

# **Application of Ion-Mobility and Advanced Statistical Methods for Small Molecule Profiling**

*John Shockcor*

*Director of Metabolic Profiling Business Development  
Visiting Fellow, Dept of Biochemistry, University of Cambridge*

- I have 2 sample groups A and B
  - *Are the groups different? If so:*
    - *What has higher in A*
    - *What has lower in A*
    - *What is absent in A*
    - *What is unique to A*

- I have 2 sample groups A and B

- *Are the groups different? If so:*

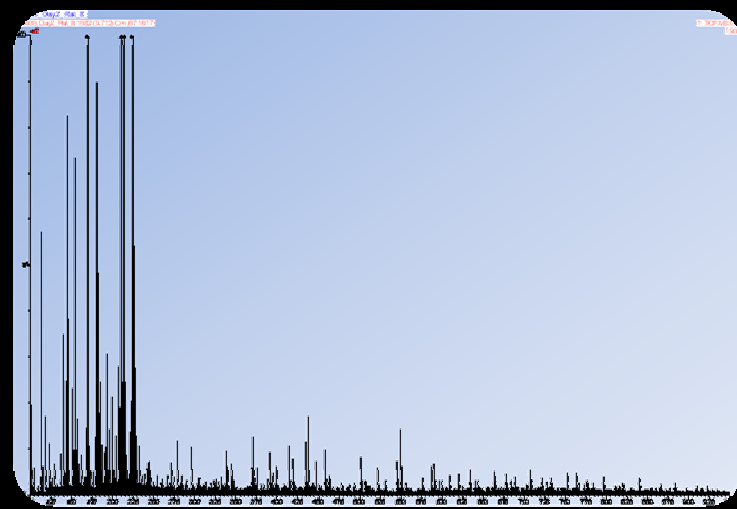
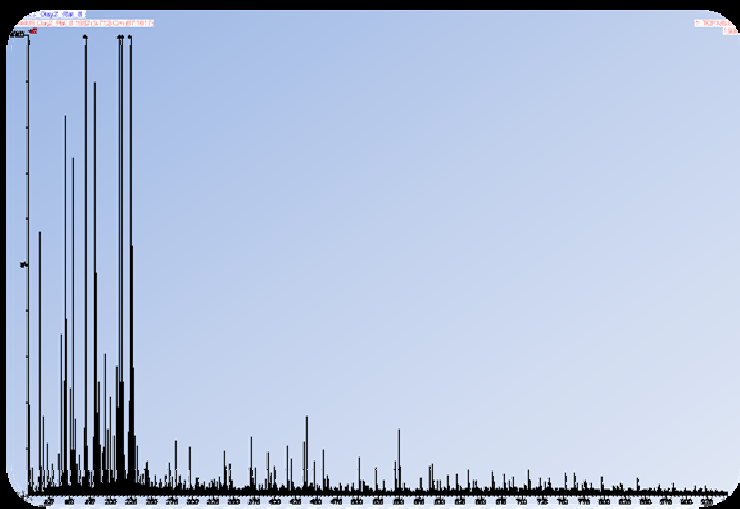
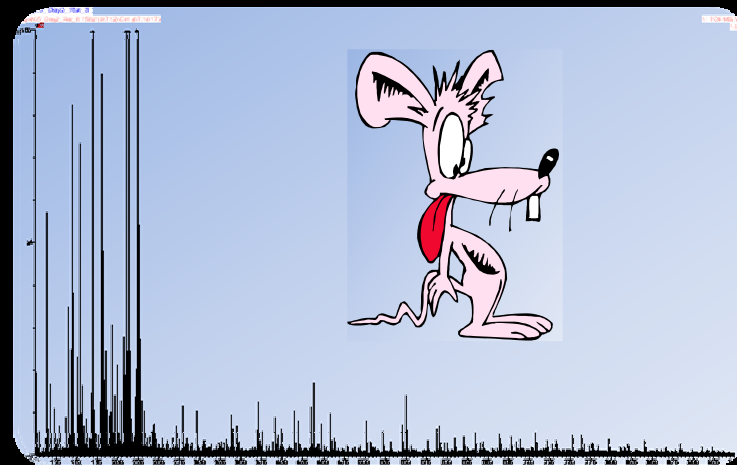
- *What has higher in A*
- *What has lower in A*
- *What is absent in A*
- *What is unique to A*

These are MARKERS of the difference between A and B

# How is Do We Find These Markers?

**A Manual Approach**  
**Think about doing a rigorous comparison of just**  
**these 4 spectra (~2,000 masses or metabolites in each).**

**Waters**  
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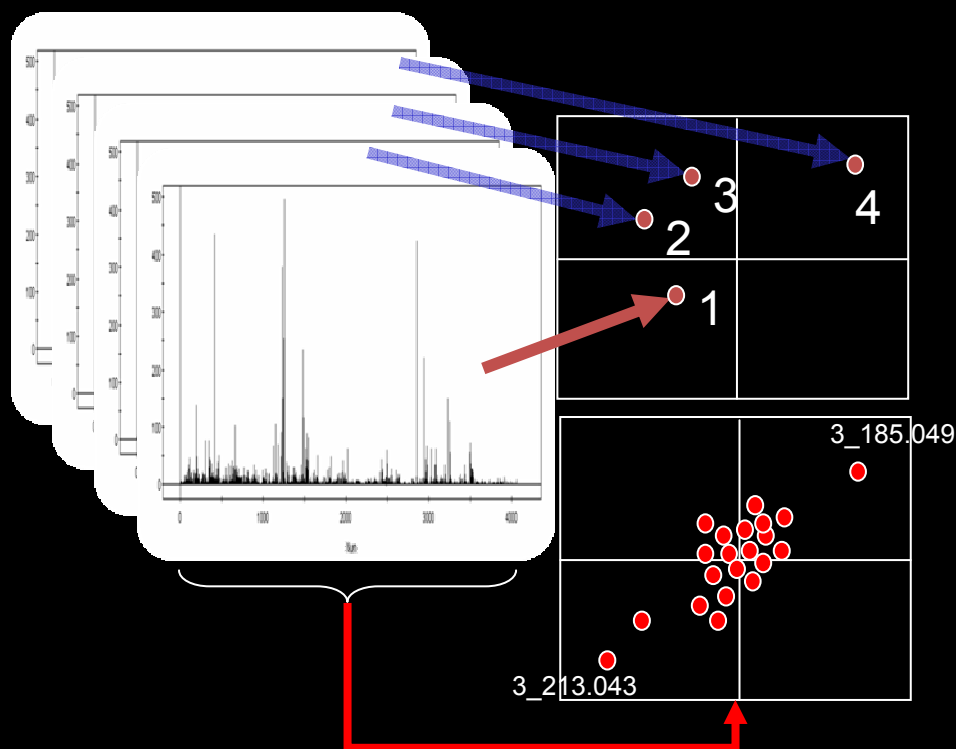
# A Solution to The Problem

- It is possible to mine the data using multivariate statistics.
- We first analyze the groups using GC or LC/MS
- We then tabulate all the observed masses and their chromatographic retention times with advanced computational methods.
  - These mass/retention time pairs become the variables used for statistical analysis.

## ***A Solution to The Problem***

- Multivariate statistics then allows us to reduce thousands variables (mass/retention time pairs) down to a simple 2 or three dimensional maps.
- These maps shows the difference, if any, between the groups and provides us with a list of the variables which contribute to the difference.

# How Spectral Information is displayed



- Spectrum (observation) becomes a point in PCA **Scores plot**

- Variables (m/z\_RT) shown in PCA **Loadings Plot**

- Using plots together allows trends in the sample spectra to be *interpreted* in terms of m/z



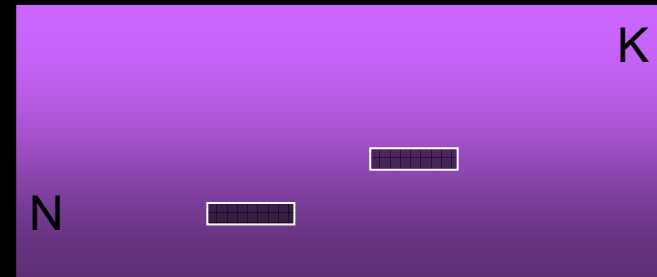
# *Why Choose to use Multivariate Statistics?*

## Why not :

- *Hierarchical Clustering*
  - *Heat make*
  - *ANOVA*
  - *T tests*
- 
- *With MarkerLynx it is possible to export your data to any statistical program you like.*

# Why Use Multivariate Analysis?

- Short and wide data sets
  - Few observations (N)
  - Many variables (K)
  - Noisy data
  - Missing data/excluded regions
  - Multiple objectives
- Implications
  - High degree of correlation (Many variables are related)
  - Difficult to analyse with conventional methods
- Require methods for simplification and visualisation



# Multivariate Statistics The Basics

# **Principle Component Analysis PCA**

**A multivariate statistical approach that  
facilitates the identification of differences or  
similarities between groups**

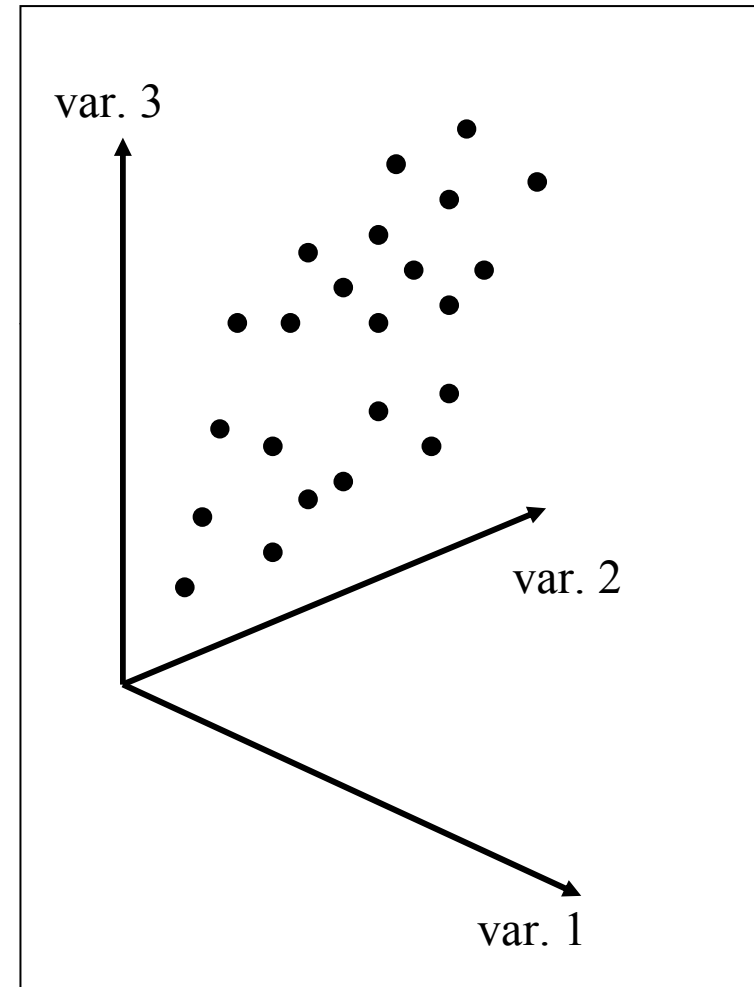
# Data preparation

Data table → variable space

	var. 1	var. 2	var. 3
1			
2			
3			
4			
5			
6			
N			

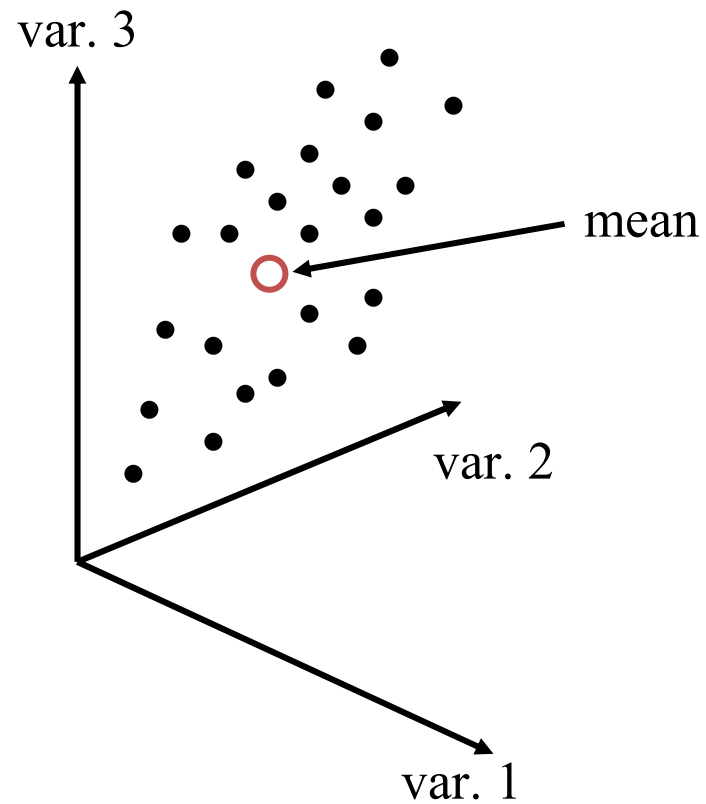
→

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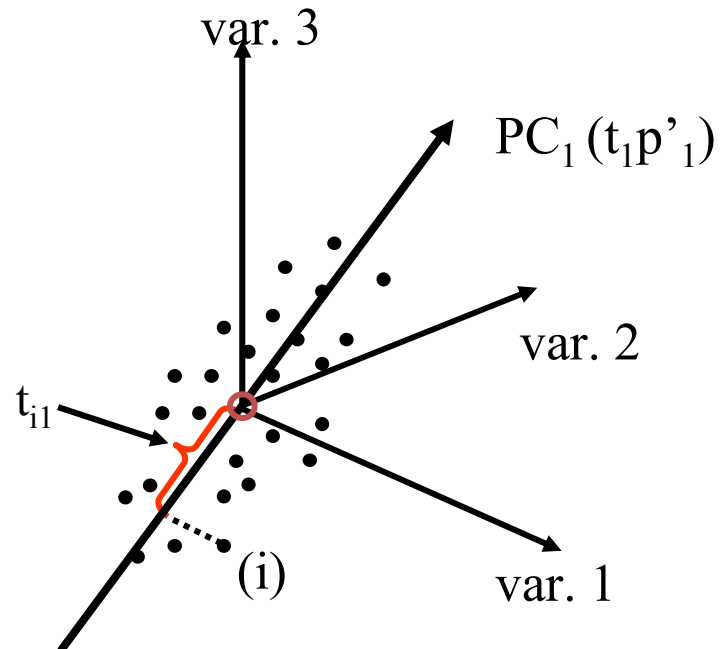


The whole table yields a swarm of points in variable space

- Centering – move centre of point swarm to the variable origin



# PCA theory – step by step

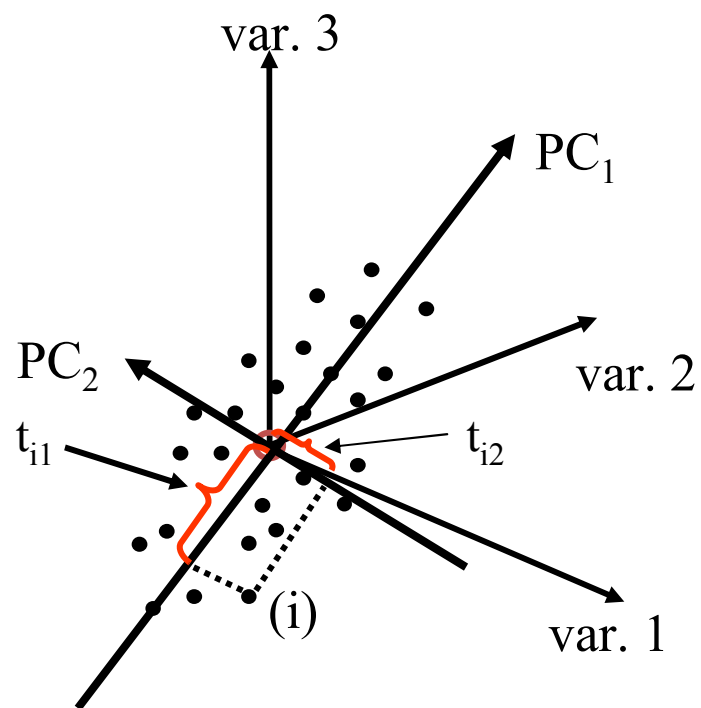


The first principal component ( $PC_1$ ) is set to describe the largest variation in the data, which is the same as the direction in which the points spread most in the variable space

The Score value ( $t_{i1}$ ) for the point  $i$  is the distance from the projection of the point on the 1:st component to the origin.

$PC_1$  hence is the first latent variable in a new coordinate system that describes the variation in the data.

