



New and Fully Automated Workflow for Alcohol Consumption and Drugs of Abuse Monitoring from one Single Blood Droplet

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Minimally invasive sampling

Dried Blood Spot Collection Instruction

Here are the ten steps which you should follow for a successful PEth DBS sampling

Step 1: Please wash your hands

Step 2: Open your DBS set and spread out the content on a clean table. The drying agent can be put back into the minigrip bag as this will be used at the end of the sampling process. Afterward set up the drying rack:



Step 3: Wipe the target finger with the isopropyl alcohol pad and allow the finger to air dry.

Step 4: Twist off the protective cap on the sterile safety lancet.

Step 5: Place the open end of the lancet against the sterilized finger, making sure that the placement is slightly off-center. To activate the lancet, firmly press the lancet against the puncture site. A click should be heard, once the lancet is activated.

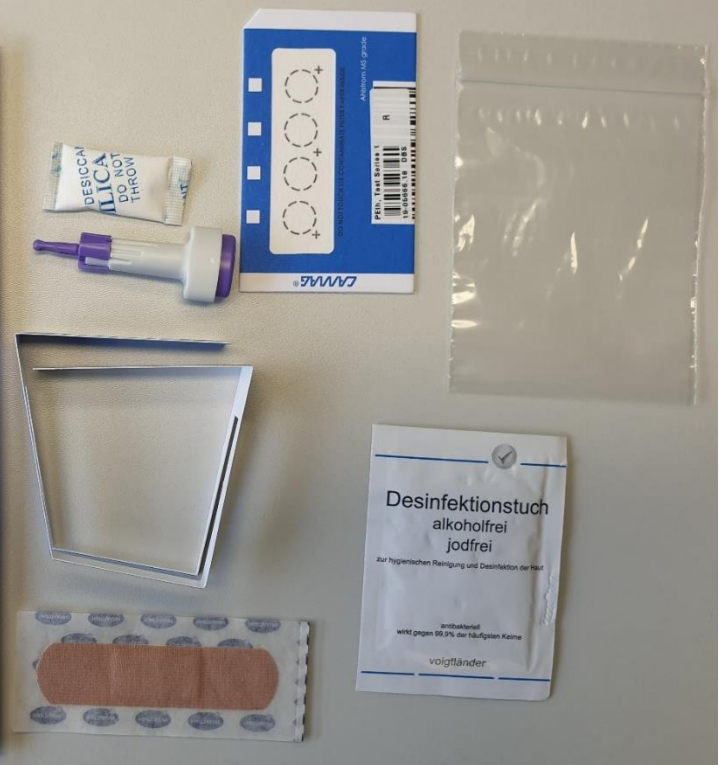
Step 6: Wait for the formation of a large blood drop before attempting to fill the DBS card. There should be a big enough blood drop to reasonably assume that it will fill the collection circle in a single attempt. **Do not layer successive drops of blood on the same spot!**

Step 7: Try to fill all the four collection circles on the card. Avoid massaging the finger to squeeze out more blood, as this will only cause the flow of interstitial fluid.

Step 8: Place the card on the drying rack for at least three hours. The filter paper must not touch any surface during the sampling and drying process.

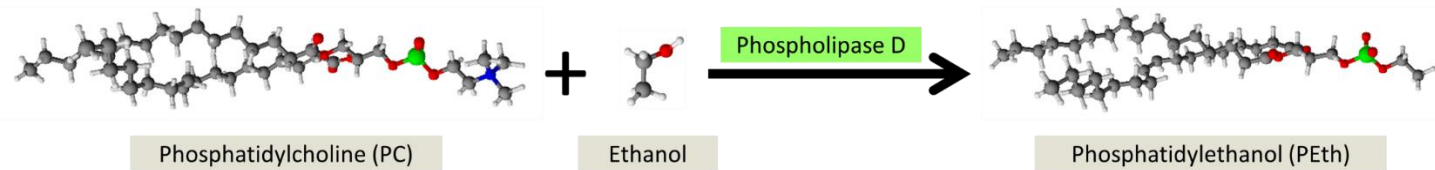
Step 9: Put the provided band-aid on the site of sampling to stop the blood flow.

