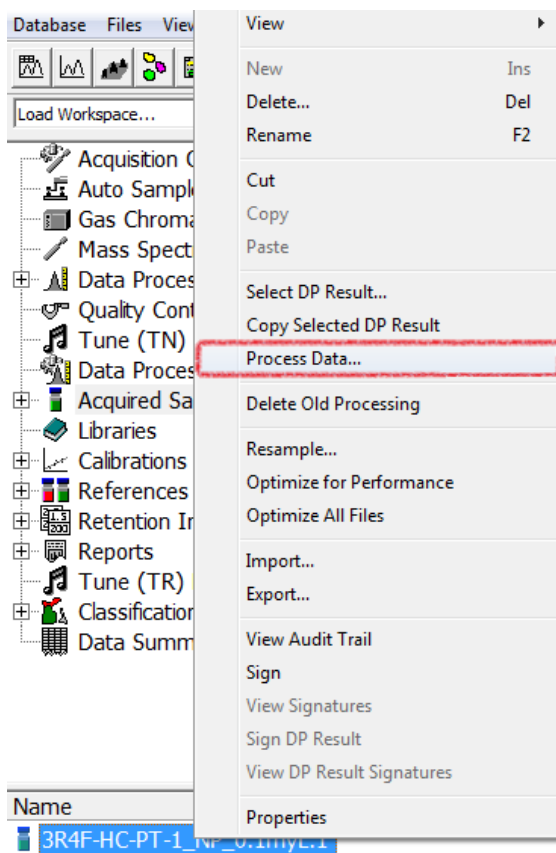



Figure 3. Processing of the pool sample.

- **Repeated processing of the pool sample with classification and RI method**
 - computing of the baseline
 - finding peaks above the baseline
 - identifying peaks by library search (select only “ISTDs_RIMs” library)
 - integration of the peaks (area, height)
 - calculation of retention index
 - classification (exclusion of, e.g. bleed, artefact peaks like isopropanol including tailing regions)

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☒ Baseline - computes baseline
☒ Peak Find - finds peaks above the baseline
☒ Library Search - identifies all peaks found
☒ Calculate Area / Height - computes the area and height of peaks without a calibration
☒ Retention Index Method

☒ Filter peaks by classification

CLASSIFICATION

Add...
Remove

Select the retention index method to convert retention time to retention index:

RIM
Select ...

☒ Check Retention Index Analytes

Criteria:

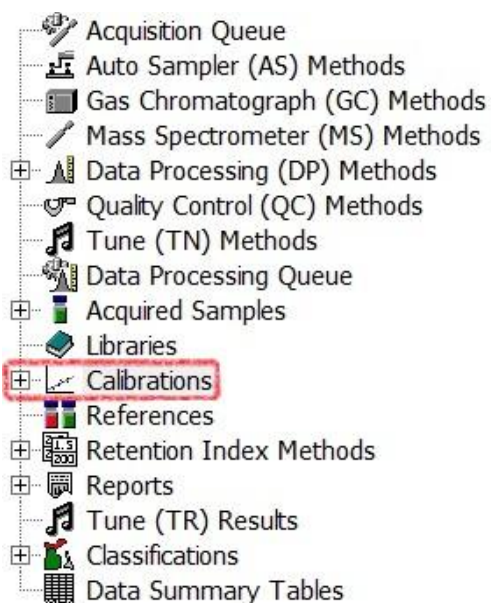
☒ Maximum allowed retention index variation.
20

Options:

☒ Update the retention times of retention index analytes.

Figure 4. Processing steps that need to be activated in the DPM of the repeated processing.

- **Evaluate the data and create a new calibration of the pool sample**
 - evaluate correct finding of ISTD and RI compounds
 - sort according to Quant S/N, delete peaks with S/N <50
 - flag false/noise peaks
 - import processed and flagged data into new calibration
 - select quantitation parameters in the calibration



Name
 Volatile_Pool sample-S/N 250

Figure 5. Creating a “New” calibration under tab “Calibrations”.