# PCA theory – step by step

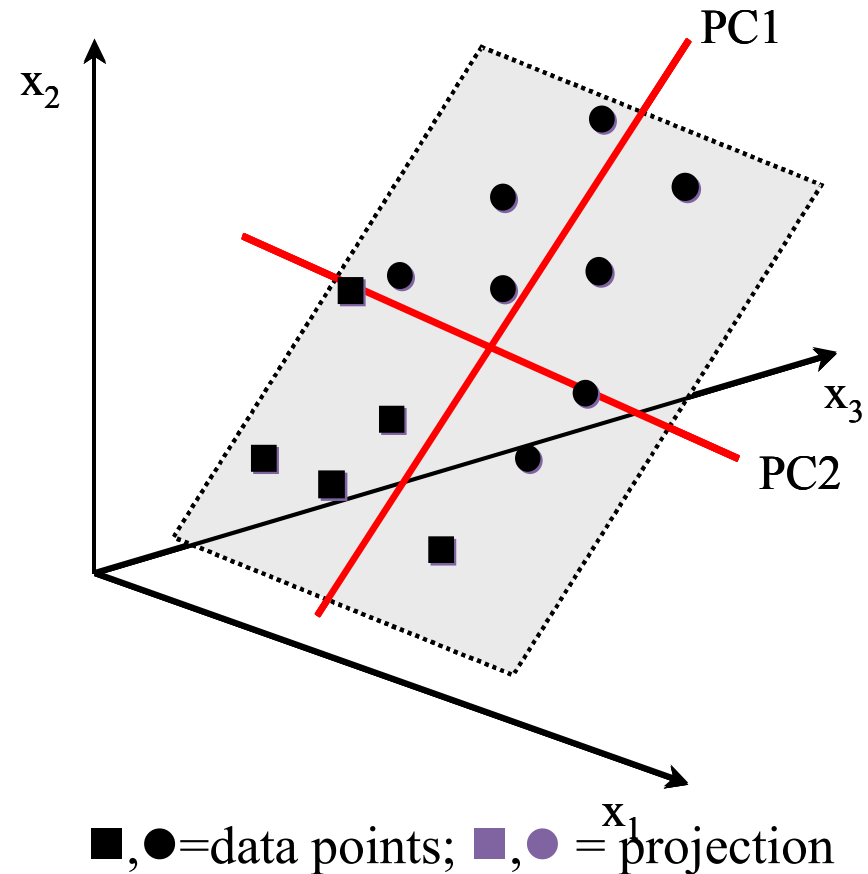


The second principal component ( $PC_2$ ) is set to describe the largest variation in the data, Perpendicular (orthogonal) to the 1:st component



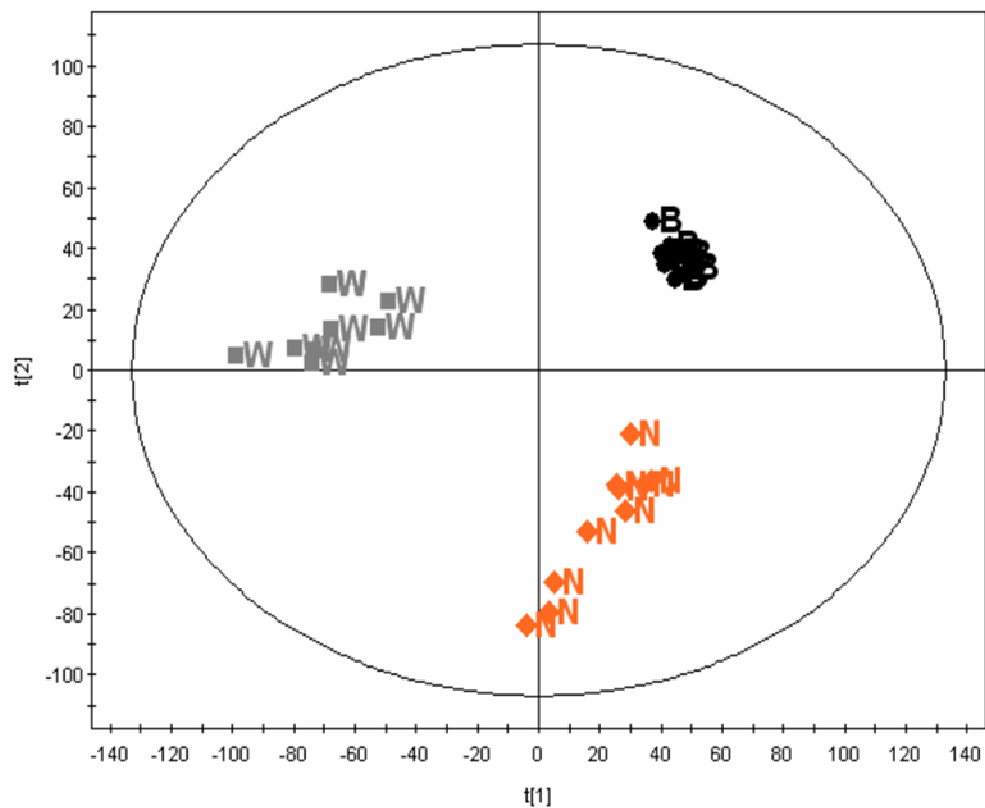
# PCA theory – step by step

- This is the scores plot similarities or differences between samples can now be seen.
- A corresponding loading plot describes the variables relationships
  - allows interpretation of the scores plot by showing which variables are responsible for similarities and differences between samples.
- The perpendicular distance from the object to the projection on the plane is the residual of the two PCs.
- Two PCs make a plane (window) in the K-dimensional variable space. The points are projected down onto the plane which is lifted out and viewed as a two dimensional plot.



# Scores plot example

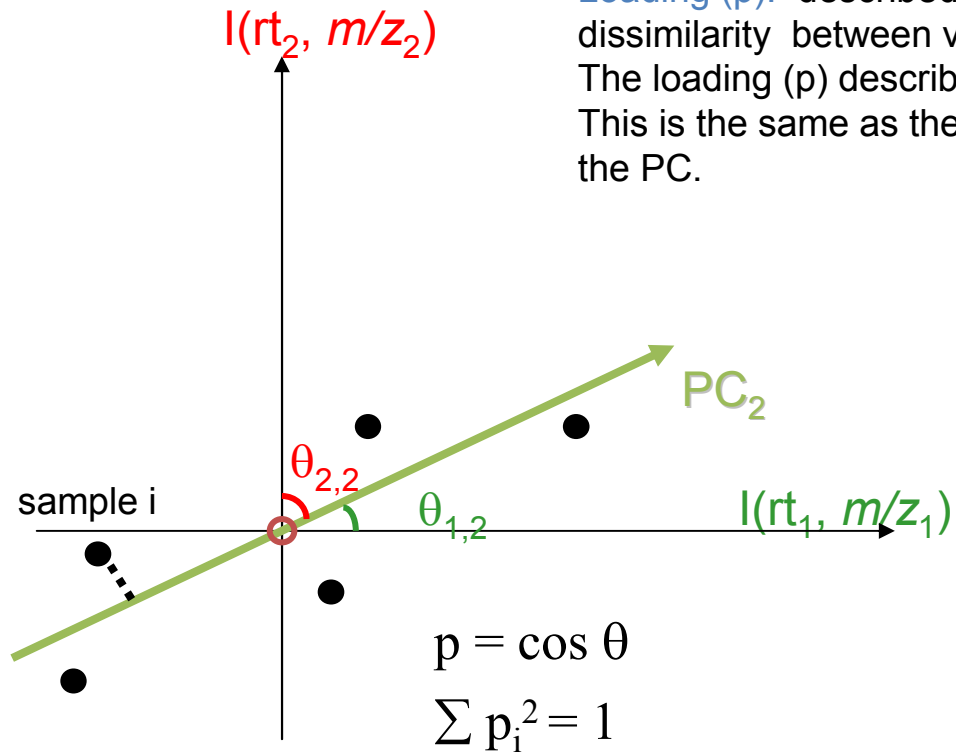
PCA Mouse Urine  
White, Black & Nude Mice



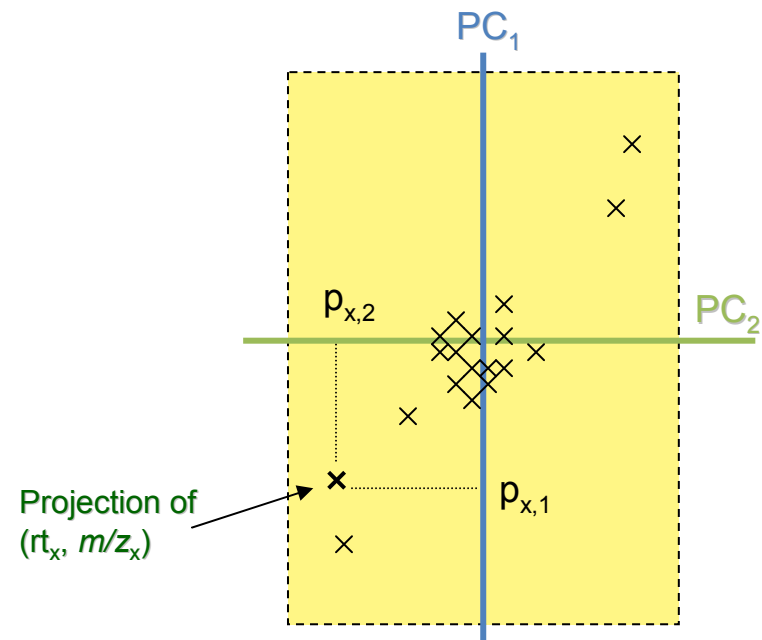
Ellipse: Hotelling T2 (0.95)

SIMCAP+ 10.5 - 03/09/2004 11:07

# The Loadings Plots



**Loading (p):** described the variation in the variable direction i.e. similarity/dissimilarity between variables, and also explains the variation in scores. The loading (p) describes the original variables importance for respective PC. This is the same as the similarity in direction between the original variable and the PC.



With  $p_{x,1} = \cos(\theta_{x,1})$  and  $p_{x,2} = \cos(\theta_{x,2})$   
 and  $\theta_{x,1}$  : angle between axe  $(rt_x, m/z_x)$  and PC1  
 and  $\theta_{x,2}$  : angle between axe  $(rt_x, m/z_x)$  and PC2

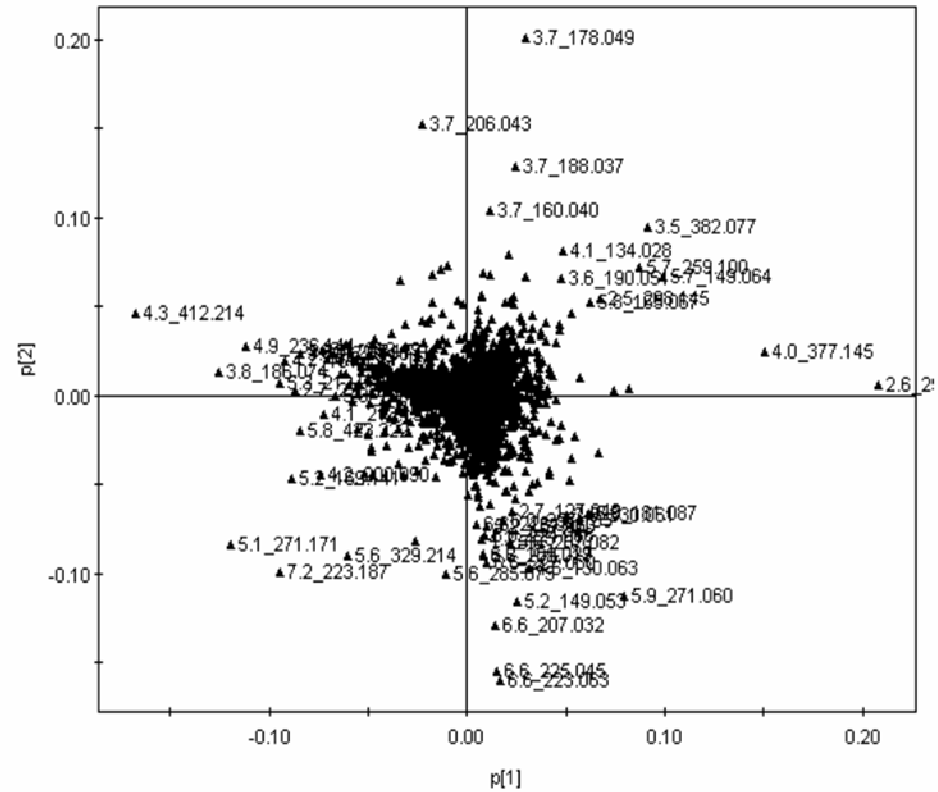
The **loading (p)** is described as the cosine of the angle between the original variable and the PC.