Step 10: Once the card is dried (after min. 3 h), put it back in the minigrip bag and note the barcode on the card to your smartphone. **Without your personal barcode, you will not be able to identify your sample after the analysis.**



Fully Automated Determination of Phosphatidylethanol

Formation of Phosphatidylethanol



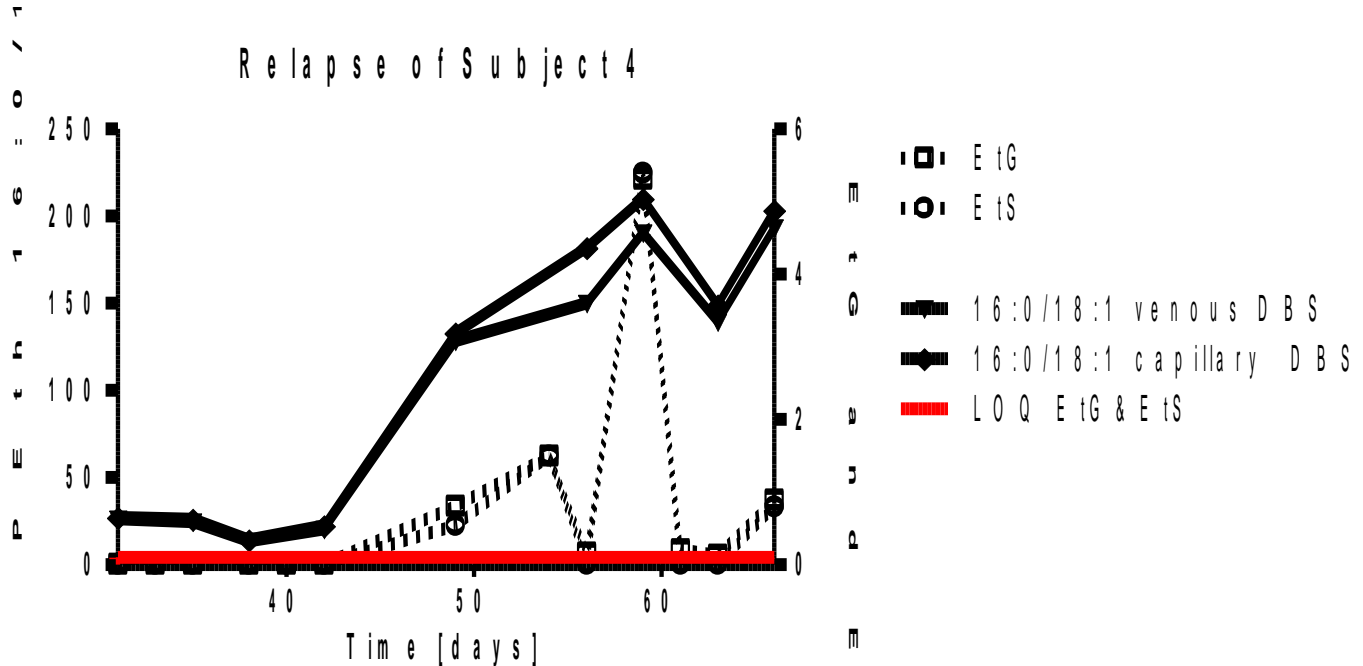
- PEth is a group of phospholipids that serve as direct alcohol marker
- PEth 16:0/18:1 and PEth 16:0/18:2 are most abundant in human blood
- PEth is used for the assessment of alcohol consumption behaviour
- PEth has a half-life of 3-12 days
- PEth is not stable in liquid blood, unless stored at -80°C
- Dried Blood Spots are the matrix of choice for PEth