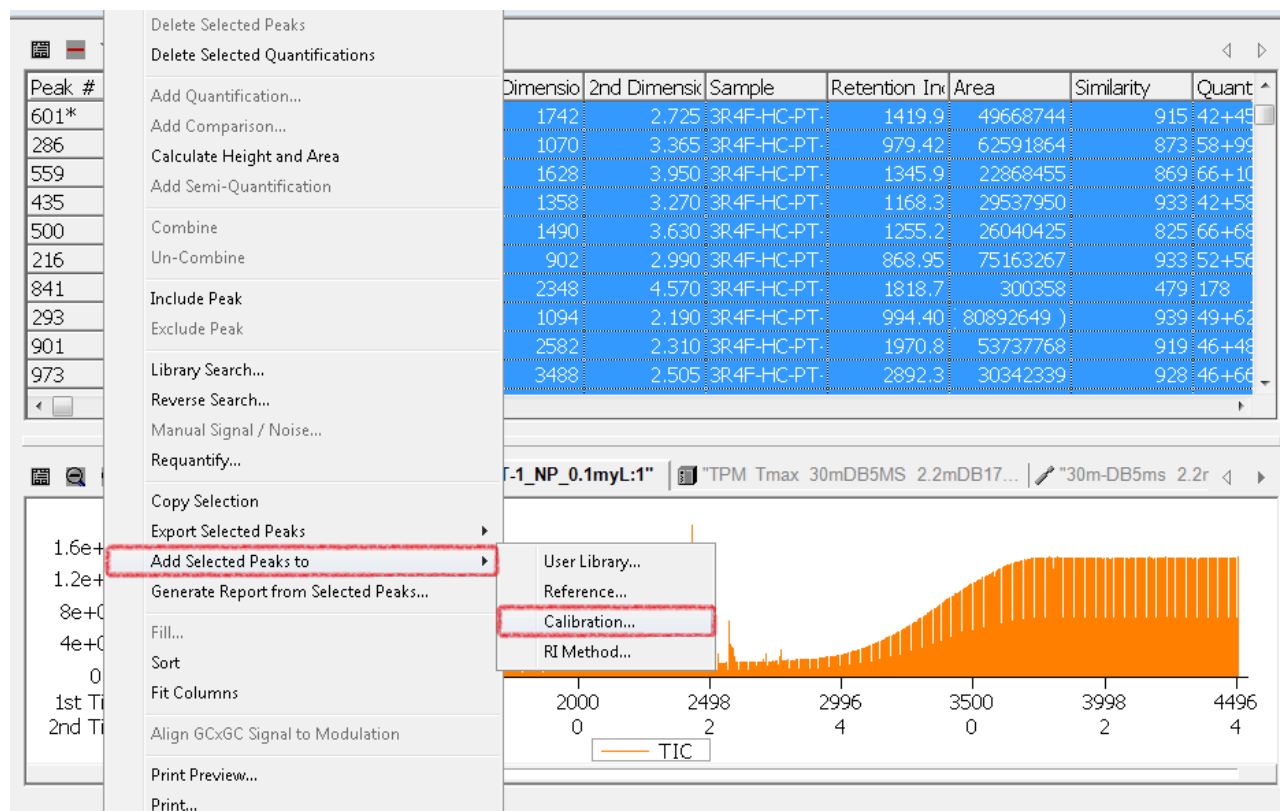



Figure 6. Select the processed pool sample, select all peaks and add selected peaks to calibration.

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- Acquisition Queue
- Auto Sampler (AS) Methods
- Gas Chromatograph (GC) Methods
- Mass Spectrometer (MS) Methods
- Data Processing (DP) Methods
- Quality Control (QC) Methods
- Tune (TN) Methods
- Data Processing Queue
- Acquired Samples
- Libraries
- Calibrations
- References
- Retention Index Methods
- Reports
- Tune (TR) Results
- Classifications
- Data Summary Tables

Analyte	1st Dimension R.I. Deviation	R.I. Deviation	S/N Threshold	Force Origin	Min Valid Concentration	Max Valid Concentration
1	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
2	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
3	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
4	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
5	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
6	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
7	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
8	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
9	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
10	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
11	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
12	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
13	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
14	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
15	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
16	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
17	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
18	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
19	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
20	18.000	0.30000	10.000	Force Origin	0.0000	1000000000
21	18.000	0.30000	10.000	Force Origin	0.0000	1000000000

Figure 7. Selection of the quantitation parameters. Values have to be filled down.

4.4.7.1.2 Comparison of the Whole Sample Set against the Reference Peak List and Export Data

- **Prepare a report-file folder structure for the export of the .csv files**

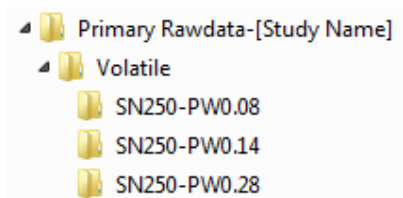



Figure 8. Folder structure for the export of the .csv files.

- **Prepare three quantitation methods with alternating peak widths in the 2nd dimension**
 - computing of the baseline
 - finding peaks above the baseline
 - disable library search
 - calculation of retention index
 - apply calibration
 - enable export of the peak information in ASCII CSV format

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Select the task or tasks you wish to perform from the list below.


- ☒ Baseline - computes baseline
- ☒ Peak Find - finds peaks above the baseline
- ☐ Library Search - identifies all peaks found
- ☐ Calculate Area / Height - computes the area and height of peaks without a calibration
- ☒ Retention Index Method
- ☐ Classifications
- ☒ Apply Calibration(s) - computes the absolute concentration of peaks based upon a calibration
- ☐ Apply Reference(s) - computes the relative concentration of peaks with respect to a reference
- ☐ Semi Quantification - computes concentration based on another analytes calibration curve
- ☐ Tune Check
- ☐ Tailing Factor Check - checks to see if the analytes have an acceptable peak shape
- ☐ Calibration Check
- ☐ Blank Check - checks to make sure none of the analytes exceed their blank concentration
- ☐ Report - prints selected reports for each sample
- ☒ Export peak information in ASCII CSV format
- ☐ Export data in Andi MS format (.cdf)
- ☐ Export data file

Add the calibrations to use for quantification to the list below:

Volatile_Pool sample-S/N 250 	Add... Remove Promote Demote
--	---------------------------------------

Figure 9. Processing steps that need to be activated in the DPM of the final three methods.

- method 1: peak width 0.08 sec
- method 2: peak width 0.14 sec
- method 3: peak width 0.28 sec
- keep remaining parameters consistent

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Enter baseline tracking info below:

#	Start	End	Mode
1*	Start of Run	End of Run	Default

Add
Remove

Enter the baseline offset below (0.5-3.0):

0.8

Examples:
 0.5 Through the middle of the noise
 1.0 Just above the noise

Enter the number of data points that should be averaged for smoothing below:

Auto

☒ GCxGC Parameters

1st Dimension

Enter the expected peak width in seconds below.

☐ Peak widths broaden throughout the chromatographic run

Peak Width	Retention Time	Peak Width values should be the expected number of slices multiplied by the modulation period. Typically, 3 to 6 slices per analyte are expected. Example: 6 slices x 4 sec. modulation period = Peak Width of 24
12		

2nd Dimension

Match Required to combine: 850

☒ Override the allowed second dimension R.T. shift for combine

Early 0.150

Late 0.050

Enter the expected peak width in seconds below: (as measured from baseline to baseline)

☐ Peak widths broaden throughout the chromatographic run

Peak Width	Retention Time	For broadening, two peak widths may be specified at two different retention times. All peak widths will be extrapolated from these two points.
0.08		

Subpeak Settings

Minimum S/N: 5

Integration Approach:

☒ Traditional

☐ Adaptive


☒ Filter peaks by classification

CLASSIFICATION

Add...