# Example Loadings Plot

PLS Software



### Mice Loadings Plot

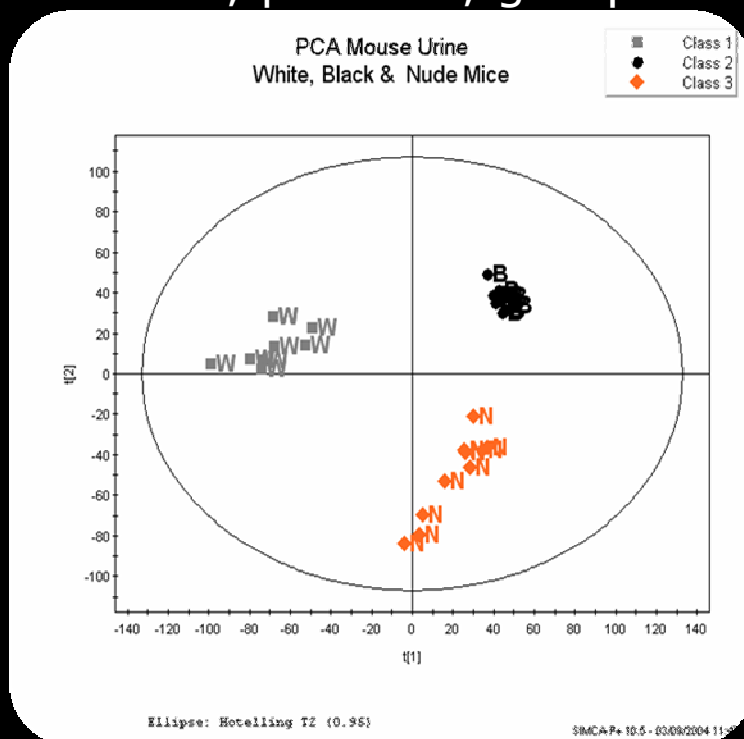


SIMCA-P+ 10.5 - 28/07/2004 10:07

# Interpretation of PCA

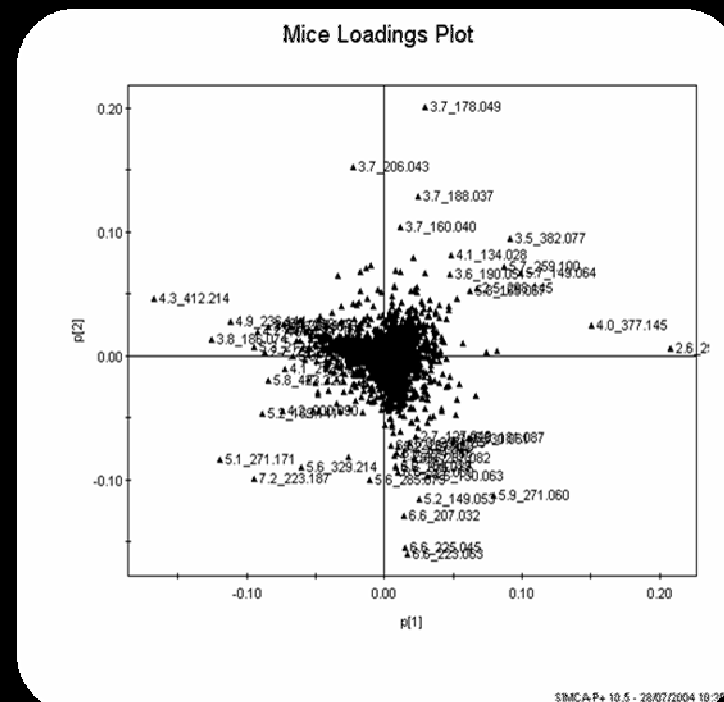
## Scores

- Observations (spectra)
- Trends, patterns, groups



## Loadings

- Variables (m/z)
- Correlation, influence

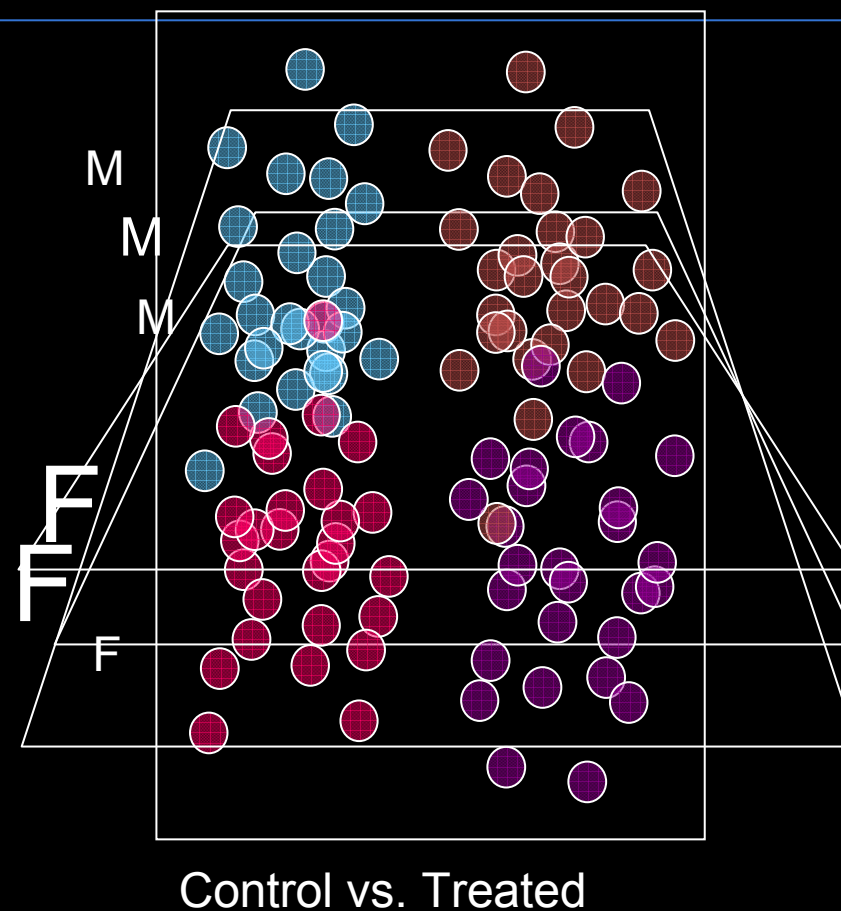


# Advanced Methods

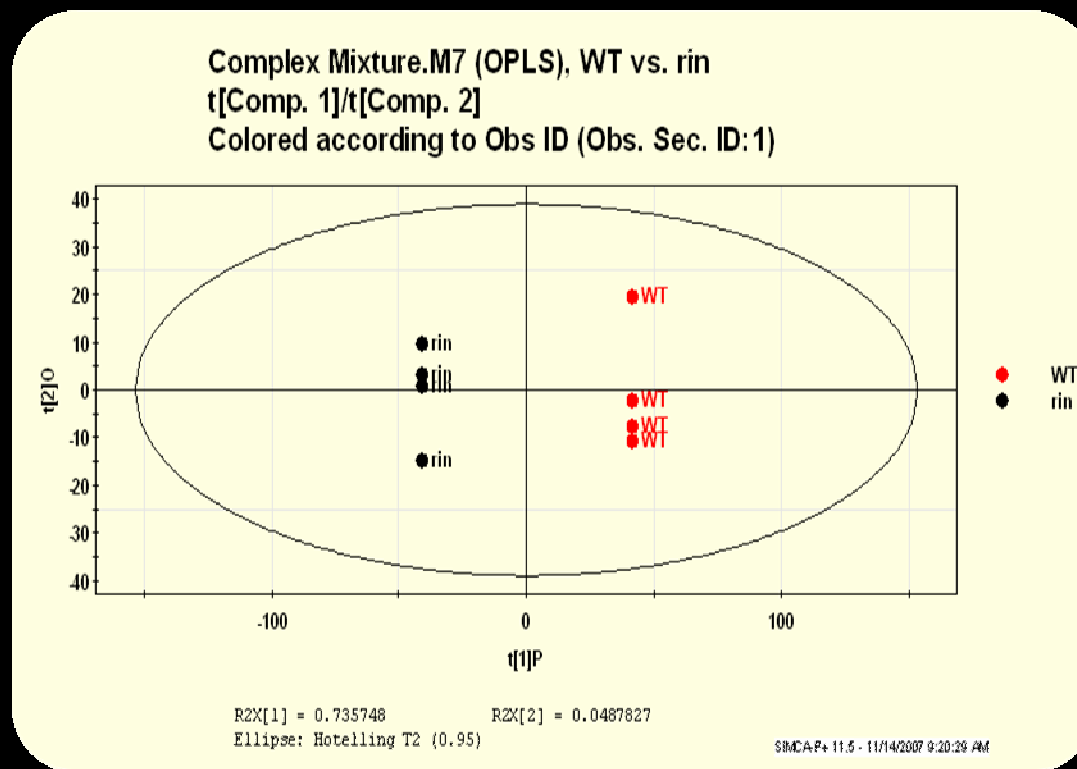
## OPLS and the S-Plot

# Coping with unwanted variation

- Often the effect we are looking for is masked by other unwanted variation
- OPLS is able to rotate the projection so that the model focuses on the effect of interest
- Here we want to focus on **control vs. treated** but **gender** is the bigger influence on X
- OPLS causes a rotation so that the first OPLS component shows the between class difference



Within group variation



Between group variation

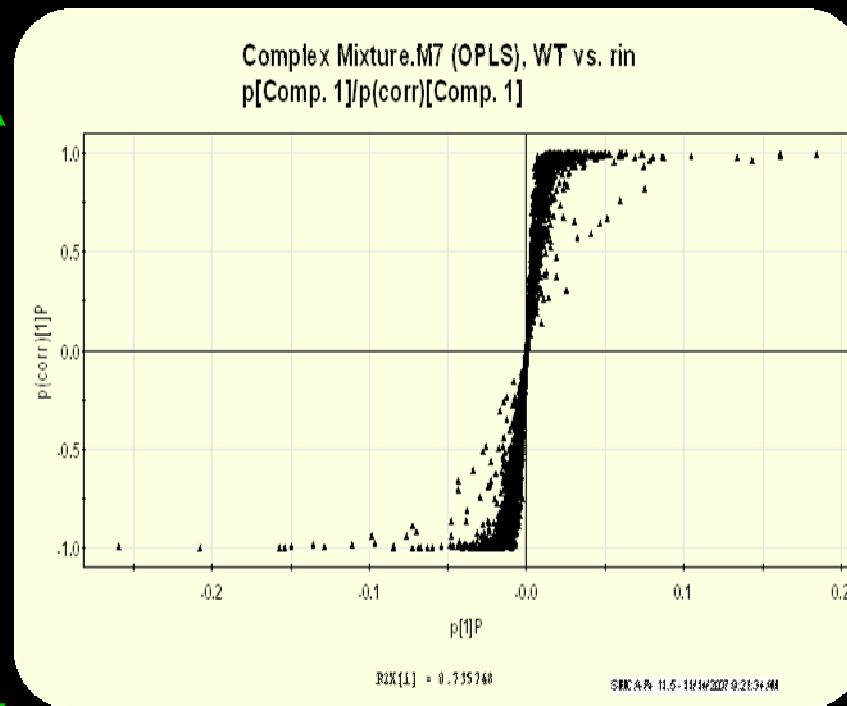


# The S-Plot for OPLS-DA

Developed by A team of scientists from:

- The University of Umea
- Umetrics
- Waters

Variable Confidence (correlation)



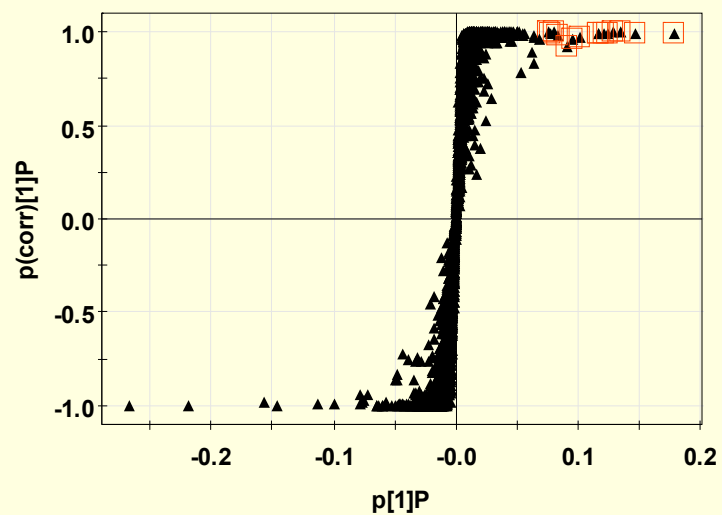
Variable Contribution (covariance)

Wiklund S, Johansson E, Sjöström L, Mellerowicz EJ, Edlund U, Shockcor JP, Gottfries J, Moritz T, Trygg J.

Visualization of GC/TOF-MS-Based Metabolomics Data for Identification of Biochemically Interesting Compounds Using OPLS Class Models. Anal Chem. 2008 Jan 1;80(1):115-122.

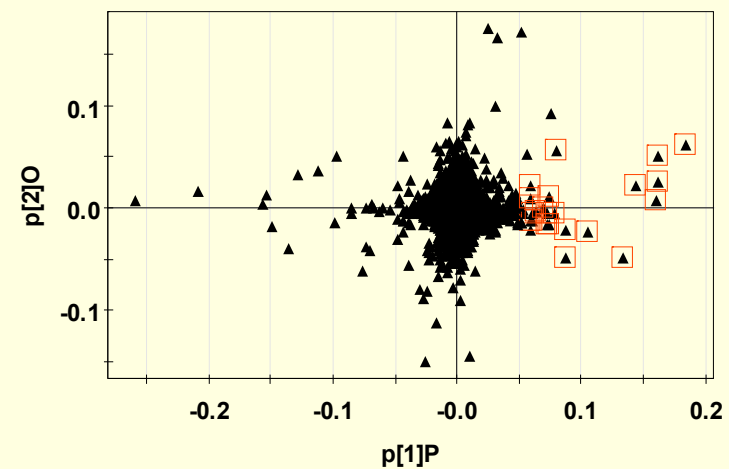
# S-Plot vs Loadings High in Wild Type

Complex Mixture.M6 (OPLS), WT vs. nor  
 $p[\text{Comp. 1}]/p(\text{corr})[\text{Comp. 1}]$



R2:0.710  
SIMCA-P+ 11.5 - 11/14/2007 6:46:18 AM

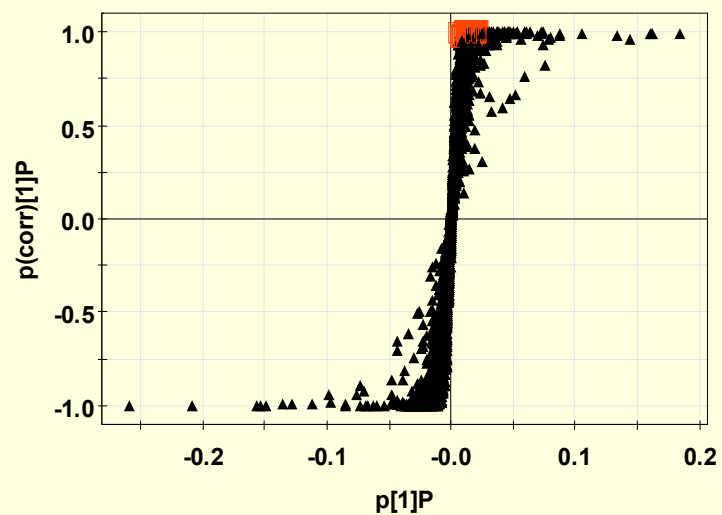
Complex Mixture.M7 (OPLS), WT vs. rin  
 $p[\text{Comp. 1}]/p[\text{Comp. 2}]$   
Colored according to model terms



R2X[1] = 0.730  
SIMCA-P+ 11.5 - 11/14/2007 6:49:37 AM

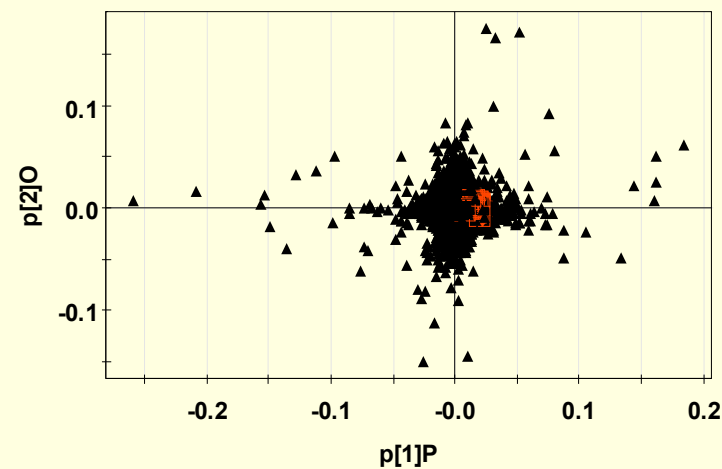
# S-Plot vs Loadings High in Wild Type

Complex Mixture.M7 (OPLS), WT vs. rin  
 $p[\text{Comp. 1}]/p(\text{corr})[\text{Comp. 1}]$



R2 = 0.710  
SIMCA-P+ 11.5 - 11/14/2007 6:53:11 AM

Complex Mixture.M7 (OPLS), WT vs. rin  
 $p[\text{Comp. 1}]/p[\text{Comp. 2}]$   
Colored according to model terms



R2X[1] = 0.730  
SIMCA-P+ 11.5 - 11/14/2007 6:53:43 AM

# MarkerLynx XS Software Demo

# ***Ion-Mobility /oa-TOF Mass Spectrometry And its Application to the Study of Lipids***

***John Shockcor***

***Director of Metabolic Profiling Business Development, Waters Corp.  
Visiting Fellow, Dept of Biochemistry, University of Cambridge***

- Separation of ions as they drift through a gas under the influence of an electric field
- Rate of drift is dependant on the ion's mobility through the gas
- Mobility is dependant on factors such as,
  - Size
  - Shape
  - Charge

# History of IMS

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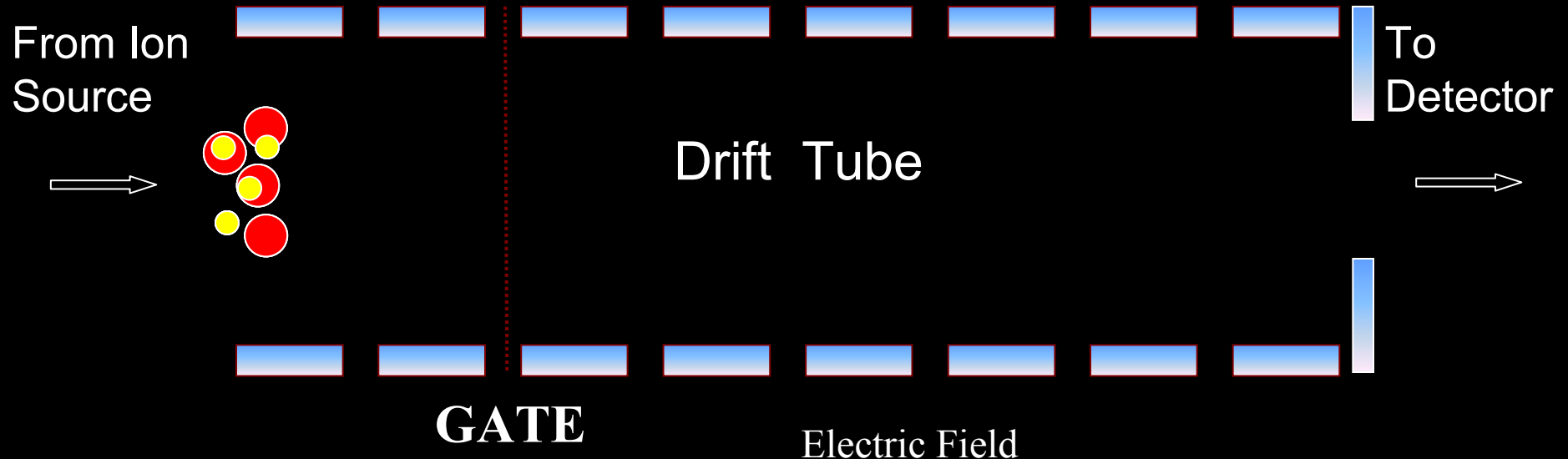


Thomson, J. J.; Rutherford, G. P.,  
"Conduction of Electricity Through  
Gases", Dover, NY, 1928.

Thomson, J. J.; "Rays of Positive  
Electricity", Green and Co., London,  
England, 1933.