Gnann et al. - Formation of phosphatidylethanol and its subsequent elimination during an extensive drinking experiment over 5 days. Alcohol Clin Exp Res. 2012

Schröck et al. - Phosphatidylethanol (PEth) detected in blood for 3 to 12 days after single consumption of alcohol—a drinking study with 16 volunteers. Int J Legal Med. 2017

⁴Gnann et al. - Identification of 48 homologues of phosphatidylethanol in blood by LC-ESI-MS/MS. Anal Bioanal Chem. 2010

Applications for Phosphatidylethanol Alcohol Withdrawal and Dishabituation Therapy



General Experimental Setup

Fully Automated PEth Determination

Required Setup

- CAMAG DBS-MS 500 autosampler
- 2× binary LC-MS pump
- Mass spectrometer (e.g. Shimadzu 8050)
- Switching valve



Automated DBS Processes

Optical card recognition



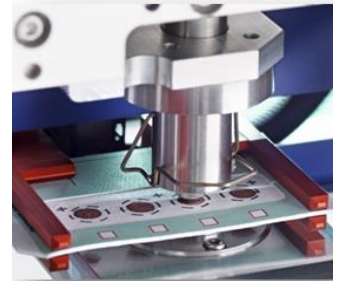
- Photo documentation
- Spot recognition
- Barcode reader
- Recognition of spot size, roundness, and center.

Internal standard application



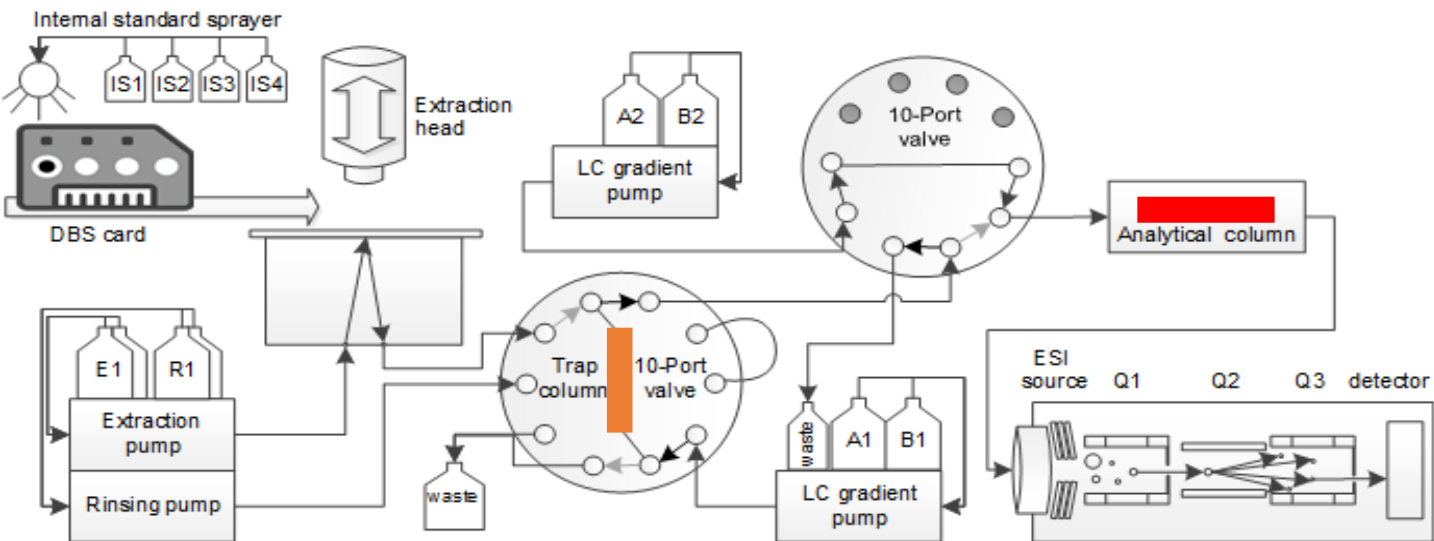
- Spray application of internal standard compensates for extraction bias
- 5-40 μL