Figure 10. Alternate peak width in 2D (green square); keep remaining parameters constant (red squares).

- choose header "@SampleName[]"
- export all peaks, except "Contaminants / Unknowns"
- ensure export of peak information **in the right order**

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Header: [Leave Blank if no header information is desired]

Functions...

@SampleName()

Field Separator
☒ Comma
☐ Tab

Filter
☒ Calculate area percentage from filtered peaks only
☒ Quantified
☒ Analytes ☒ Surrogates ☒ Internal Standards
☒ Match
☒ Out of Tolerance
☐ Contaminants / Unknowns
☒ Not Found

Sort by:
 Quantification ☒ Ascending ☐ Descending

Then by:
 ☒ Ascending ☐ Descending

Then by:
 ☒ Ascending ☐ Descending


Information not exported Exported Information

Actual Tailing Factor Analyte Id Analyte Range Analyte Type Apexing Masses Area % BaselineModified Calculated Ion Ratio 1 Calculated Ion Ratio 2 Calculated Ion Ratio 3 Calibration Classifications Comment Conc. Concern Conc. Conv. Units Conc. Units Concerns Contributor Conv. Conc.	Add >> << Remove	Quantification Retention Index Area 1st Dimension Time (s) 2nd Dimension Time (s) Concentration R.T. (s) Expected Analyte R.T. (s) Similarity Quant S/N Type CAS standard Formula Exact Mass UniqueMass Name Quant Masses Full Width at Half Height
--	---------------------	---

Promote Demote

Figure 11. Critical parameters that have to be inserted, deactivated or given in the right order.

- **Process all samples using the final quantitation methods 1, 2 and 3**

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4.4.7.1.3 Transfer of the Final Calibration into a Library

- Create a new user library in ChromaTOF and name it according to the study
- Select all entries of the final ChromaTOF calibration and add them to the newly created user library
- Ensure to deactivate the box “Enter additional user information for each spectrum”

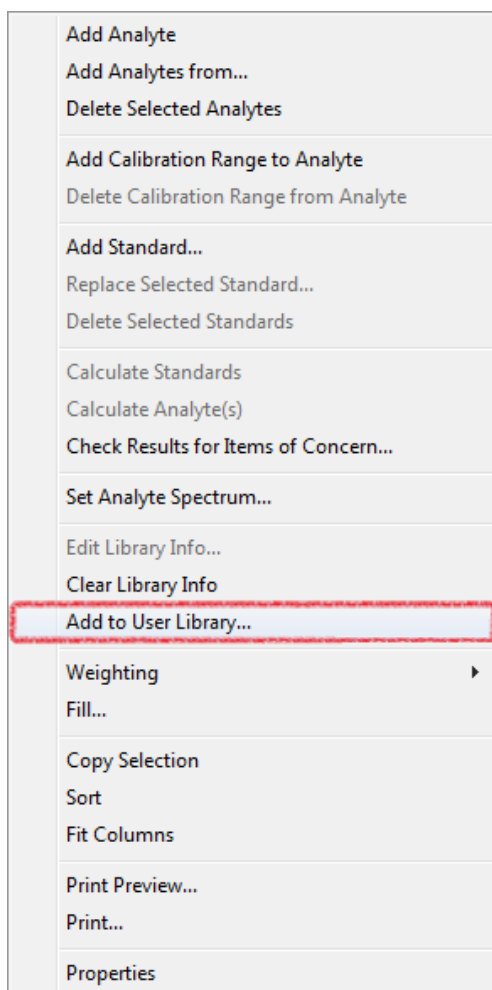



Figure 12. Adding information from a calibration to a user library.

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4.4.7.2 Submitting Metadata to CASI Pre-processor, CASI and CASI Post-processor

A step-by-step description is presented in *PMI-RRP-FOR-111491* - Submitting metadata for CASI pre-processor, CASI, CASI post-processor (*RDNEU*). All the steps have to be documented.

Two files are needed as input in order to run through all the CASI processes. Both files have to be saved in the study folder "...\\Primary Raw data-[Study name]\\Volatile\\".

The file "Concentration_ISTDs.txt" is generated from the respective volatile sheet in *PMI-RRP-FOR-111487* - Chemicals, solvents, solutions and internal standard amount used for NTDS GCxGC-TOF (*RDNEU*). The file has to be saved with the exact name "Concentration_ISTDs.txt". The group names (column → test item) in "Concentration_ISTDs.txt" have to be in accordance with the groups defined in the exported file names.

The JCAMP file "Library.HPJ" is generated by converting the library, which was created in **Section 4.4.7.1.3**, with lib2nist converter. Here, no naming convention is necessary.

4.4.7.2.1 CASI Pre-processor

CASI Pre-processor performs a fully automated batch processing, which includes replacement of saturated signals by the approximate value, alignment of the data, calculation of RI and 2DrelRT means, and determination of the maximum peak area for each signal within the three quantitation methods. In case the max area of an ISTD is not between 50 and 200 % of the mean of max area values across all samples the value is replaced by the mean of the max area.