# Conventional ion mobility spectrometers

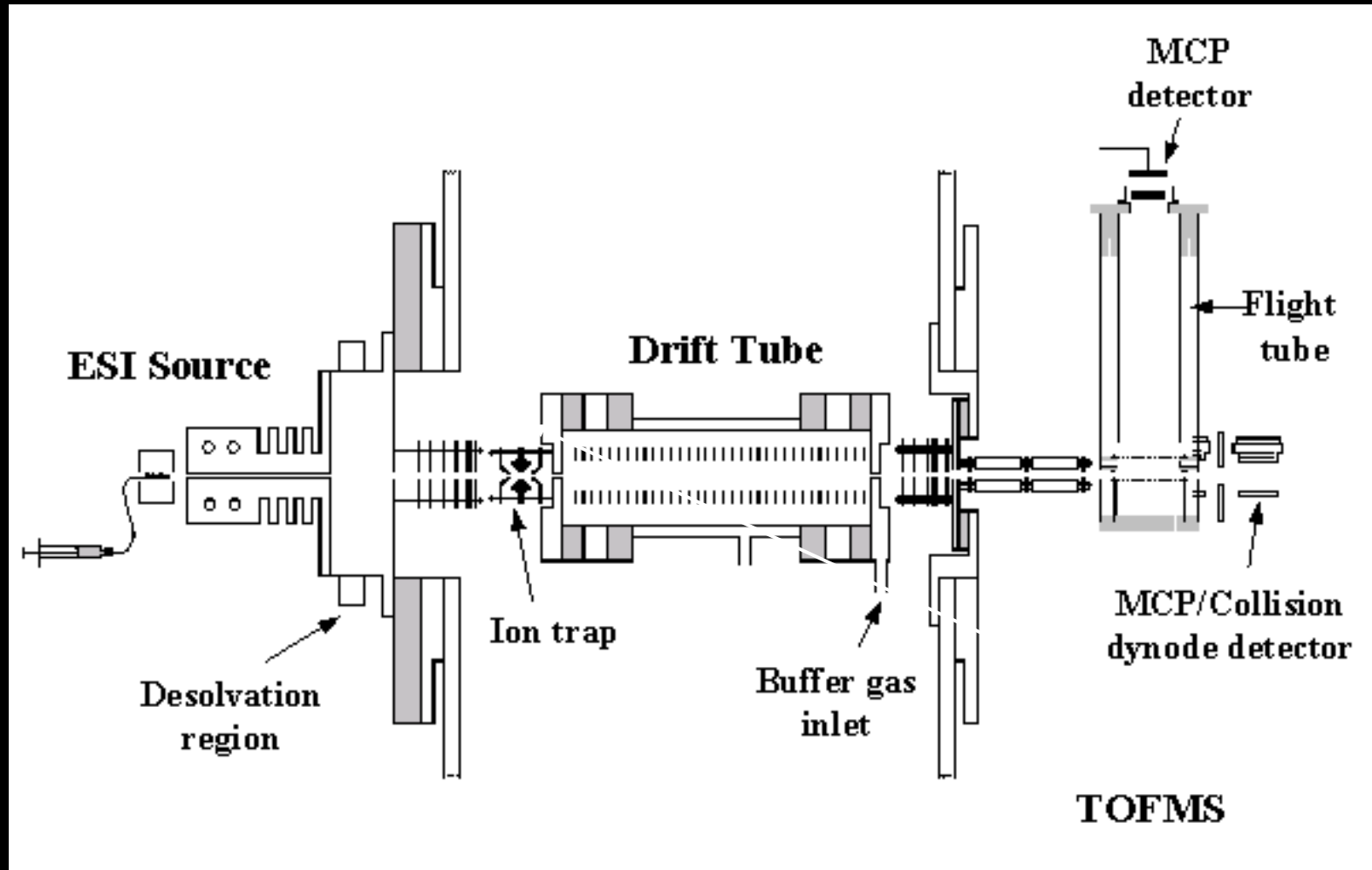
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- High Mobility Ion
- Low Mobility Ion



*Clemmer et al. introduced an accumulating ion trap upstream to increase duty cycle [1997]*



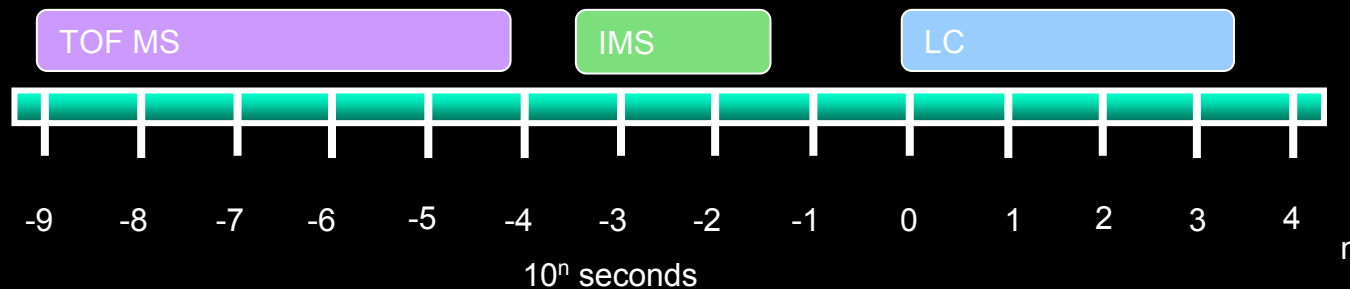
However: Drift tubes suffer from diffusion losses

Driving Field E



# Ion Mobility Spectrometry Perspective:- The Benefits

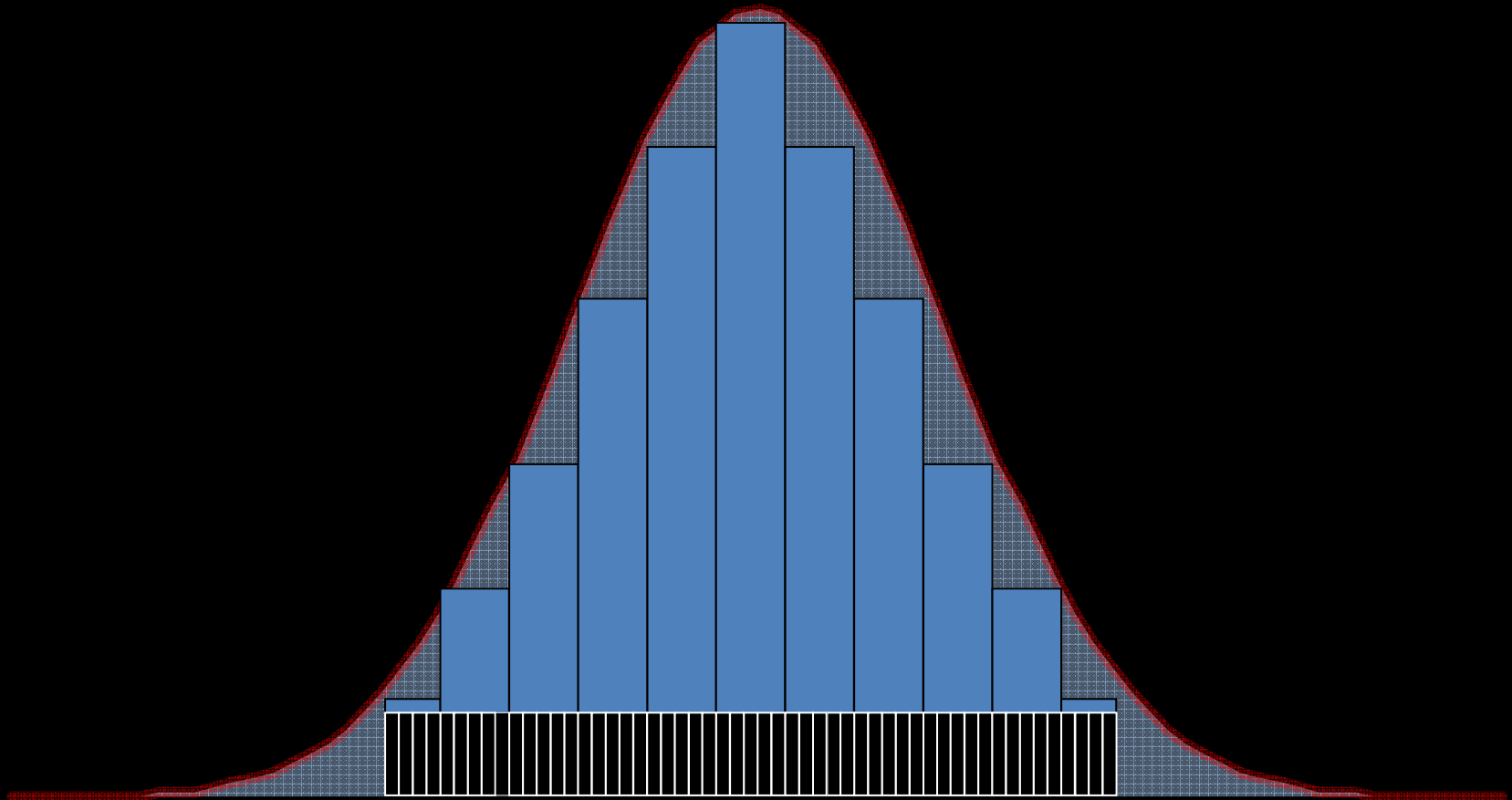
- Rapid orthogonal separation capability



- Improve peak capacity
- Provide novel functionality
- Enhance performance of the mass spectrometer
- IMS is an orthogonal separation
- How can T-Wave technology be implemented ?

# IMS Timing

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→ MS:  $\mu\text{sec}$

→ IMS run: msec

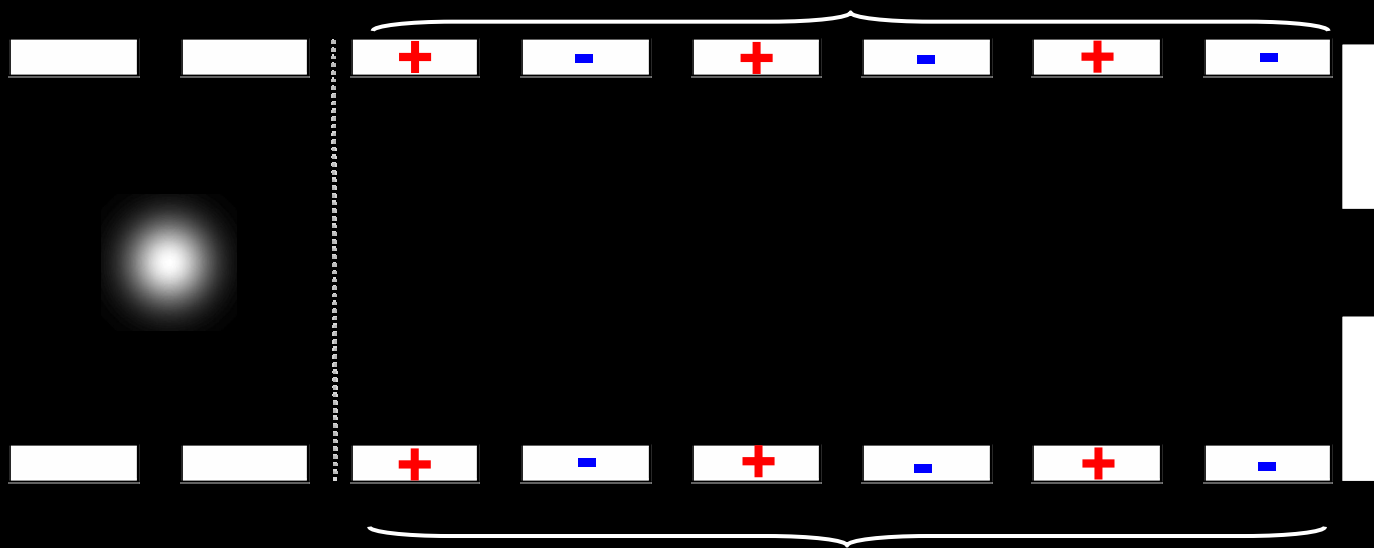
→ Chromatographic peak: sec

Adding RF gives radial confinement and greater sensitivity

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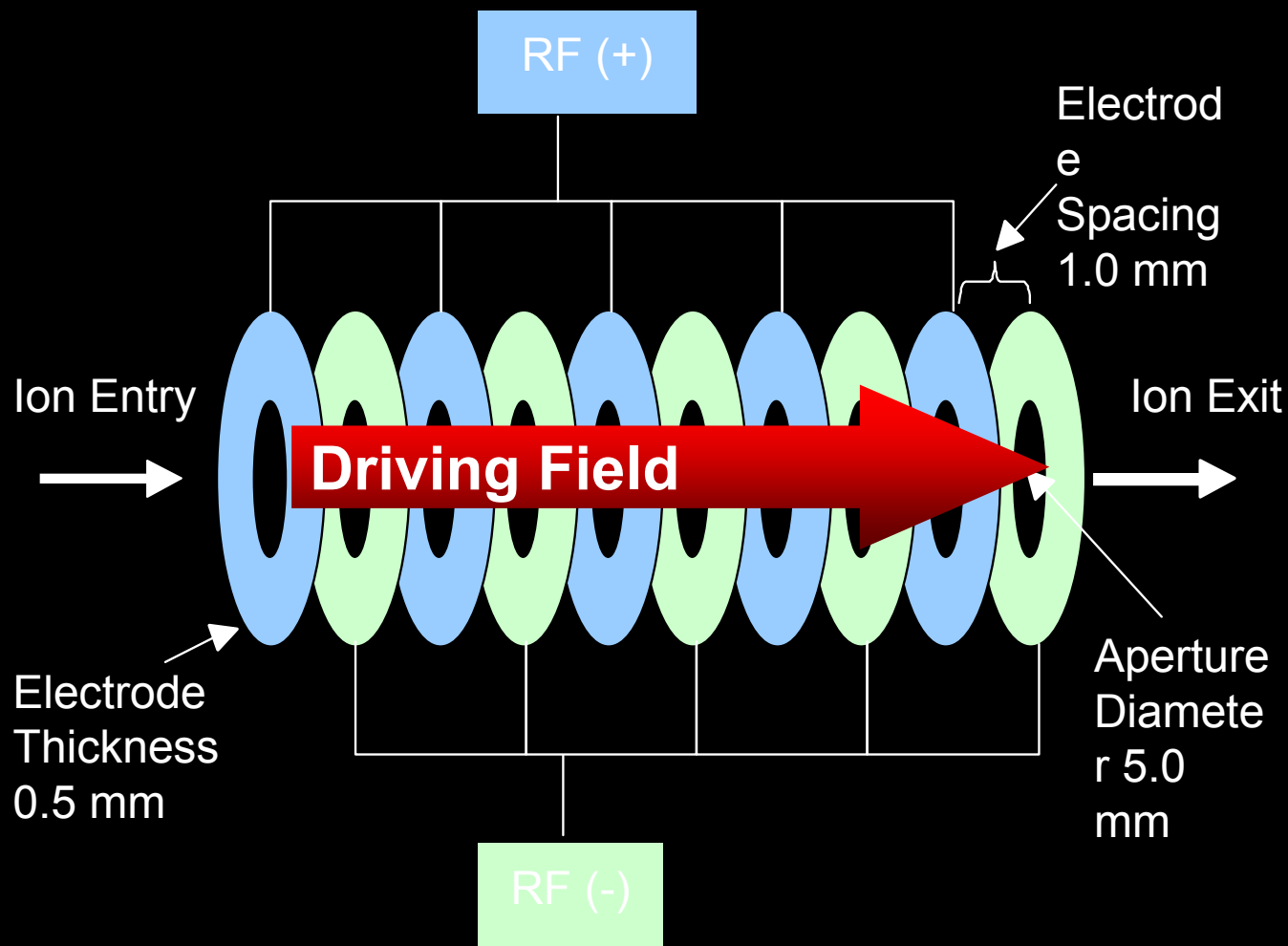
Driving Field E