Extraction



- Extraction under pressure
- 4 mm \varnothing subpunch
- Variable volume
- Wash station

Detailed Instrumental Setup



Trapping column: Synergy Polar RP, 20 mm

Analytical column: Luna RP-C5, 50 mm

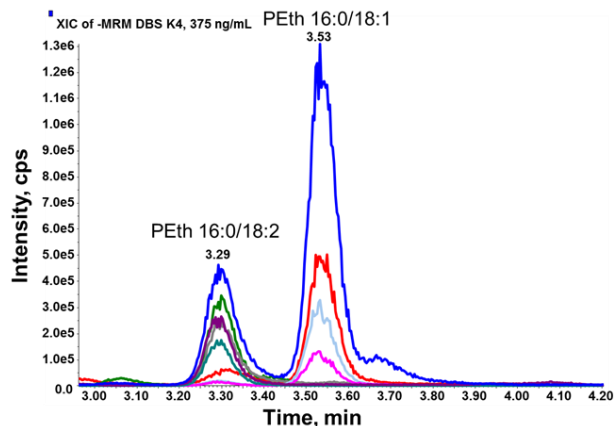
Sample preparation: 2 min

LC-MS/MS run : 5 min

Total runtime, overlapped: 5 min

Fully Automated Determination of Phosphatidylethanol

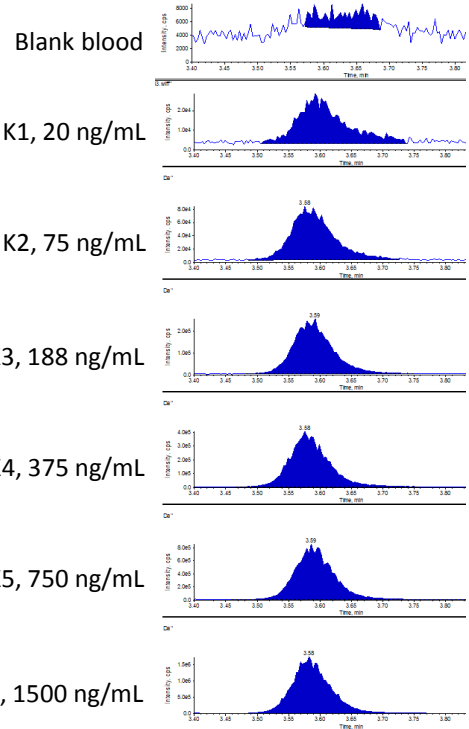
- Analytes
 - PEth 16:0/18:1
 - PEth 16:0/18:2
 - PEth 16:0/18:1- D_5
 - PEth 16:0/18:2- D_5
- Range: 20-1500 ng/mL (six-point calibration)
- QC: 20, 45, 1180 ng/mL
- Extraction: 40 μ L (40 μ L/min)
 - (34.5/15/50/0.05, H₂O/MeCN/2-Propanol/FA)



Compound	Q1 [m/z]	Q3 [m/z]	Dwell time [msec]	DP [volts]	EP [volts]	CE [volts]	CXP [volts]	RT [min]
PEth 16:0/18:1 SRM 1	701.3	255.2	20	-32	-10	-40	-14	3.53
PEth 16:0/18:1 SRM 2	701.3	281.3	20	-20	-10	-40	-14	
PEth 16:0/18:1- D_5 SRM 1	706.3	255.3	20	-20	-10	-40	-14	
PEth 16:0/18:1- D_5 SRM 2	706.3	281.1	20	-32	-10	-40	-14	
PEth 16:0/18:2 SRM 1	699.5	279.4	20	-5	-10	-40	-14	3.29
PEth 16:0/18:2 SRM 2	699.5	255.3	20	-5	-10	-40	-14	
PEth 16:0/18:2- D_5 SRM 1	704.5	279.5	20	-5	-10	-40	-14	
PEth 16:0/18:2- D_5 SRM 2	704.5	255.3	20	-5	-10	-40	-14	