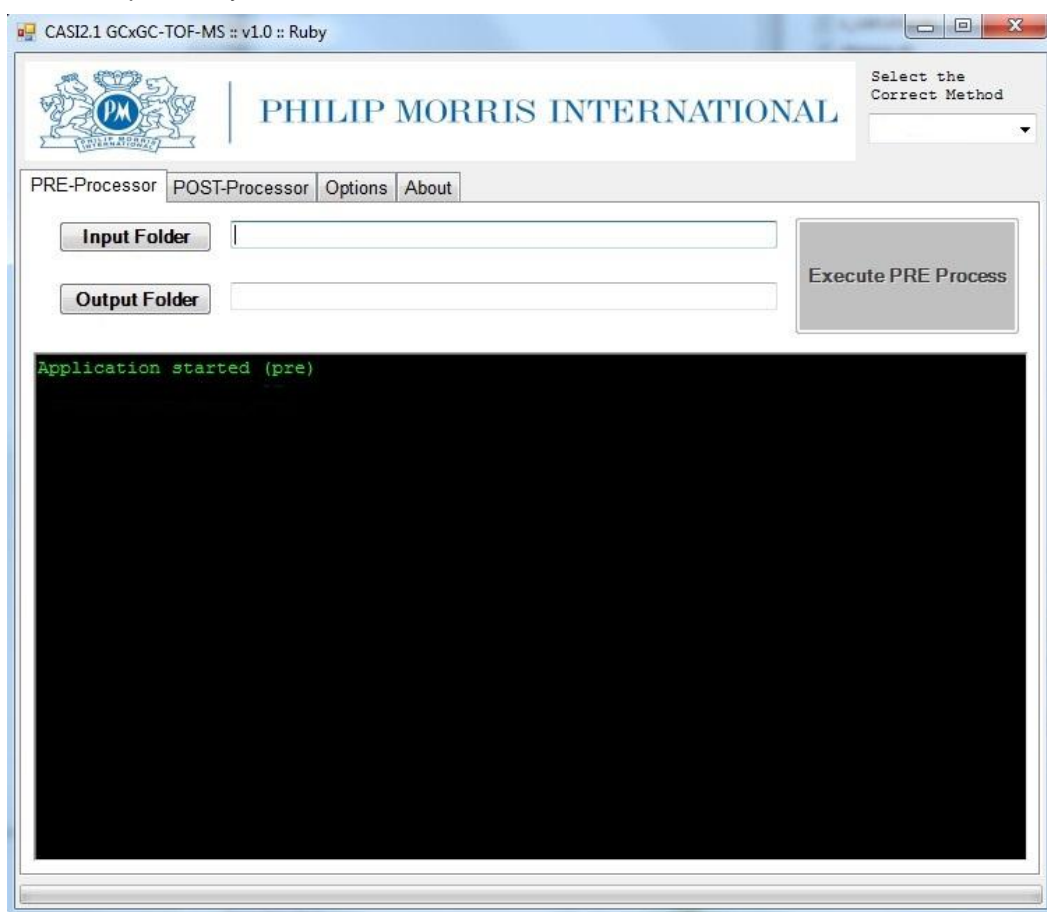



Figure 13. User interface of CASI Pre- and Post-processor.

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CASI Pre-processor outputs in total four files, two warning files and two files that are needed for further processes.

The file “warning.txt” lists all signals, which (A) were saturated and therefore replaced or (B) could not be found in respective samples.

The file “warning-area-dcompounds.txt” lists the max areas of the ISTDs that were out of the defined range and thus replaced (original max area values are shown).

The file “input-postprocess.txt” contains the accumulated information and is required as an input file for CASI Post-processor.

The file “casi_input.txt” comprises average RI and 2DrelRT values, which are needed for CASI.

4.4.7.2.1 CASI

Computer Assisted Structure Identification is a powerful platform that enhances the accuracy of compound structure identification and accelerates and standardizes the identification process. CASI's automatic identification process operates on-the-fly and facilitates a higher confidence in the correct assignment of mass spectra to the right compounds as relevant structures are associated with chromatographic values, including models for retention index, 2-dimensional relative retention time and boiling point.

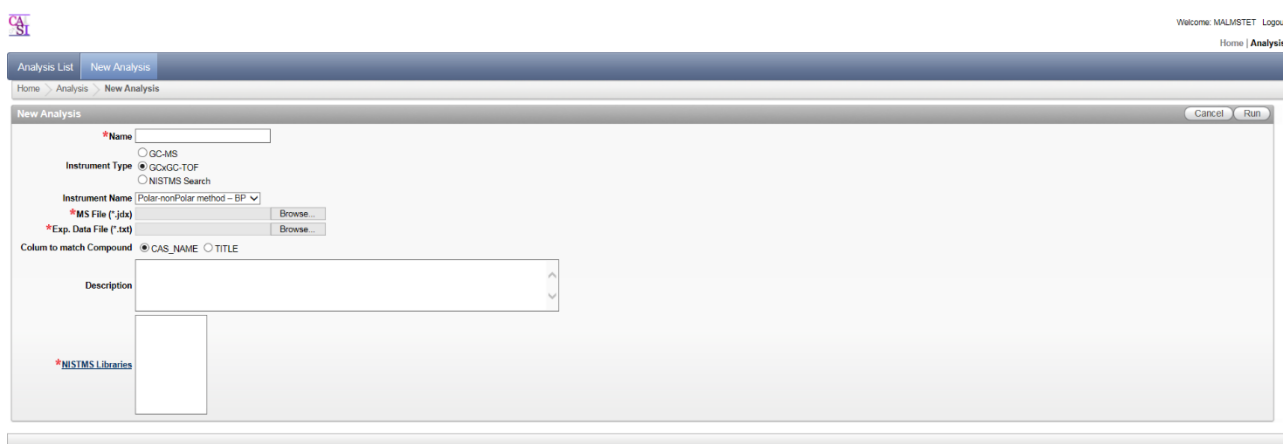



Figure 14. User interface of CASI.

A user manual for CASI is available in EDMS ([PMI-RRP-WKI-111624](#)).

CASI requires two files, the “Library.HPJ”, which was converted from the original library with lib2nist converter, and the “casi_input.txt” generated by the CASI Pre-processor.