RF

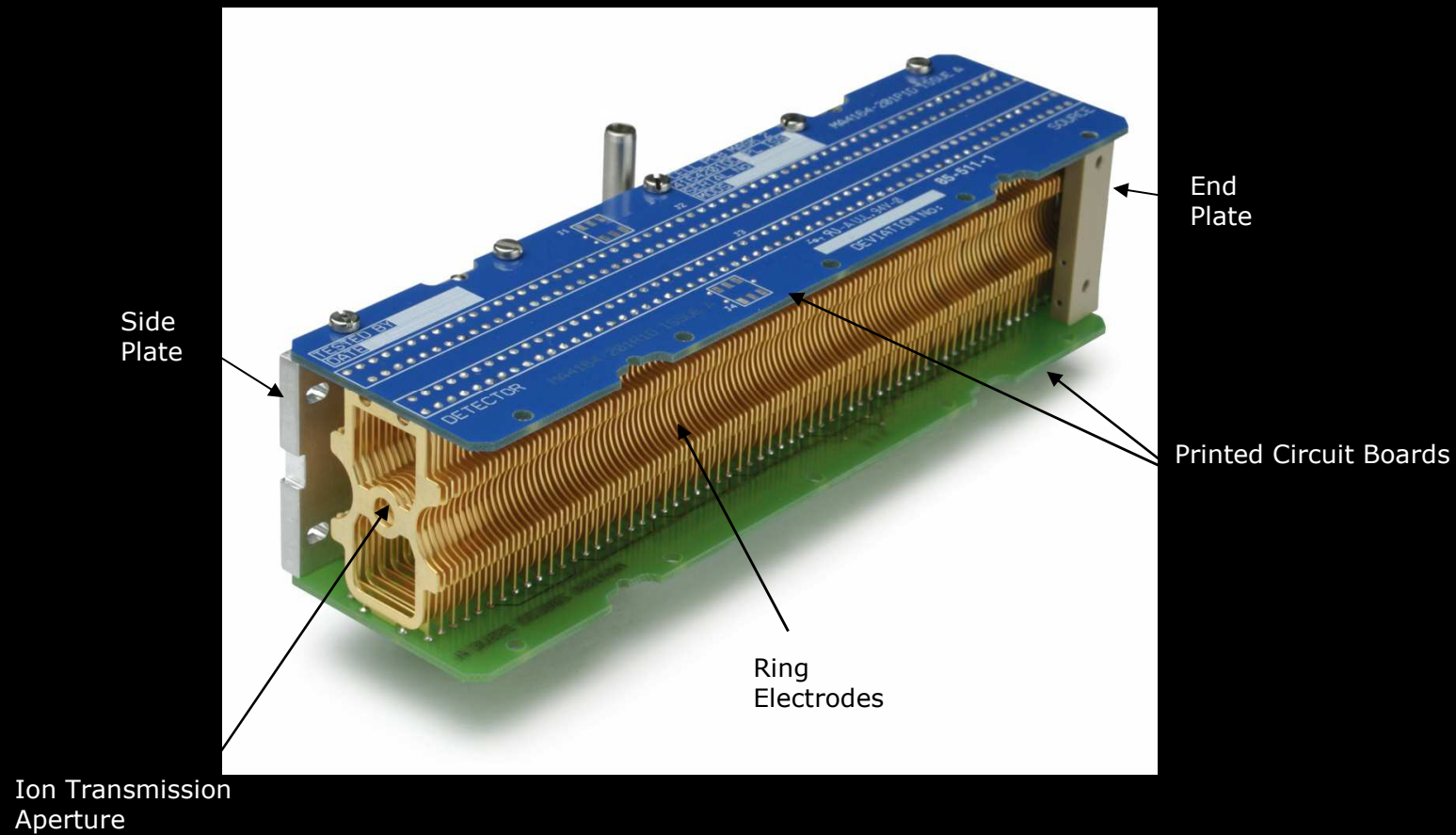


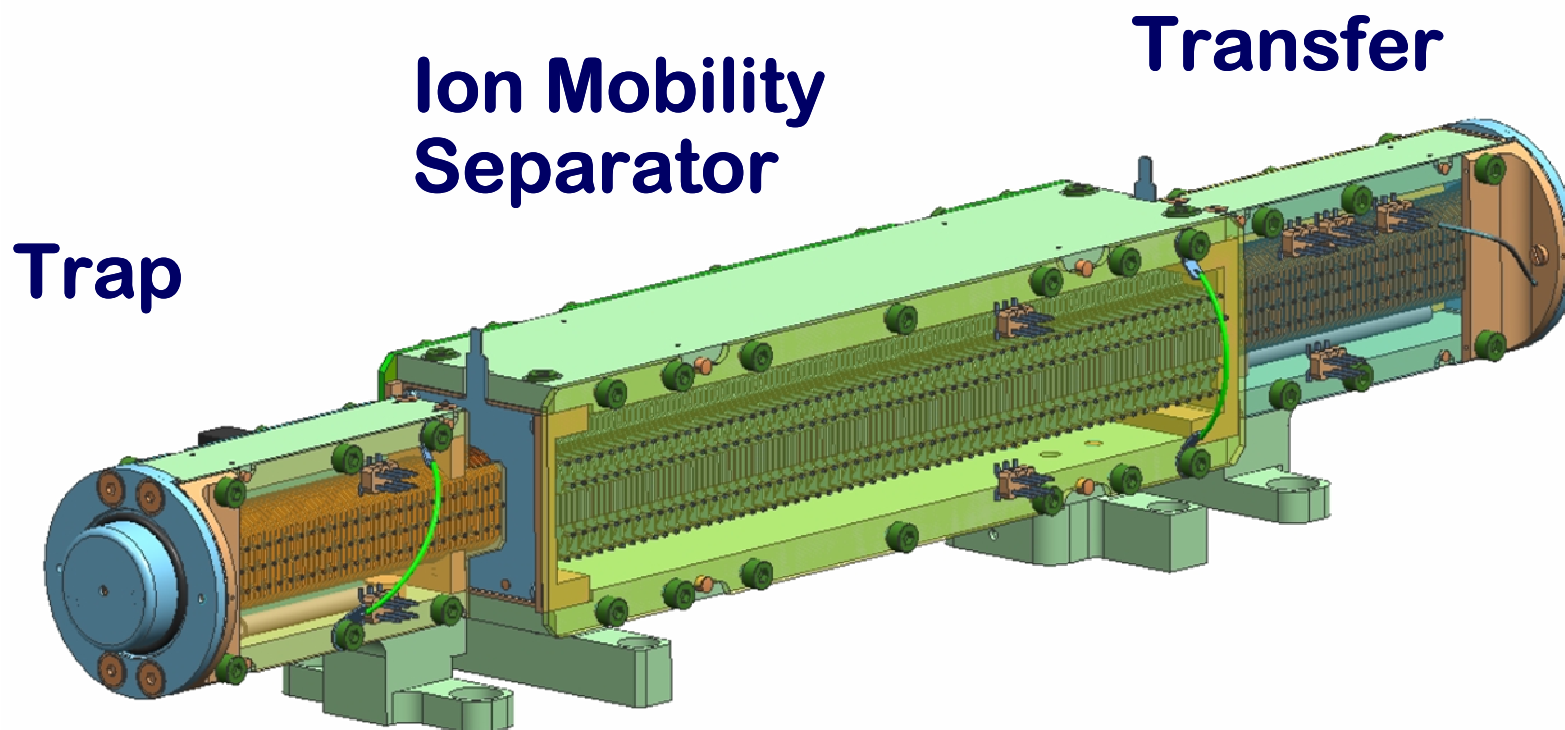
# An RF-Only Stacked Ring Ion Guide transports ions with 100% efficiency

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# Traveling Wave Device



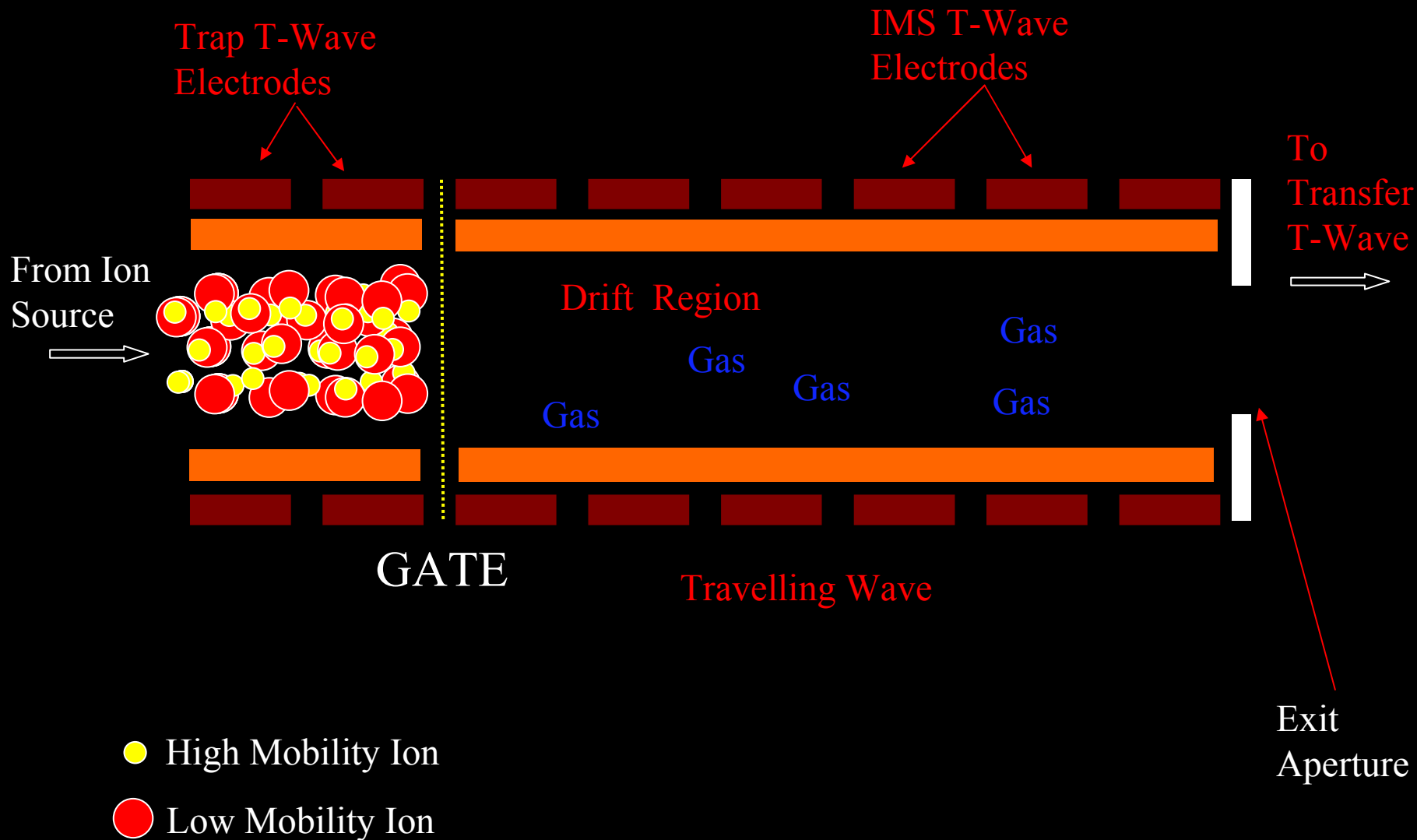


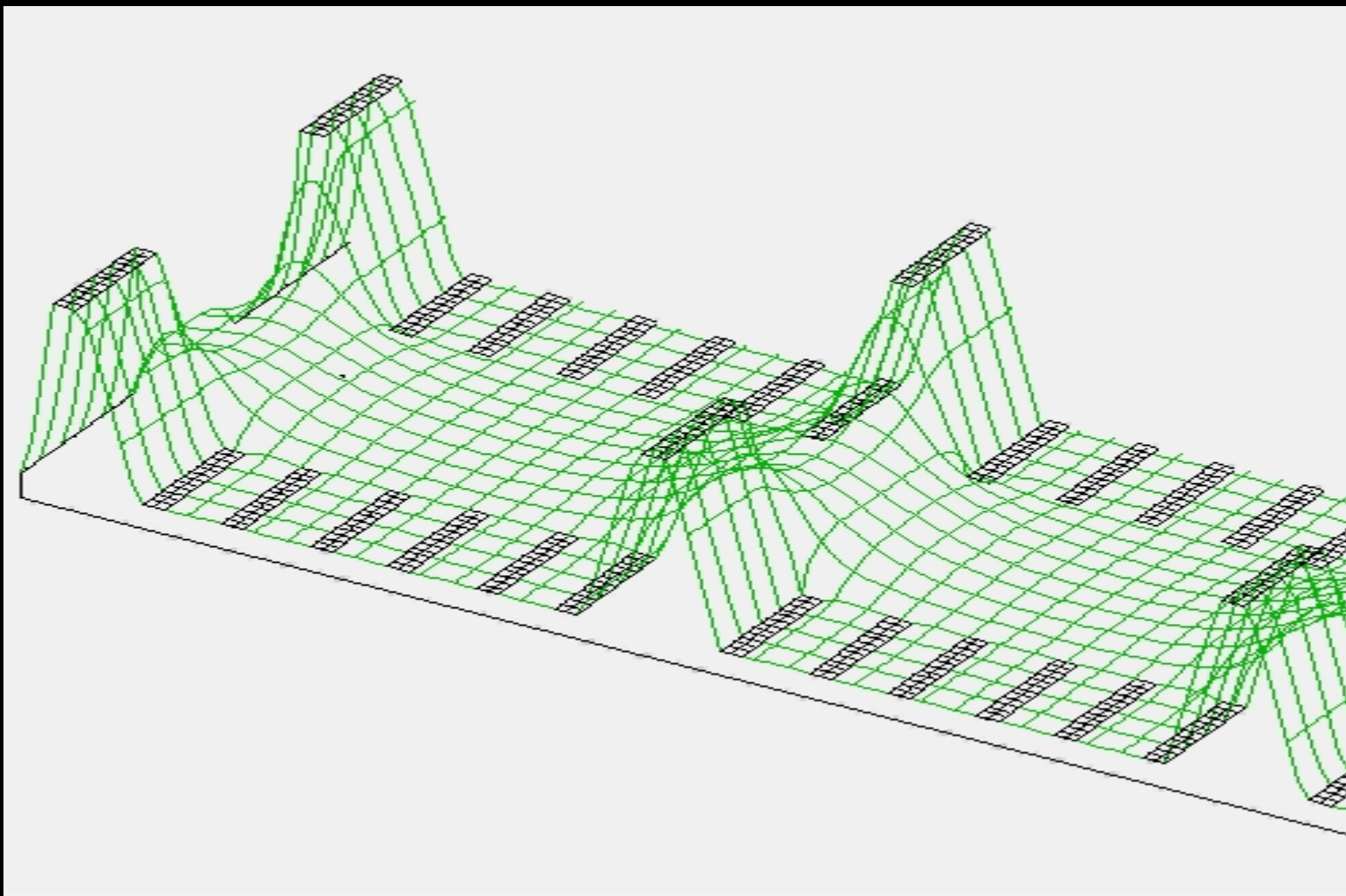
Fragmentation (CID) can be induced in both the TRAP and TRANSFER regions ( $\sim 10^{-3}$  mbar). For IMS analysis helium is admitted into the Ion Mobility Separator ( $\sim 0.5$  mbar)



# Synapt HDMS System TriWave - High Duty Cycle High Transmission

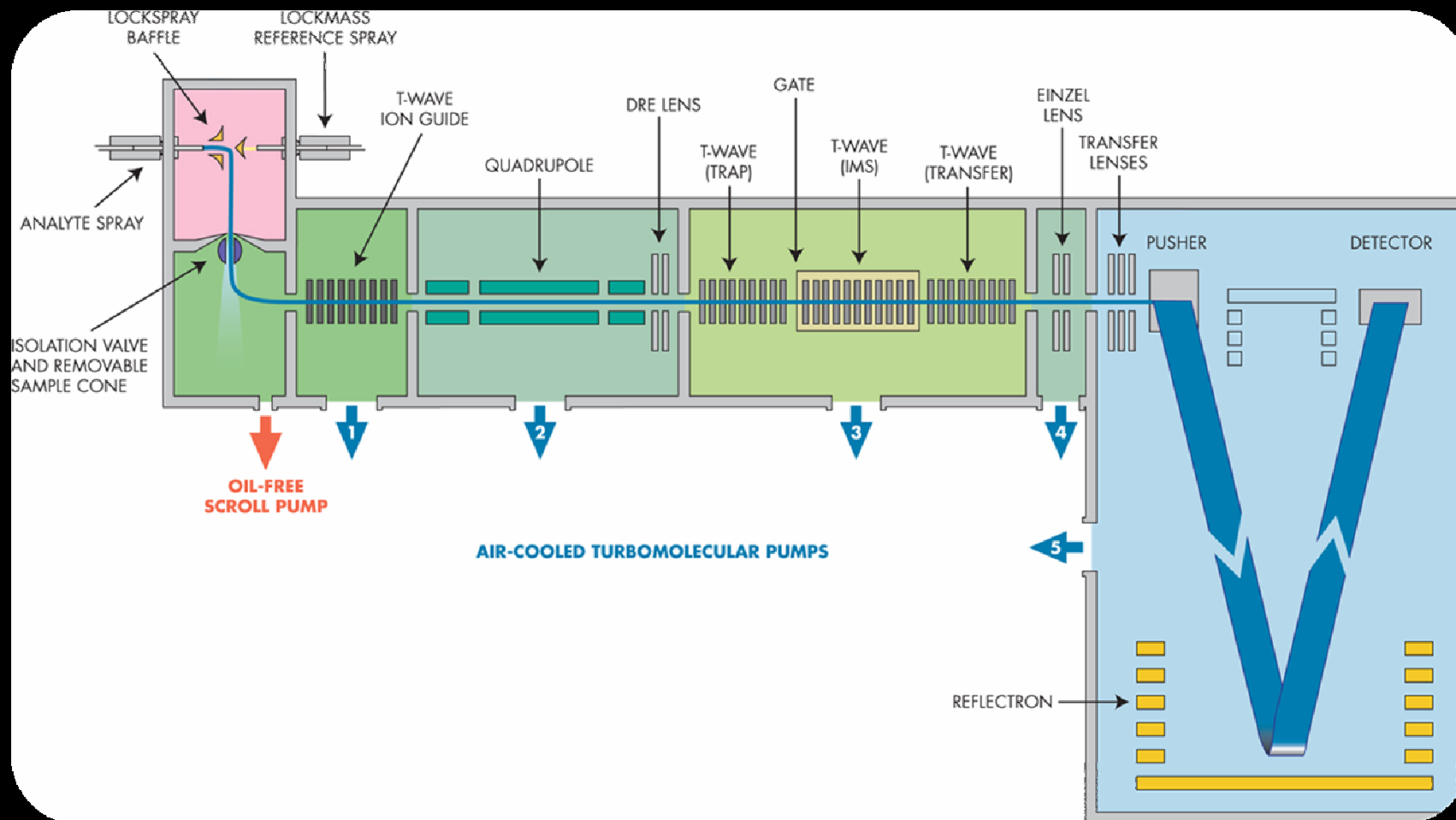
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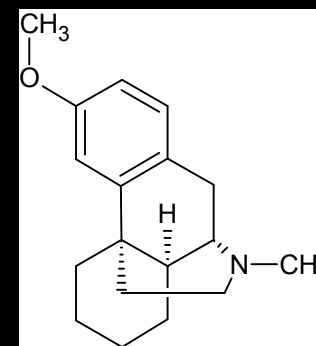
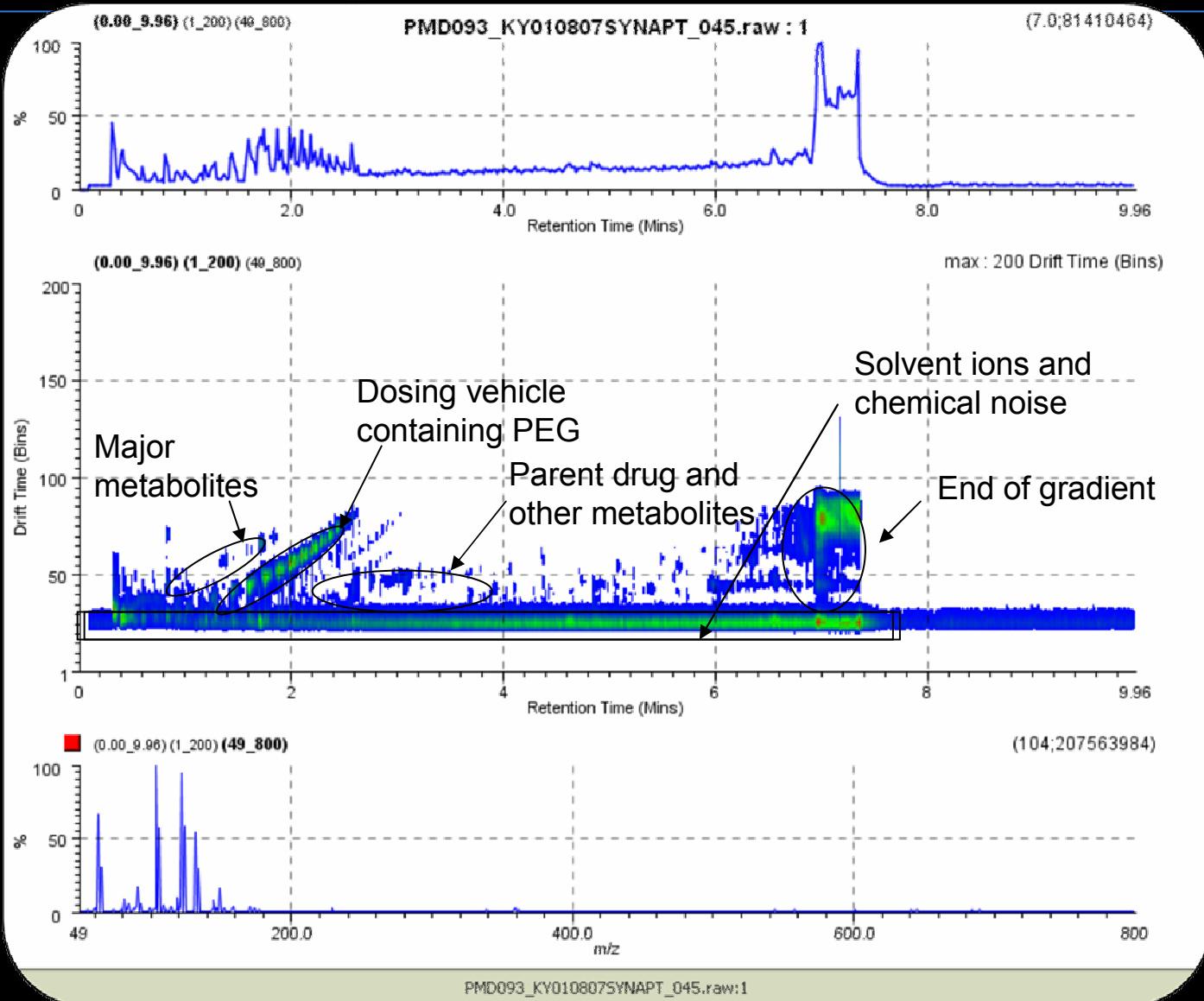