Validation Parameter

- Linearity:
 - 0.9980 ± 0.0016 (range: 0.9954-0.9996) for PEth 16:0/18:1
 - 0.9974 ± 0.0005 (range: 0.9953-0.9982) for PEth 16:0/18:2
 - extended linear range up to 2500 ng/mL with a correlation coefficient of at least 0.9975
- **LOQ at 20 ng/mL**, LOD at 10 ng/mL
- Accuracy and precision within $\pm 15\%$
- Mean extraction efficiency: 88%



Whole Blood Extraction vs Fully Automated DBS Analysis



Manual whole blood analysis

- Prepare sample labels for extraction containers
- Label all containers
- Pipette sample into Eppendorf tube
- Add extraction solvent
- Add internal standard and close tubes
- Shake
- Centrifuge
- Transfer into glass vial
- Evaporate solvent
- Reconstitute
- Cap samples
- Build batch
- Inject

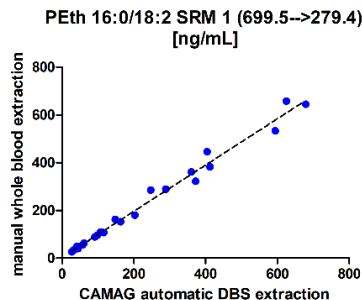
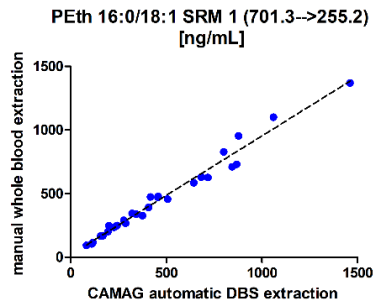


Figure 1 comparison of the automated CAMAG DBS extraction to manual whole blood extraction for 28 samples from AUD patients. (data points above LOQ)

- Whole blood, PEth 16:0/18:1, Slope: 0.9349 ± 0.02824 (R=0.9768)
- Whole blood, PEth 16:0/18:2, Slope: 0.9706 ± 0.02339 (R=0.9863)



Fully automated DBS analysis

- Add card into autosampler
- Build batch
- Hit play

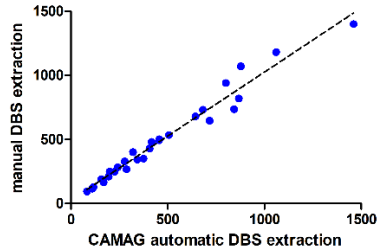
Manual Whole Spot DBS vs Fully Automated DBS Analysis



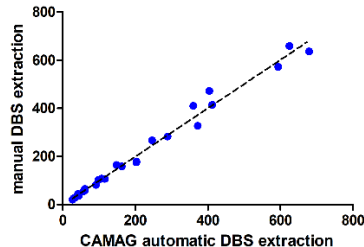
Manual DBS analysis

- Prepare sample labels for extraction containers
- Label all containers
- Cut DBS, fold, and place into Eppendorf tube
- Add extraction solvent
- Add internal standard and close tubes
- Shake
- Centrifuge
- Transfer into glass vial
- Evaporate solvent
- Reconstitute
- Cap samples
- Build batch
- Inject

PEth 16:0/18:1 SRM 1 (701.3→255.2) [ng/mL]



PEth 16:0/18:2 SRM 1 (699.5→279.4) [ng/mL]