When the CASI process is finished the “casi_report_ntds.txt” and the “casi_report.sdf” are exported. Both files are uploaded to the Pipeline Pilot script “IS_determination_volatile_GC×GC”. The script performs group-type classification, assigns each compound to a specific internal standard (according to rules defined in **Section 4.5.2**) and merges the data into one file. The merged file is saved as “casi_report_ntds.txt” (ensure the correct name). The file is further required to run CASI Post-processor.

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4.4.7.2.2 CASI Post-processor

CASI Post-processor aligns the data comprised in “casi_report_ntds.txt” to the data of the file “input-postprocess.txt”. Semi-quantification is performed according to specific rules, which are defined in **Section 4.5.2**. The output file of CASI Post-processor is the file “concentration.txt”, which contains the final processed data.

4.4.7.2.3 Manual Excel Processing

Before the CASI processors were developed the metadata was processed manually in a predefined MS Excel workflow. The individual steps are briefly described point by point in the following:

- open .csv file and delete saturation comments in field "area"
- sort table: field "standard" and then "quantification" ascending
- sort standards for "standard" descending
- verify ISTD and RT-INDEX alignment => correction if necessary
- rename .csv data into [SNx]-[Pwy]-[sample name]-[repetition number]-[method], e.g. SN250-PW0.14-3R4F_HC1-V.xls
- repeat first 5 steps for all .csv files
- generate EXCEL reference calculation file
- import compound name, area data and information on sample, measurement-no., S/N and PW into EXCEL
- verify correct data-table alignment (conditional format, compare names)
- correction of misalignments in data
- get maximum area of values from the different integration parameters
- prepare NIST format library from final calibration file, prepare chromatography file for CASI, including calculation of 2DrelRT, data have to be averaged
- align CASI results with chromatography data
- perform analysis on elemental composition
- copy worksheet and transform formulas to values
- check ISTD areas according to criteria:
 - area must be within 50% and 200% of mean area
 - non-accepted areas are replaced by mean area of valid dataset
- semiquantify all samples according to rules described in **Section 4.5.2**
- copy worksheet e.g. 3 times (depending on the number of comparisons) and transform formulas to values
- rename as table P1reg vs P2reg / P1reg vs 3R4F / P2reg vs 3R4F
- perform t-test on the data sets
- sort tables for p-values, separate data with p-values >0.05 as "not significantly different"
- calculate EFFECT, INDEX and RANK

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- sort for RANK, split tables in positive and negative list, sort for absolute values within categories
- verify results (manually)

The time-consuming manual processing procedure has been replaced and each step verified by CASI Pre- and Post-processor.

4.4.7.3 Pipeline Pilot Processing

The Pipeline Pilot script “NTDS_Comparison and Report” is specifically dedicated to perform t-tests and ranking on the dataset. In addition the script transforms all of the information into a suitable reporting format. Therefore the “concentration.txt” has to be uploaded to the webport, the study name/comparisons entered and the process executed. The output file is a final report file in Excel format.

The user guide “User Guide Pipeline Pilot Web Port Protocols”, Elyette Martin, version 1.0 describes all the available Pipeline Pilot webport protocols (available on DISCO).

4.5 Calculation and Records

4.5.1 Calculation of the Second Dimension Relative Retention Time

For the calculation of the second dimension relative retention time a experimental model was developed. The 2DrelRT is derived from second dimension peaks in relation to hypothetical reference points based upon linear regressions of deuterated n-alkanes (**Figure 15**). The n-alkanes are used to generate a hypothetical second dimension retention time reference system, compensating for systematic shifts (such as different column length or gas flow) but not for any shifts related to analyte-stationary phase interaction, as these shifts are dependent upon individual compound properties.

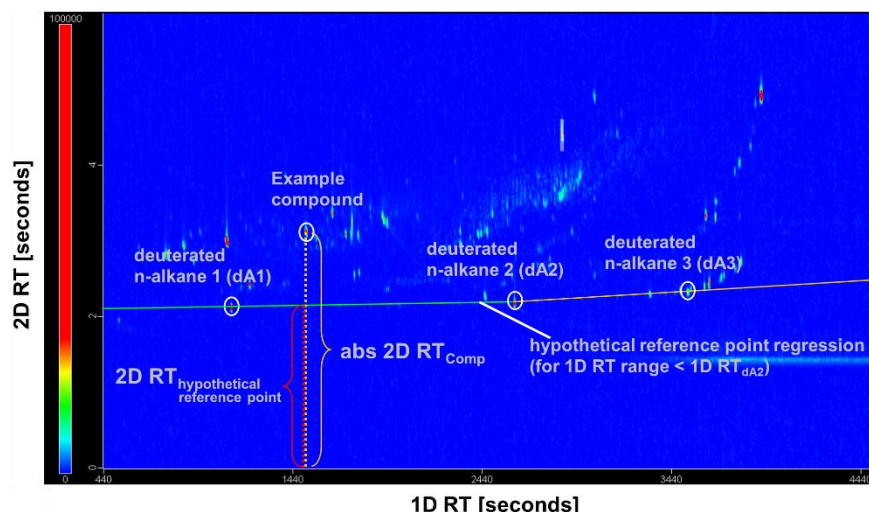



Figure 15. Principals of the second dimension relative retention time generation. Hypothetical reference points (full line) are derived from the linear regression of the experimentally measured retention times of deuterated n-alkanes in the two-dimensional separation space.

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The second dimension relative retention time of a compound is calculated as follows:

$$2DrelRT = \frac{abs_2DRT}{2DRT_{hrf}} \quad (1)$$

where abs_2DRT is the measured second dimension retention time of the compound and 2DRT_{hrf} is the second dimension retention time of the hypothetical reference point.