# Hybrid Quadrupole / IMS / oa-ToF

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# Removing Interferences

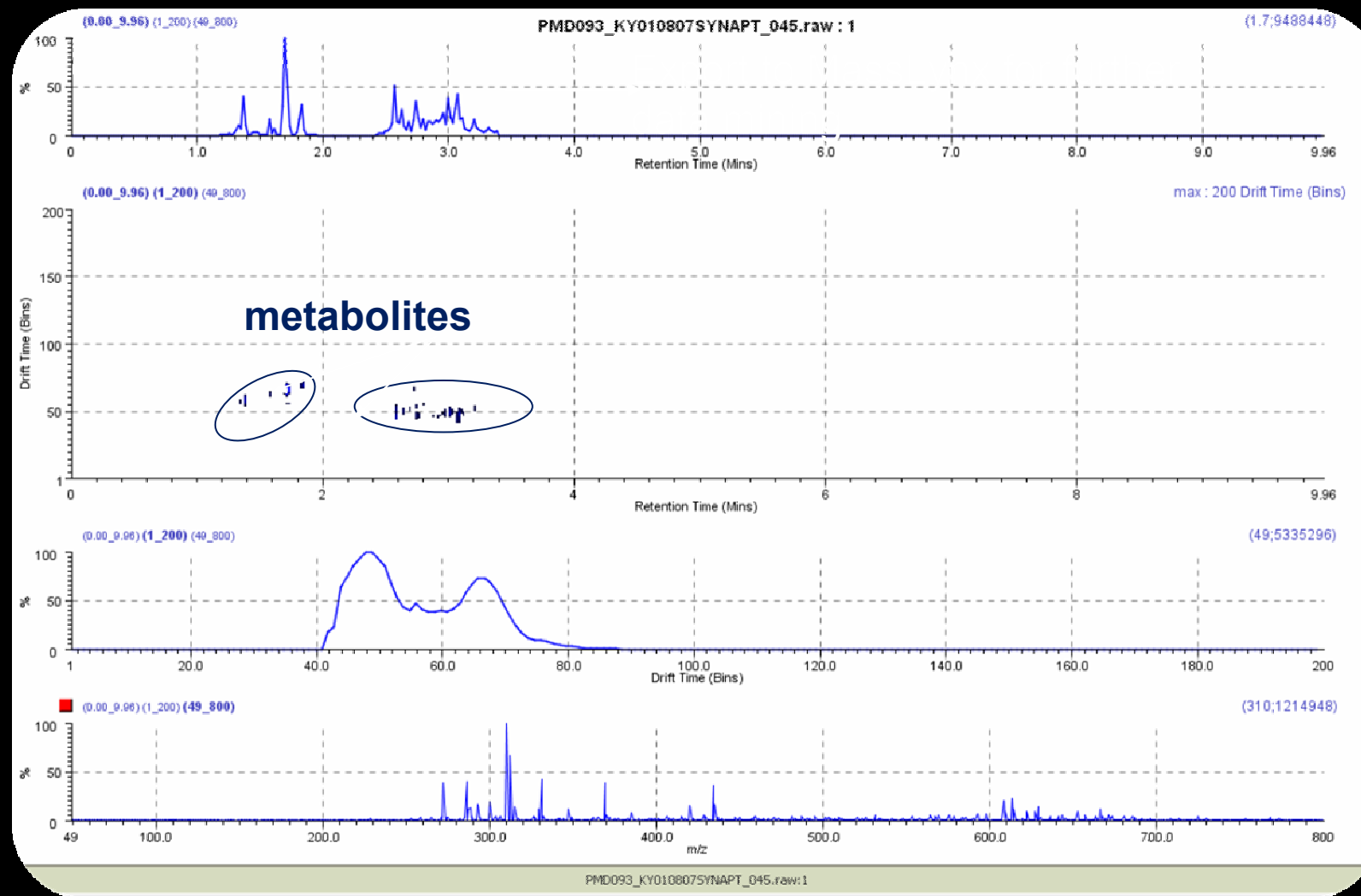


Dextromethorphan

# Data clean-up step using the drift time function

Waters

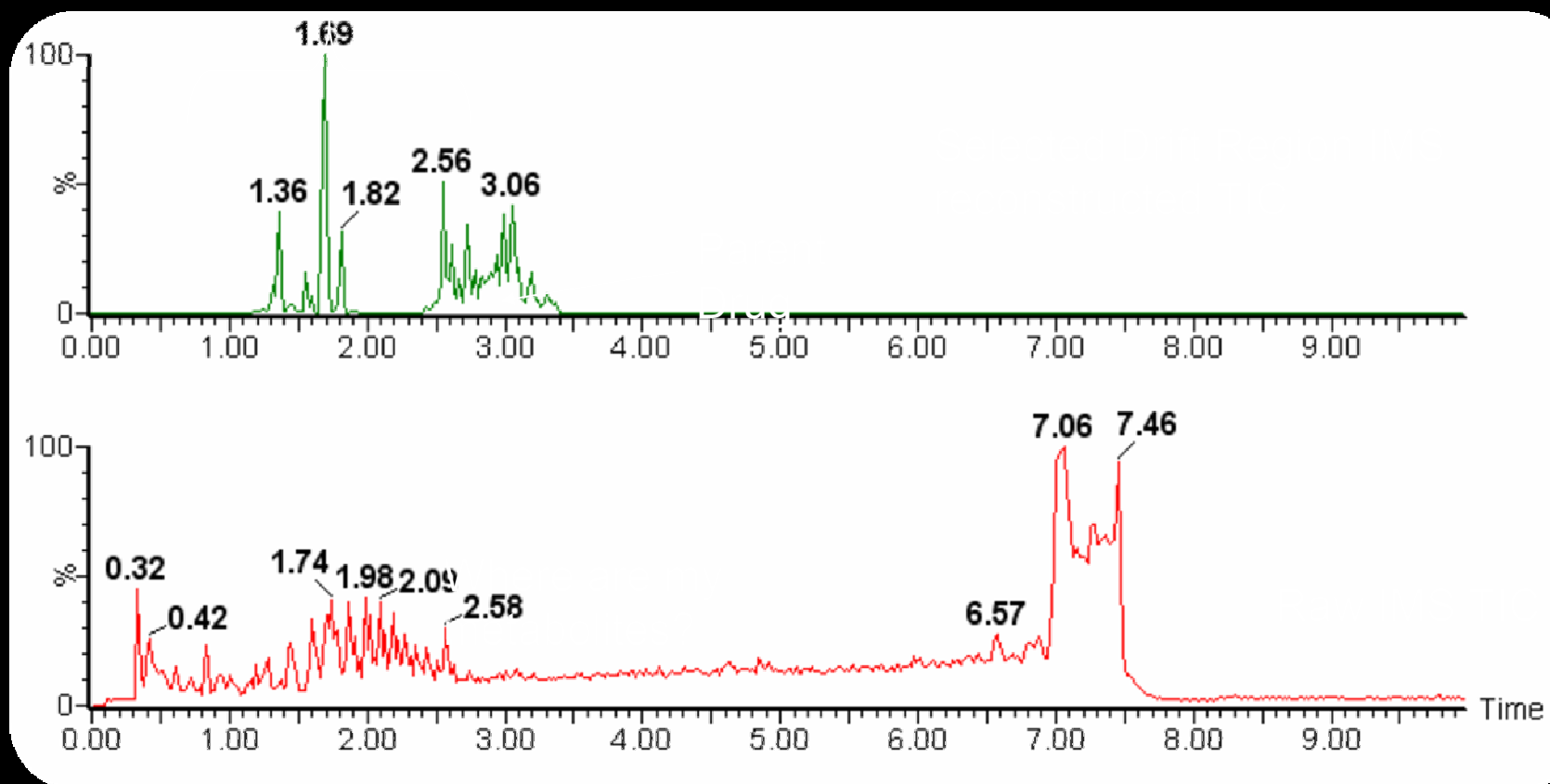
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# Metabolite search by UPLC-IMS-TOF

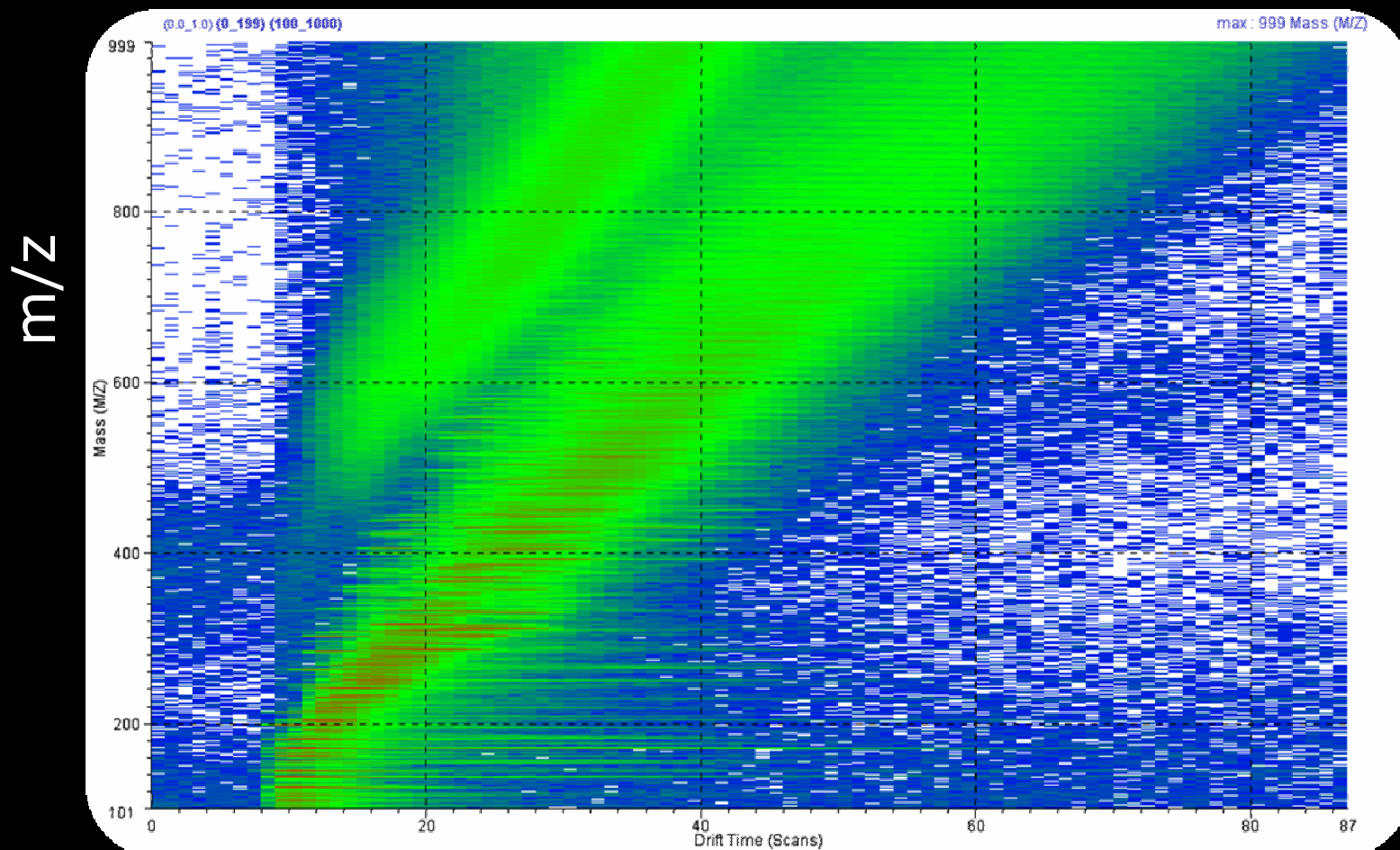
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## Metabolites



# Urine Infusion on SYNAPT™ HDMS

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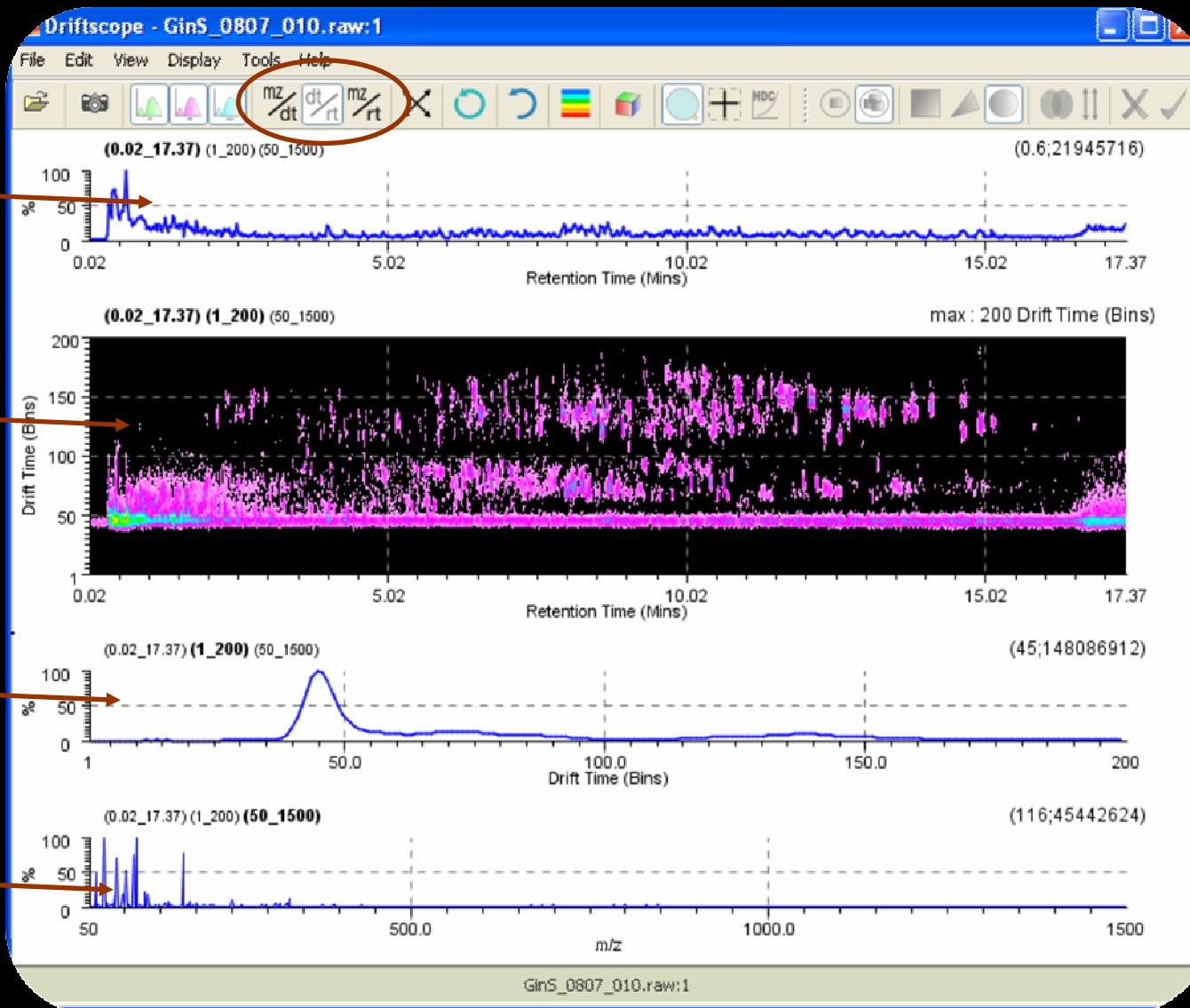