Fully automated DBS analysis

- Add card into autosampler
- Build batch
- Hit play

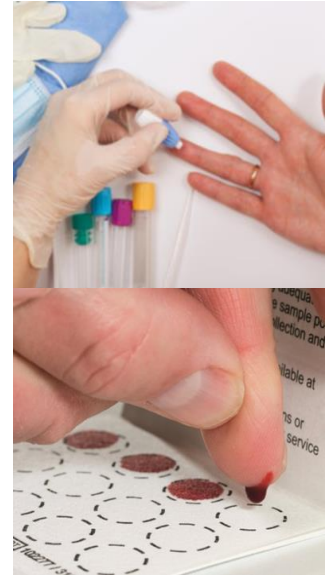
Figure 1 comparison of the automated CAMAG DBS extraction to manual DBS extraction for 28 samples from AUD patients.(data points above LOQ)

- Manual DBS, PEth 16:0/18:1, Slope: 0.9995 ± 0.03644 (R=0.9666)
- Manual DBS, PEth 16:0/18:2, Slope: 1.006 ± 0.02542 (R=0.9849)

Fully Automated, Library Based Screening

The Advantages of Screening in DBS

- Minimally invasive sampling process
- Sampling is possible on site, without healthcare professionals
- Blood is the matrix of choice to tell if somebody is under the influence
- DBS are stable at room temperature
- No biohazard label
- Reduced storage and shipping costs
- Fully automated processes are available



Forensic Toxicology Database for LC-MS/MS By Shimadzu

- **MRM & Spectral Library Database**
- **Two separation conditions available**
 - **ODS** (Phenomenex Kinetex XB-C18 (2.1 mmI.D. x 100 mmL., 2.6um))
 - **Biphenyl** (Restek Raptor Biphenyl (2.1 mmI.D. x 100 mmL., 2.7um))
- The ODS method contains information on 1,250 compounds and the Biphenyl method contains 1,281 compounds.



Compound List Creation Tool

MRM or Spectral
Library
Screening?



No.	Results	Compound Name
1	OK	Cocaine
2	OK	Methamphetamine
3	OK	Heroin
4	OK	Amphetamine
5		
6		
7		
8		
9		
10		
11		

Insert target
compounds to
build compound
list



Compound List Creation Tool

Test - Notepad

File Edit Format View Help

Name	Type	m/z(1)	m/z(2)	Ret. Time	Unit	Ref.(1) m/z(1)	Ref.(1) m/z(2)	Ref.(1) Ratio	Ref.(1) Allowance	Ref.(1) Rel Allowance	Conc.(1)	Band	ProcessStartTime	ProcessEndTime	Ref. Mode	Pk. Select	Calc.	
1	Minimum Repeat Time			Exec Condition	Order	Intensity	Dependent Scan	Start m/z(3)	Dependent Precursor Ion m/z(3)	Dependent Start Time(5)	Dependent End Time(5)	Dependent Acquisition Mode(3)	Dependent Polarity(3)	Dependent Event Time(5)	Dependent Acquisition Mode(1)	Dependent Interface Voltage(5)	Depen	
Cocaine	3	304.15	182.25	4.409		304.15	82.1	0	0	1	0	0	0	0	0	0	0	0
Methamphetamine	3	150.12	91.05	3.466		150.12	119.1	0	0	1	0	0	0	0	0	0	0	0
Heroin	3	370.16	58.15	4.31		370.16	44.1	0	0	1	0	0	0	0	0	0	0	0
Amphetamine	3	136.1	91.05	3.36		136.1	119.05	0	0	1	0	0	0	0	0	0	0	0



Import custom target list into the default screening LC-method



Start optimization:

- LC parameters
- MS compound window

Instrument Parameters View

Normal Advanced End Time: 6.00 min

MS Interface Data Acquisition LC Time Prog. Pump Column Oven Controller

Positive Negative End Time: 6.000 min MS Program Edit Valve and MS Program...