For a given compound that elutes between deuterated n-alkane standard compound 1 and compound 2, the 2DRT_{hrf} is calculated using the linear equation y=ax+b:

$$2DRT_{hrf} = \frac{2DRT_{dA2} - 2DRT_{dA1}}{1DRT_{dA2} - 1DRT_{dA1}} \times 1DRT + \left(2DRT_{dA1} - \frac{2DRT_{dA2} - 2DRT_{dA1}}{1DRT_{dA2} - 1DRT_{dA1}} \times 1DRT_{dA1} \right) \quad (2)$$

where $a = \frac{2DRT_{dA2} - 2DRT_{dA1}}{1DRT_{dA2} - 1DRT_{dA1}}$ is describing the slope and b is calculated by substituting x using the known values for dA1.

The equation resolved using the known values for dA1 for b=y_{dA1}-ax leads to


$$b = 2DRT_{dA1} - \frac{2DRT_{dA2} - 2DRT_{dA1}}{1DRT_{dA2} - 1DRT_{dA1}} \times 1DRT_{dA1}$$

where dA1 and dA2 are deuterated n-alkane 1 and 2, respectively, and 1DRT and 2DRT are the first and second dimension retention time of the respective molecules.

4.5.2 Semi-quantification of Compounds


The calculation of peak areas (integration) for a high number of diverse compounds is a critical step due to the different chromatographic behavior of individual compounds. In order to enhance the quality of the integration process, the samples are processed three times using different peak integration parameters as described in **Section 4.4.7.1.2**. Then, the maximum value of the integration results for each component will be used for further calculation.

For semiquantification, each compound will be referred to one of the internal standards. Every internal standard is allocated to a certain compound class. If a compound cannot be classified by a corresponding internal standard or is unknown a secondary classification according to 2DrelRT applies. A detailed description of the rules is given in **Table 13**.

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Compound	Case of Known Compounds	Case of Unknown Compounds
Acetone-d6	internal standard for ketones with RI ≤ 590	-
Benzene-d6	internal standard for aromatic hydrocarbons	-
2-Butanone-d5	internal standard for ketones with RI > 590	-
Butyraldehyde-d8	internal standard for aldehydes	-
Cyclohexene-d10	internal standard for unsaturated cyclic hydrocarbons	internal standard for compounds with 2DrelRT ≤ 1.173 (in general corresponds to nonpolar unknowns)
Cyclopentane-d10	internal standard for saturated cyclic hydrocarbons	-
1,2-Dichloroethane-d4	internal standard for Cl-containing compounds	-
Dimethyl sulfide-d6	internal standard for S-containing compounds	-
Ethyl acetate-d8	internal standard for esters	internal standard for compounds with 2DrelRT > 1.173 and ≤ 1.788 (in general corresponds to nonpolar to medium polar unknowns)
Furan-d4	internal standard for compounds with at least one ether function and at least one double or aromatic bond	-
Methacrylonitrile-d5	internal standard for N-containing compounds	internal standard for compounds with 2DrelRT > 1.788 (in general corresponds to medium polar to medium polar aromatic or basic unknowns)
3-Methylhexane-d16	internal standard for branched hydrocarbons (saturated and unsaturated)	-
Propylene oxide-d6	internal standard for ethers (cyclic and non-cyclic), no double or aromatic bond, RI ≤ 600	-
Tetrahydrofuran-d8	internal standard for ethers (cyclic and non-cyclic), no double or aromatic bond, RI > 600	-
n-Hexane-d14	retention-index marker 2, internal standard for linear hydrocarbons (saturated and unsaturated)	retention-index marker 2

Table 13. Assignment of compound classes to specific ISTDs.

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4.5.3 Extraction of Significant Differences

The extraction of significantly different compounds between the different test items is done by applying a two-tailed two-sample t-test with unequal variances (heteroscedastic) on the data set (2 groups, 3--5 replicates). The results provide the probability (p) of significant differences between two samples and/or test items. Comparisons with $p \leq 0.05$ will be considered to be significantly different. On the contrary, compounds with $p > 0.05$ will be excluded from further calculations/processing.

TTEST(Dataset Lx, Dataset Ly, tails, type)

Lx: measured values of test item 1 to be compared with Ly

Ly: measured values of test item 2 to be compared with Lx

tails = 2; two-tailed distribution

type = 3; heteroscedastic

4.5.4 Ranking of Detected Compounds

The sorting of significantly different compounds by their relevance is done by applying an empirically developed ("RANK") formula on the t-test filtered data set.

This "RANK" formula mathematically combines two criteria:

- difference of the variable ("Effect" (%))
- abundance of the variable ("Average Concentration" (e.g., µg/cig. or µg/article, or µg/mg TPM)).

$$\text{RANK} = \frac{\text{Effect}^3}{1000} \times \text{Average Concentration}$$


$$\text{Effect} = \frac{(\text{Ly}-\text{Lx})}{(\text{Ly}+\text{Lx})} \times 100$$

$$\text{Average Concentration} = \frac{\text{Lx}+\text{Ly}}{2}$$

The data set is divided into positive ($\text{Lx} > \text{Ly}$) and negative ($\text{Lx} < \text{Ly}$) rank values and sorted by increasing absolute rank values for the positive as well as the negative effect. A lower rank value shows more significant differences than a higher rank value.

4.5.5 Flexible Filtering

The final processed data can be filtered according to e.g. fold change or a concentration cut-off can be applied depending on the request or individual requirement.

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4.5.6 Results Recording/Data Transfer/Documentation

A detailed description for data management is given in **PMI-RRP-FOR-111519** - NTDS GCxGC-TOF-Data Management (**RDNEU**). The form summarizes all the administrative data, certificates, paper-rawdata, method specific forms and sample naming information that are needed for the study, and the GCxGC-TOFMS rawdata, processed data, CASI Processor data and result tables that are generated during the study with the respective location of storage. To conclude the study all steps have to be documented in **PMI-RRP-FOR-111519**, saved electronically in the study folder, printed and stored in the study binder.