Drift Time

# IMS Data Review in Drift Scope

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LC Chromatogram



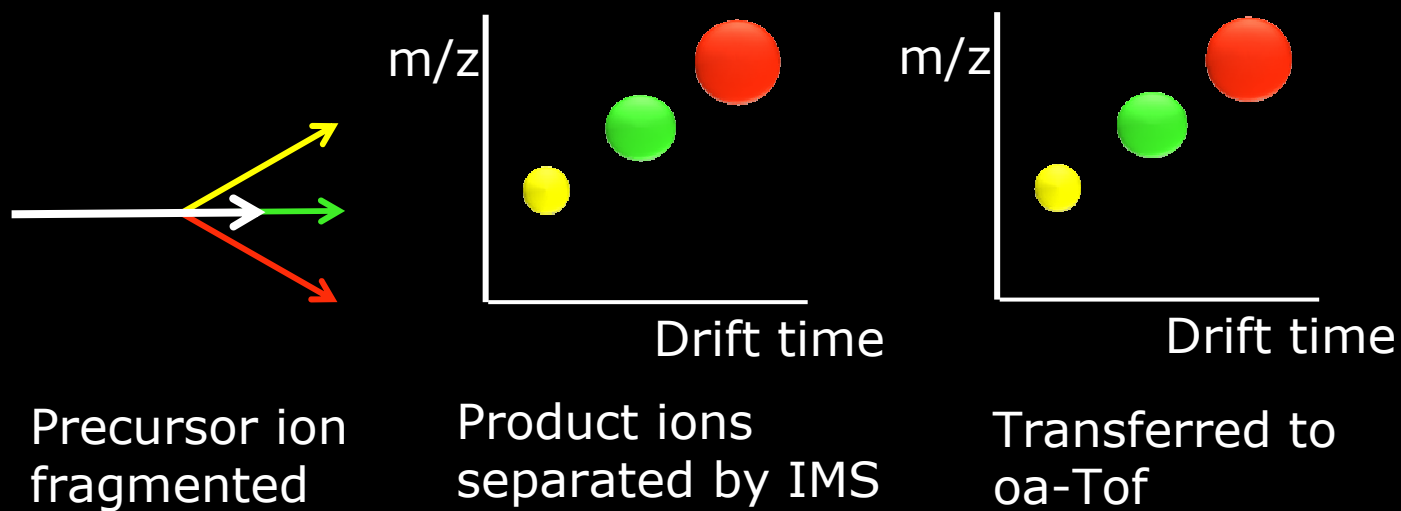
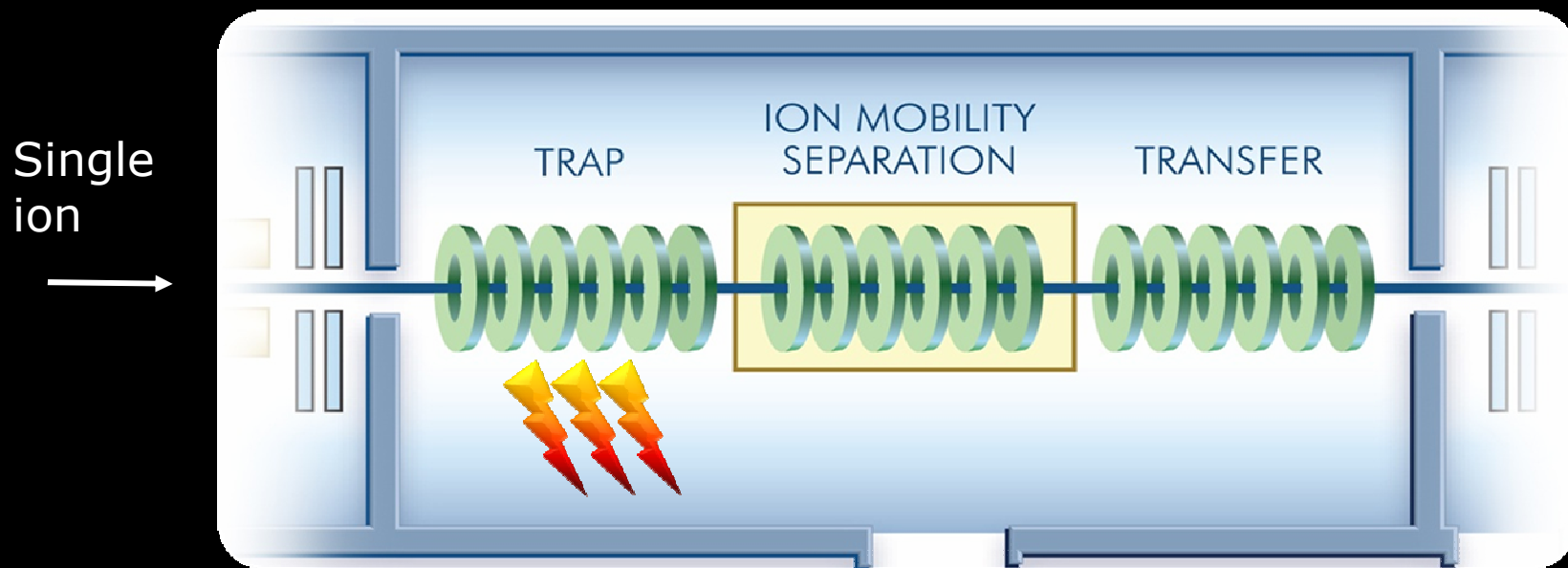
IMS Drift Scope

Drift Time Plot

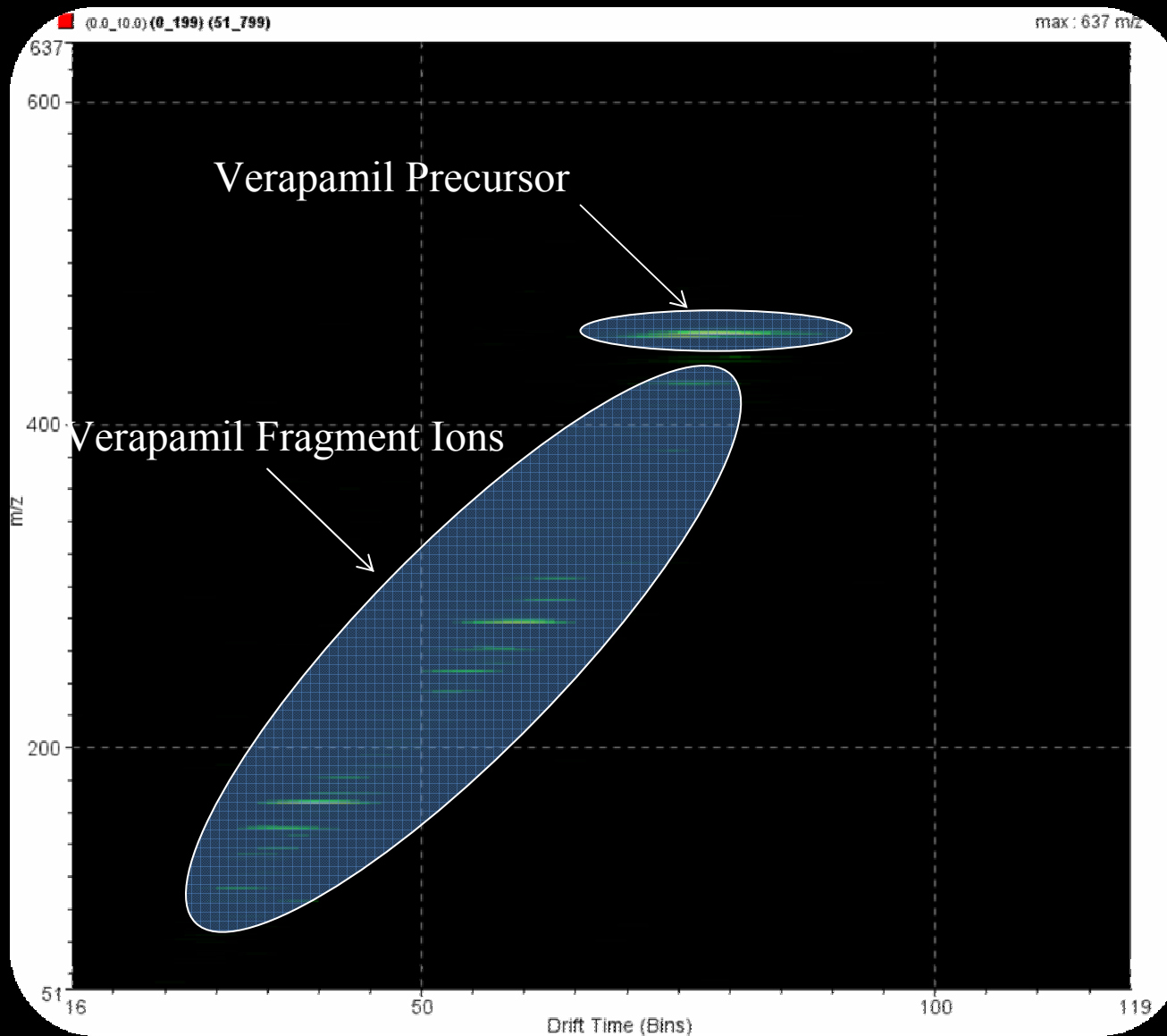
Mass Spectrum



# Trap fragmentation (CID-IMS)

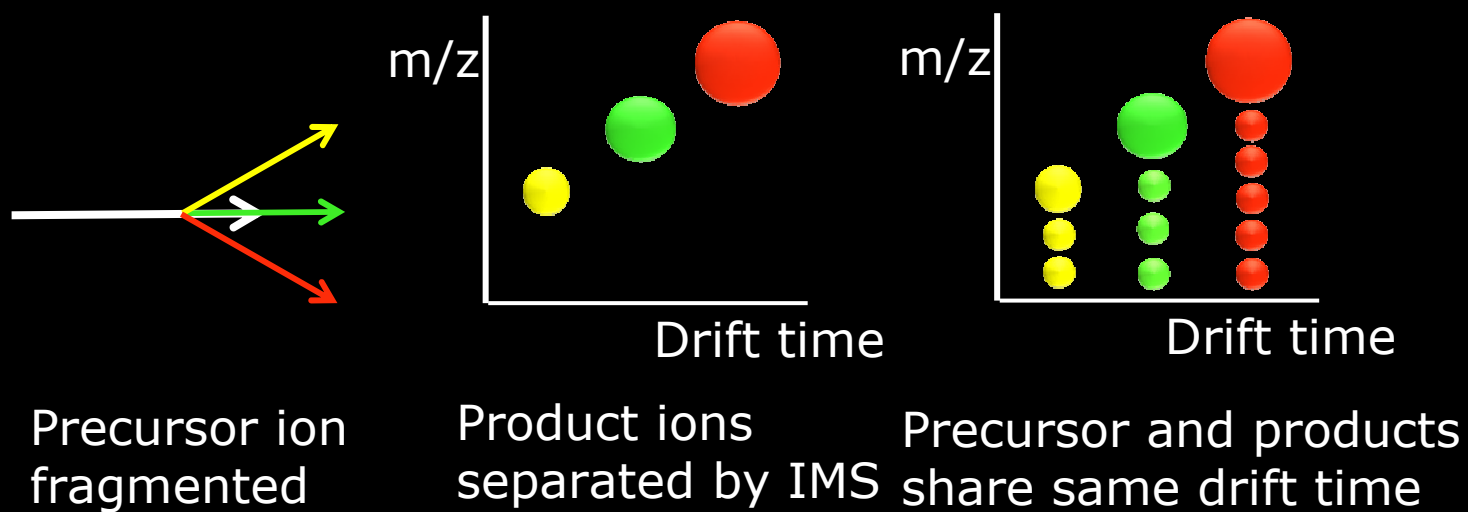
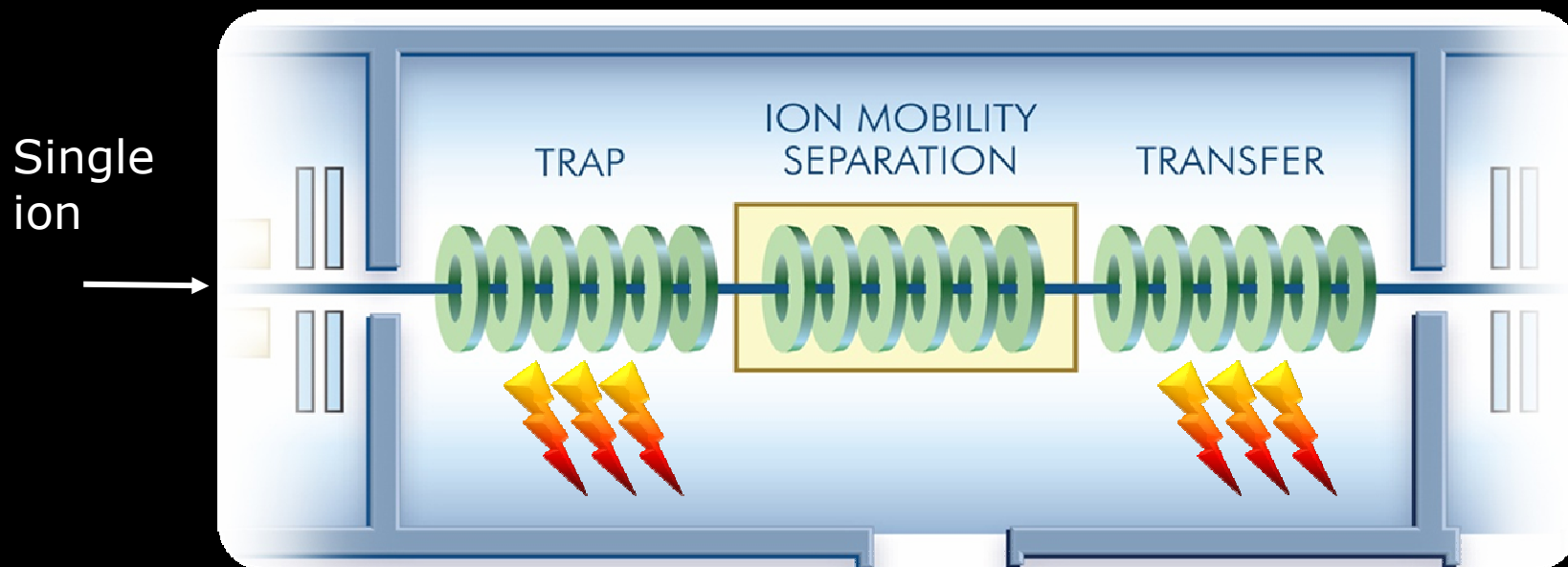