MRM(+), Product Ion Scan(+), Precursor Ion Scan(+), Neutral Loss Scan(+), SIM(+), Scan(+)

CD Gas, CID Gas, Attenuation, Loop Time

Type	Event#	±/∓	Compound Name	m/z	Time (0.000 min - 6.000 min)
MRM	1	+	Egonine Methyl Ester	250.10	
Product Ion Scan	2	+	>CE-15.0	20.00	194.10
Product Ion Scan	3	+	>CE-30.0	20.00	194.10
Product Ion Scan	4	+	>CE-45.0	20.00	194.10
MRM	5	+	0_IS_Egonine Methyl Ester-D		
MRM	6	+	Morphine	286.15	165.10
Product Ion Scan	7	+	>CE-15.0	20.00	296.15
Product Ion Scan	8	+	>CE-30.0	20.00	296.15
Product Ion Scan	9	+	>CE-45.0	20.00	296.15
MRM	10	+	0_IS_Morphine-D	289.15	15
MRM	11	+	0_IS_Morphine-D	289.15	15

Steps: Acq. Time: 0 - 6 min Compound Name: Egonine Methyl Ester

Ch	Precursor m/z	Product m/z	Pause Time (msec)	Dwell Time (msec)	Q1 Pre Bias(V)	CE	Q3 Pre Bias
CH1	200.10	182.10	1.0	1.0	-10.0	-10.0	-21.0
CH2	250.10	82.10	1.0	1.0	-10.0	-25.0	-17.0

Instrument Parameters View

Normal Advanced End Time: 6.00 min

MS Interface Data Acquisition LC Time Prog. Pump Column Oven Controller

Time	Module	Command	Value	Comment
1.00	Pump	Auto H Conc	25	
2.00	Pump	Pump B Conc	95	
3.00	Pump	Pump B Conc	95	
4.00	Pump	Pump B Conc	1	
5.00	Pump	Pump B Conc	5	
6.00				

Download, Load Data, Data print

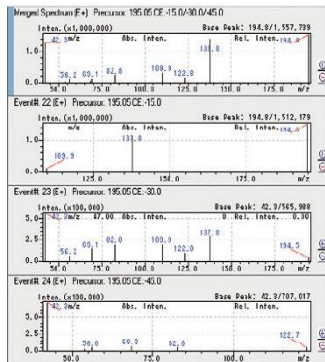
Chromatogram



MS/MS Spectrum with three different collision energies (CE)

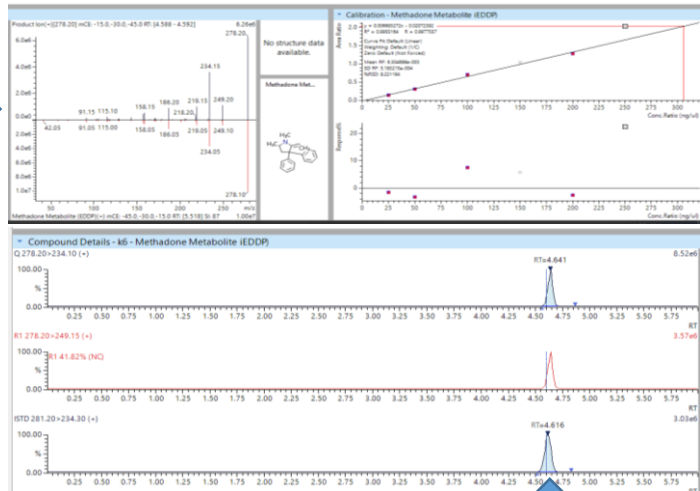
MRM Transitions for the quantification

Compound Identification by Merged Spectra



Merged Spectrum

MS/MS Spectra with three different CE



Qualifier, Quantifier, and IS

Merged spectra using three MS/MS spectra with three different CE helps to increase the confidence in reporting