Initial raw data are generated on the instrument acquisition computer, which are then copied including all study relevant instrument methods using the ChromaTOF inbuilt archiving functionality to a central data repository (currently HPC data share \\rd-hpc-samba.app.pmi). Autosampler sequences are copied to the same repository.

The initial raw data and all related data are restored on a local data evaluation computer using the ChromaTOF inbuilt restore from archive function. The data are deleted from the acquisition computer when the ChromaTOF data processing is finished successfully, provided that no file was corrupted during transfer.

Intermediate results (.csv files) of the data processing are stored in the primary raw data folder of the study directory in the \\rd-hpc-samba.app.pmi data share. Processed data files including all study relevant files are backed up to the same data repository using the ChromaTOF inbuilt archiving function.


After successful data processing using CASI Pre-processor, CASI and CASI Post-processor and subsequent confirmation of the results the processed data are deleted from the data evaluation workstation. Ultimately the entire study including a complete set of raw data and processed data must be maintained on the Long Term Repository (LTR, currently PMRD LabData_NeuchatelData \\cifs.arch10.store.pmi) environment.

Study related documents	Type
Certificates of ISTDs, syringe and analytical columns	Original/printout
Smoke/aerosol generation request and protocol	Printout/signed printout

Table 14. Study related documents.

Study relevant raw data and instrument related data for backup	File-type
Instrument raw data of samples, SSTs and sensitivity test	ChromaTOF database
Acquisition methods: GC and MS methods	ChromaTOF database
Autosampler methods	ChromaTOF database

Table 15. Study relevant raw data and instrument related data for backup.

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Study relevant processed data and intermediate results for backup	File-type
Processed raw data of samples, system suitability tests and sensitivity test	ChromaTOF database
Data Processing methods: Data Processing methods, calibrations, retention index methods, classifications	ChromaTOF database
Results sensitivity test + report	Textfile (.pdf)
Results system suitability tests + report	Textfile (.csv and .pdf), Excel-form
Results sample data processing	Textfiles (.csv)
CASI Pre-processor, CASI, and CASI Post-processor input/output files	Textfiles (.txt)
Converted library	JCAMP (.HPJ)
Further Data Evaluation and Reporting files	Excel-files

Table 16. Study relevant processed data and instrument related data for backup.


Study relevant forms for backup	File-type
<i>PMI-RRP-FOR-111487</i> - Chemicals, solvents, solutions and internal standard amount used for NTDS GCxGC-TOF (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111488</i> - Storage of samples and study related materials for NTDS (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111491</i> - Submitting metadata for CASI pre-processor, CASI, CASI post-processor (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111493</i> - Sample preparation NTDS GCxGC-TOF volatile (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111494</i> - Data processing in ChromaTOF NTDS GCxGC-TOF volatile (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111495</i> - Sensitivity test and system suitability test NTDS GCxGC-TOF volatile (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111496</i> - Preparation of LECO PEGASUS 4D SYSTEM for NTDS GCxGC-TOFMS (<i>RDNEU</i>)	Excel-file, signed printout
<i>PMI-RRP-FOR-111519</i> - NTDS GCxGC-TOF-Data Management (<i>RDNEU</i>)	Excel-file, signed printout

Table 17. Study relevant forms for backup.

4.6 Testing Scope, Repeatability, Reproducibility

Type	Name	Title	Author	Version
Assay Lifecycle Management Process Validation Report	rep_AEC_033	Validation Report (Fast Validation) Non-Targeted Differential Screening (NTDS) Assay Using Two-Dimensional Gas Chromatography-Time-of-Flight Mass Spectrometry (GCxGC-TOF) September 2008 (available on DISCO)	Arno Wittig	1.0

Table 18. Documentation.

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4.6.1 Testing Scope

NTDS GCxGC-TOFMS Volatile describes an assay for the detection of the most significant differences between two complex samples. The assay is non-targeted, i.e. it is based on a comprehensive chemical characterization of complex mixtures with no predefined target compounds. Depending on the matrix the testing scope can vary and thus cannot be defined specifically.

4.6.2 Repeatability, Reproducibility

Each sample will be generated minimum in triplicate and analyzed. Blanks, SST samples, pool sample(s) and one technical replicate of each matrix will be evenly distributed across the sequence. The repeatability of the SST and technical replicate samples are assessed by means of the area values of the ISTDs.

4.6.3 Acceptability Limits

The acceptability limits of the method are described in **Section 4.4.3.1** (sensitivity test) and **4.4.3.2** (system suitability test).

In case the criteria of the sensitivity test are not met, the multiplier voltage will be increased in steps of 50-V-increments until the acceptance criteria are fulfilled (further described in Section **4.4.3.1**). If the detector voltage exceeds 1900 V a replacement has to be considered.

If the acceptance criteria of the system suitability test are not met, the deviation needs to be commented in **PMI-RRP-FOR-111495** - Sensitivity test and system suitability test NTDS GCxGC-TOF volatile (**RDNEU**). In case of multiple deviations the samples following the respective SST sample in the sequence are rendered invalid.


4.7 Safety

- The usual good practices of a laboratory are required, information is available in the "Laboratory EHS Handbook"
- Be aware of the risk assessment of the labs
- Work in an exhaust hood and wear safety glasses
- Take care of the relevant MSDS (material safety data sheets, storage location: T0.182 - 186)
- Store the inflammable products away from a heat source or a flame

4.8 Calibration and Maintenance of Instruments

Name	Title
PMI-RRP-WKI-111668	Operation of a LECO Pegasus 4D GCxGC-TOFMS system (RDNEU)

Table 19. Documentation for calibration and maintenance of the instruments.

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5 Reference Documents

Knorr, A., Monge, A., Stueber, M., Stratmann, A., Arndt, D., Martin, E., Pospisil, P., Computer-assisted structure identification (CASI)--an automated platform for high-throughput identification of small molecules by two-dimensional gas chromatography coupled to mass spectrometry, *Analytical Chemistry*, 85(23) (2013) 11216-24


Shellie, R. A., Welthagen, W., Spranger, J., Ristow, M., Zrostlikova, J., Fiehn, O., Zimmermann, R., Statistical methods for comparing comprehensive two-dimensional gas chromatography-time-of-flight mass spectrometry results: Metabolomic analysis of mouse tissue extracts, *Journal of Chromatography A*, 1086 (2005) 83-90

Zhu, S., Lu. X., Dong, L., Xing, J., Su, X., Kong, H., Xu, G., Wu, C., Quantitative determination of compounds in tobacco essential oils by comprehensive two-dimensional gas chromatography coupled to time-of-flight mass spectrometry, *Journal of Chromatography A*, 1086 (2005) 107-114

International Organization for Standardization: International Standard ISO 3308, Routine analytical cigarette-smoking machine - Definitions and standard conditions, 4th ed., 2000

International Organization for Standardization: International Standard ISO 3402, Tobacco and tobacco products – Atmosphere for conditioning and testing, 4th ed., 1999


University of Kentucky, Kentucky Tobacco Research and Development Center: The reference cigarette, Lexington: The University of Kentucky Printing Services, 2003

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6 Related Documents

Type	Name	Title
SOP	<i>PMI-RRP-SOP-111561</i>	Change control for CASI (<i>RDNEU</i>)
SOP	<i>PMI-RRP-SOP-111562</i>	Change control for CASI pre&post-processors (<i>RDNEU</i>)
SOP	<i>PMI-RRP-SOP-111686</i>	Perform Analysis (<i>RDNEU</i>)
User Guide	User Guide Pipeline Pilot.docx	User Guide Pipeline Pilot webport protocols, Elyette Martin, version 1.0 (available on DISCO)
Validation Report	rep_AEC_033	Validation Report (Fast Validation) Non-Targeted Differential Screening (NTDS) Assay Using Two-Dimensional Gas Chromatography-Time-of-Flight Mass Spectrometry (GC×GC-TOF) September 2008, Arno Wittig, version 1.0 (available on DISCO)
WKI	<i>PMI-RRP-WKI-111700</i>	Management of pipettes (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111768</i>	Management of laboratory fridges and freezers (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111784</i>	Equipment Logbook creation and content (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111729</i>	Trappage des volatiles et semi-volatiles (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111814</i>	Management and labeling of chemicals (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111668</i>	Operation of a LECO Pegasus 4D GC×GC-TOFMS system (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111624</i>	User guide for CASI (<i>RDNEU</i>)
WKI	<i>PMI-RRP-WKI-111625</i>	User guide for CASI Pre&post-processors (<i>RDNEU</i>)


Table 20. Related documents.

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7 Records

Type	Name	Title
FOR	<i>PMI-RRP-FOR-111487</i>	Chemicals, solvents, solutions and internal standard amount used for NTDS GCxGC-TOF (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111488</i>	Storage of samples and study related materials for NTDS (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111491</i>	Submitting metadata for CASI pre-processor, CASI, CASI post-processor (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111493</i>	Sample preparation NTDS GCxGC-TOF volatile (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111494</i>	Data processing in ChromaTOF NTDS GCxGC-TOF volatile (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111495</i>	Sensitivity test and system suitability test NTDS GCxGC-TOF volatile (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111496</i>	Preparation of LECO PEGASUS 4D SYSTEM for NTDS GCxGC-TOFMS (<i>RDNEU</i>)
FOR	<i>PMI-RRP-FOR-111519</i>	NTDS GCxGC-TOF-Data Management (<i>RDNEU</i>)


Table 21. Records.

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8 Revision History

Version No.	Description of change (including reason for change)	Type of change
1.0	New version	Original issue
2.0	Addition of another instrument, minor changes in the process (improvement of the overall performance)	2
3.0	Improvements of the process by implementing the use of a pool sample, changes in data storage location (LTR)	2
<i>4.0.0</i>	<i>Content transferred in the new OMSP template. Change document names into document OMSP IDs</i>	<i>2</i>

(1. Major change/new version; 2. Minor change; 3. Review without change); at least the last three major versions (i.e. 1.0, 2.0. etc.) are listed in the Revision History.

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9 Abbreviations

Abbreviation/Definition	
2DreIRT	2 nd dimension relative retention time
ARMS	advanced request management system
CASI	computer-assisted structure identification
DISCO	document improvement system customer oriented
DMF	N,N-dimethylformamide
DPM	data processing method
EDMS	electronic document management system
EI	electron ionization
FTE	full-time equivalent
GC	gas chromatography, gas chromatograph
GC×GC	comprehensive two-dimensional gas chromatography
HPC	high performance computer
ISTD	internal standard
JCAMP	joint committee on atomic and molecular physical data
LTR	long term repository
MS	Microsoft, mass spectrometer, mass spectrometry
NTDS	non-targeted differential screening
PQ	performance qualification
RIM	retention index marker
RRP	reduced risk product
S/N	signal-to-noise ratio
SOP	standard operating procedure
SST	system suitability test
TOFMS	time-of-flight mass spectrometer
TPM	total particulate matter
WKI	work instruction

Document Name: NTDS GC×GC-TOFMS Volatile (RDNEU)

Document Info : Document Number #:PMI-RRP-WKI-111621 Version #:4.0.0 Effective Date: 28-Feb-2018

Signature Trail :

Stage	Signed By	Signed On	Signed
QA Signature	Cecile Panighini	14-Feb-2018 14:23:01 CET	QA Approval
Author Approval	Martin Almstetter	08-Feb-2018 13:37:00 CET	Author Approval
Owner Approval	Arno Knorr	08-Feb-2018 12:11:21 CET	Owner Approval