https://www.shimadzu.com/an/cms/forensic_toxicology-database/index.html

Library Search

Library Hits - k6 - Methadone Metabolite (EDDP)																
#	Compound ...	Lib. SI	Theory MW	Formula	Class	Lib. Filename	RT	Adduct Ion	Precursor Ion	MS Stage	Ionization	Collision En...	Instrument	Data Filena...	Acquired By	Acquired
<input checked="" type="checkbox"/>	1 Methadone ...	87	277.1830	C20H23N	----	Library_FT...	5.518	----	278.2000		2 ESI	----	LCMS-TQ	----	----	1/1/1601 1...
<input type="checkbox"/>	2 4-F-alpha-P...	66	277.1842	C17H24FNO	----	Library_FT...	5.443	----	278.2000		2 ESI	----	LCMS-TQ	----	----	1/1/1601 1...
<input type="checkbox"/>	3 Venlafaxine	66	277.2042	C17H27NO2	----	Library_FT...	5.299	----	278.2000		2 ESI	----	LCMS-TQ	----	----	1/1/1601 1...
<input type="checkbox"/>	4 Maprotiline	61	277.1830	C20H23N	----	Library_FT...	6.284	----	278.2000		2 ESI	----	LCMS-TQ	----	----	1/1/1601 1...
<input type="checkbox"/>	5 Amitriptyline	58	277.1830	C20H23N	----	Library_FT...	6.368	----	278.2000		2 ESI	----	LCMS-TQ	----	----	1/1/1601 1...



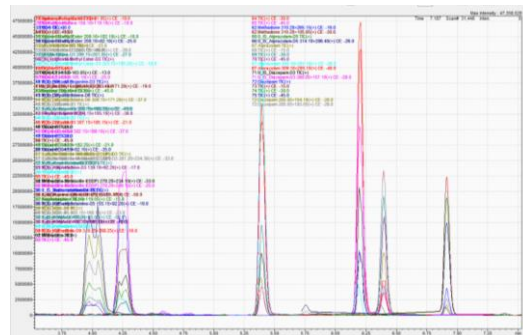
Library search based on similarity index increases confidence

Compound identification by

- Retention time
- Multiple MRM transitions (Qualifier/Quantifier)
- Merged Spectra (three different CE)
- Library Search/Similarity Index
- Internal Standard

Method Example

- Shimadzu 8050 coupled with a DBS-MS 500 autosampler
- ODS method, total runtime of 6 min
- Ex sol (20 μ l): 50-50 MeOH-H₂O, 0.1%FA, 10 mM Ammonium Formate



Quantification of Target Compounds

Six-point calibration (25, 50, 100, 150, 200, 250 ng/mL) in blank blood, one QC each

Target	Internal Standard	Linearity	QC 25 ng/mL	QC 125 ng/mL
▪ Codeine	IS Codeine-D3	r=0.994	25.7	113
▪ Dihydrocodeine	IS Dihydrocodeine-D6	r=0.976	25.7	110
▪ Amphetamine	IS Amphetamine-D3	r=0.997	26.9	125
▪ Methamphetamine	IS Methamphetamine-D5	r=0.996	27.9	123
▪ MDMA	IS MDMA-D5	r=0.993	25.3	135
▪ Cocaine	IS Cocaine-D3	r=0.991	27.1	143
▪ Benzoyl Ecgonine	IS Benzoyl Ecgonine-D3	r=0.995	29.4	131
▪ Ecgonine Methylester	IS Ecgonine Methylester-D3	r=0.995	27.2	137
▪ Methadone	IS Methadone-D9	r=0.991	25.3	148
▪ Methadone Metabolite (iEDDP)	IS Methadone Metabolite (IS iEDDP)-D3	r=0.991	31.6	143
▪ Alprazolam	IS Alprazolam-D5	r=0.975	24.8	126
▪ Diazepam	IS Diazepam-D3	r=0.981	18.0	120

Monitoring of two MRM transitions + Spectra for Library identification

And there is much more you can do!

- Vitamin D
- Nicotine and Cotinine
- Ivermectin
- Antiepileptic Drugs
- Antiretroviral Drugs
- New Born Screening
- Testosterone Panels



Thank you for your Attention!