# Trap fragmentation (CID-IMS)

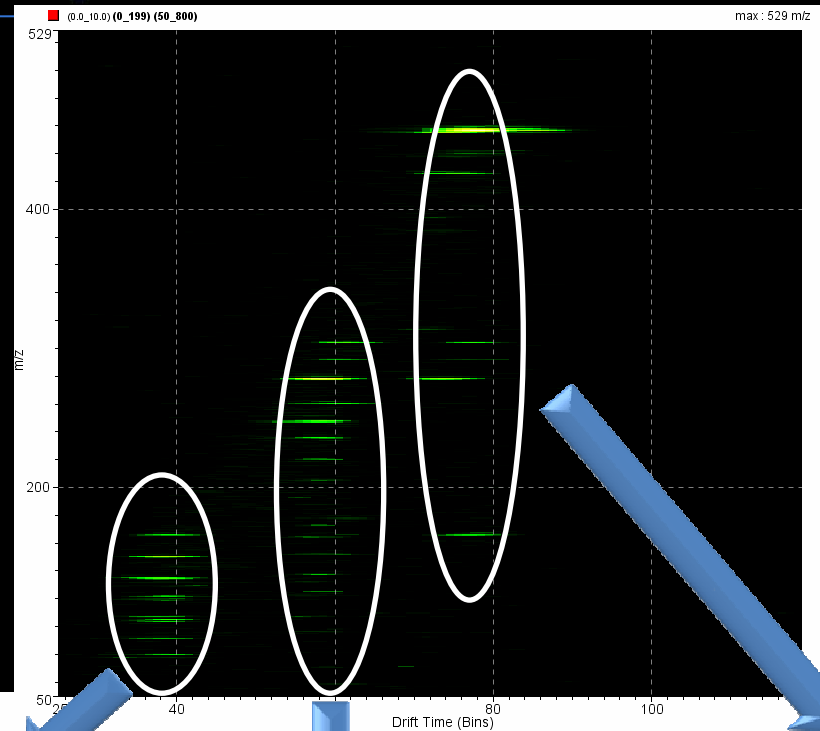


# Time Aligned Parallel Fragmentation (TAP) CID-IMS-CID

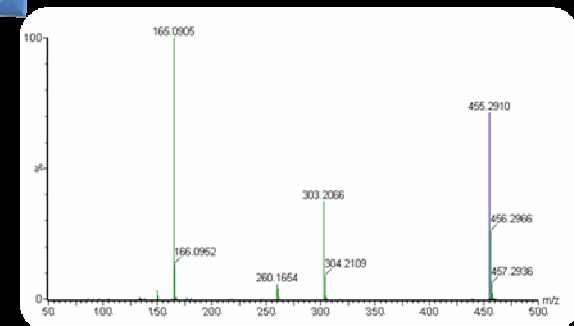
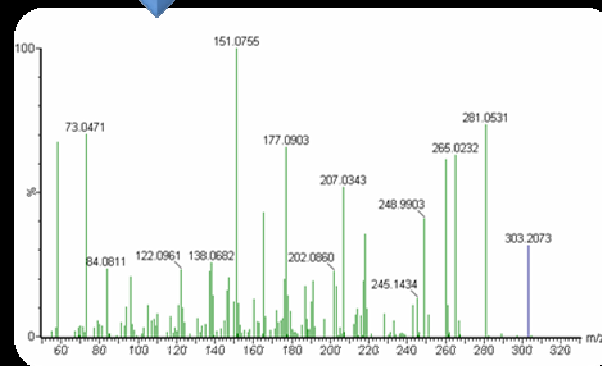
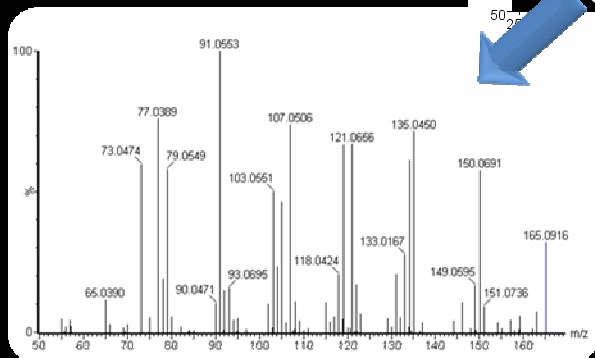
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# TAP fragmentation

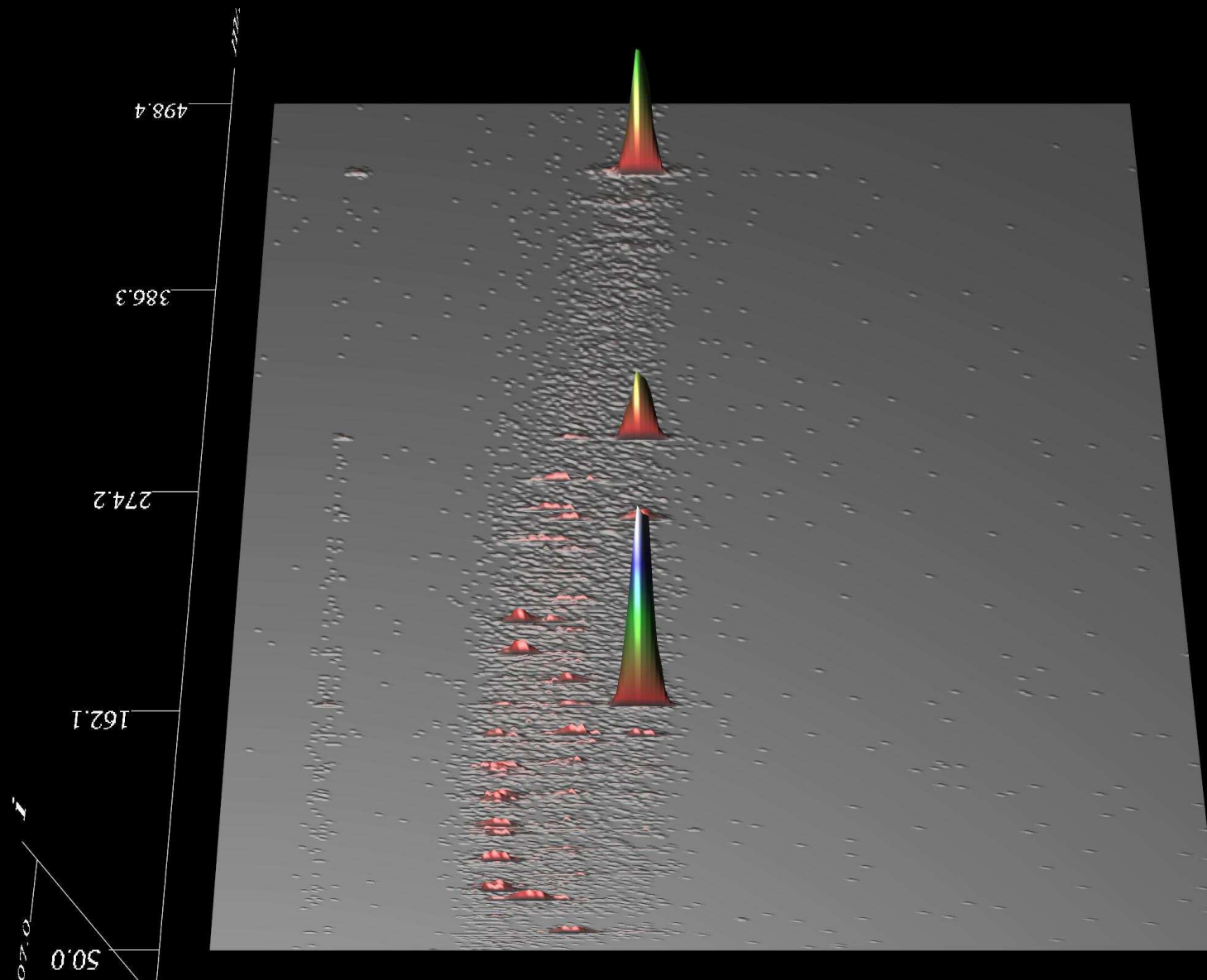


Ability to interrogate all drift time areas independently



# 3D representation of TAP for Verapamil

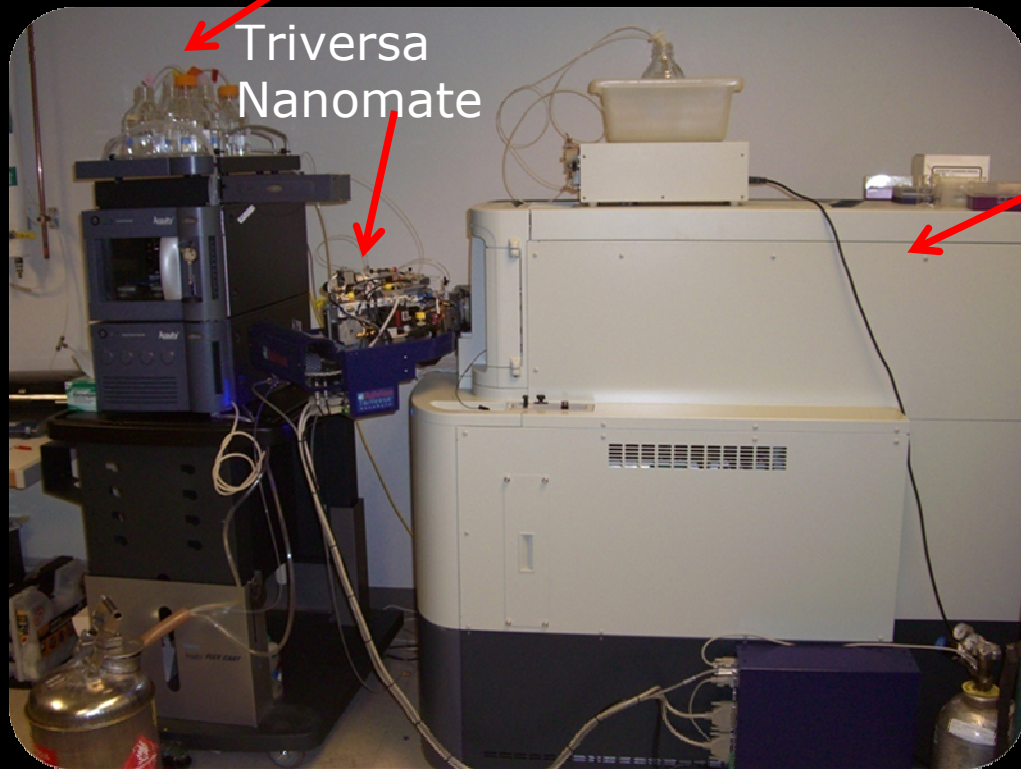
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# Lipidomics using Ion Mobility

# Instrument configuration

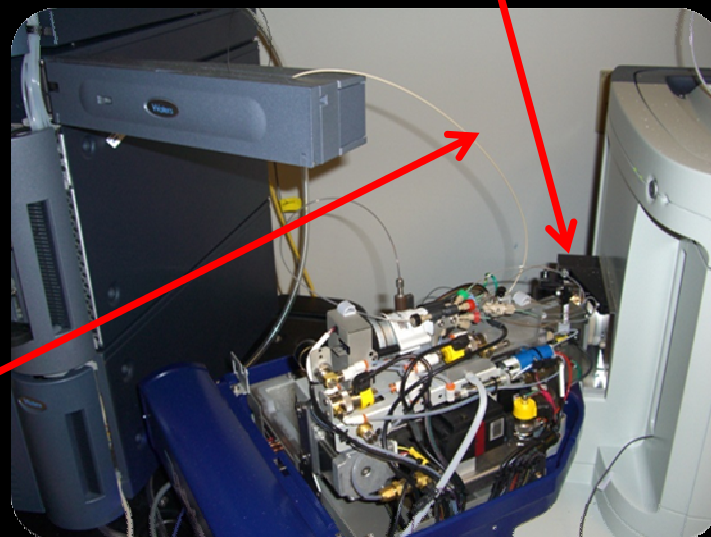
UPLC flow rate 600  $\mu\text{L}/\text{min}$



Triversa  
Nanomate

Synapt HDMS

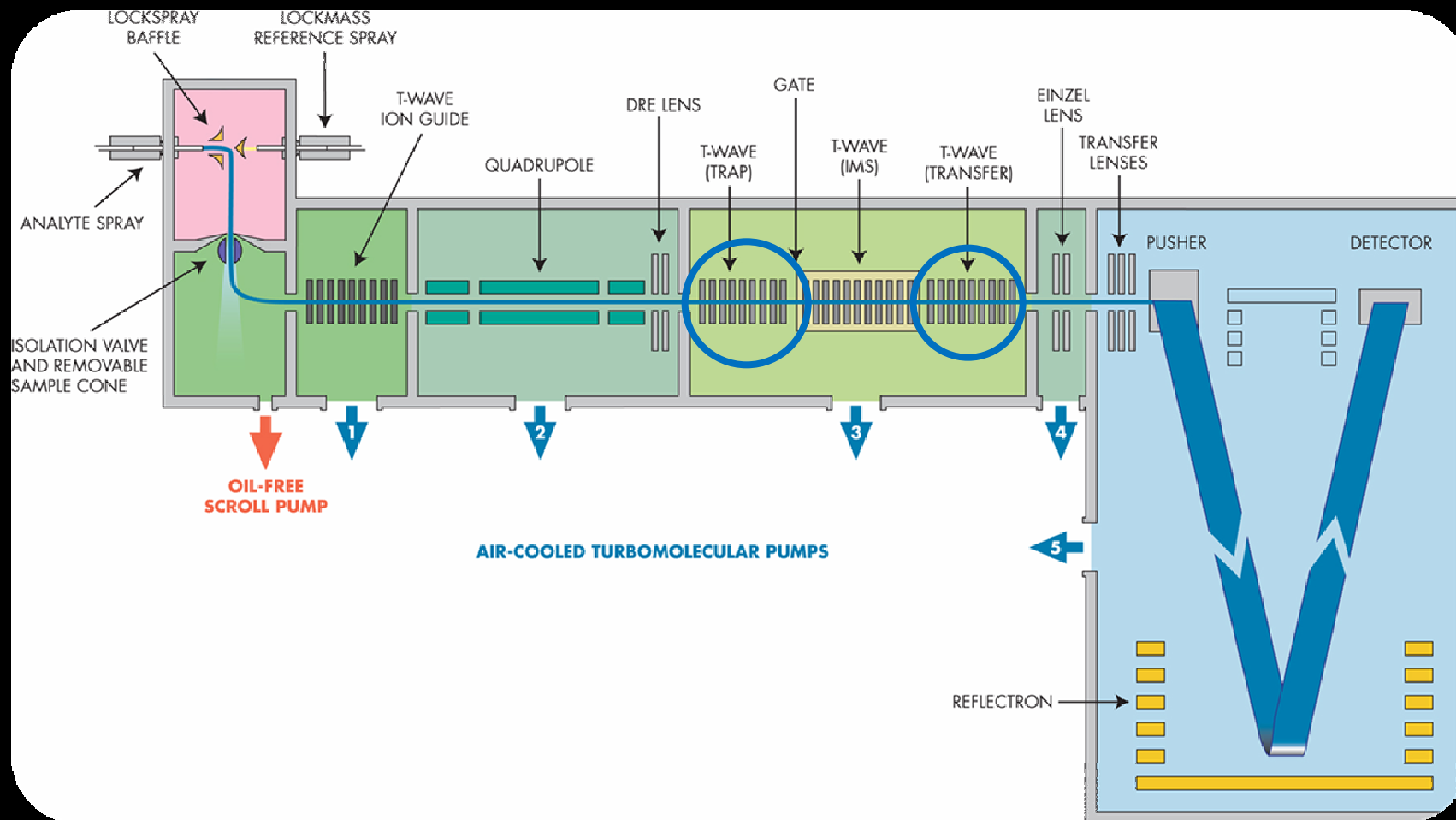
Flow rate into the Synapt  
289nL/min



UPLC Flow connected to  
Nanomate for fraction  
collection 599.7  $\mu\text{L}/\text{min}$

# Hybrid Quadrupole / IMS / oa-ToF

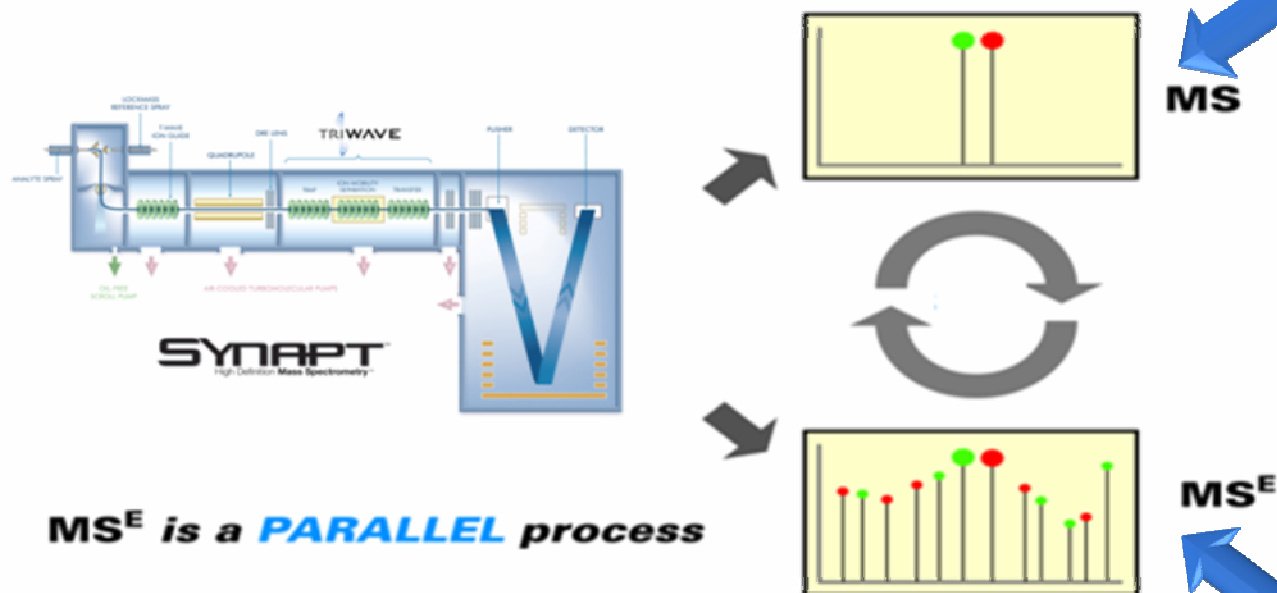
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# What is MS<sup>E</sup>?

Low collision energy mode to produce precursor ion data



MS

MS<sup>E</sup>

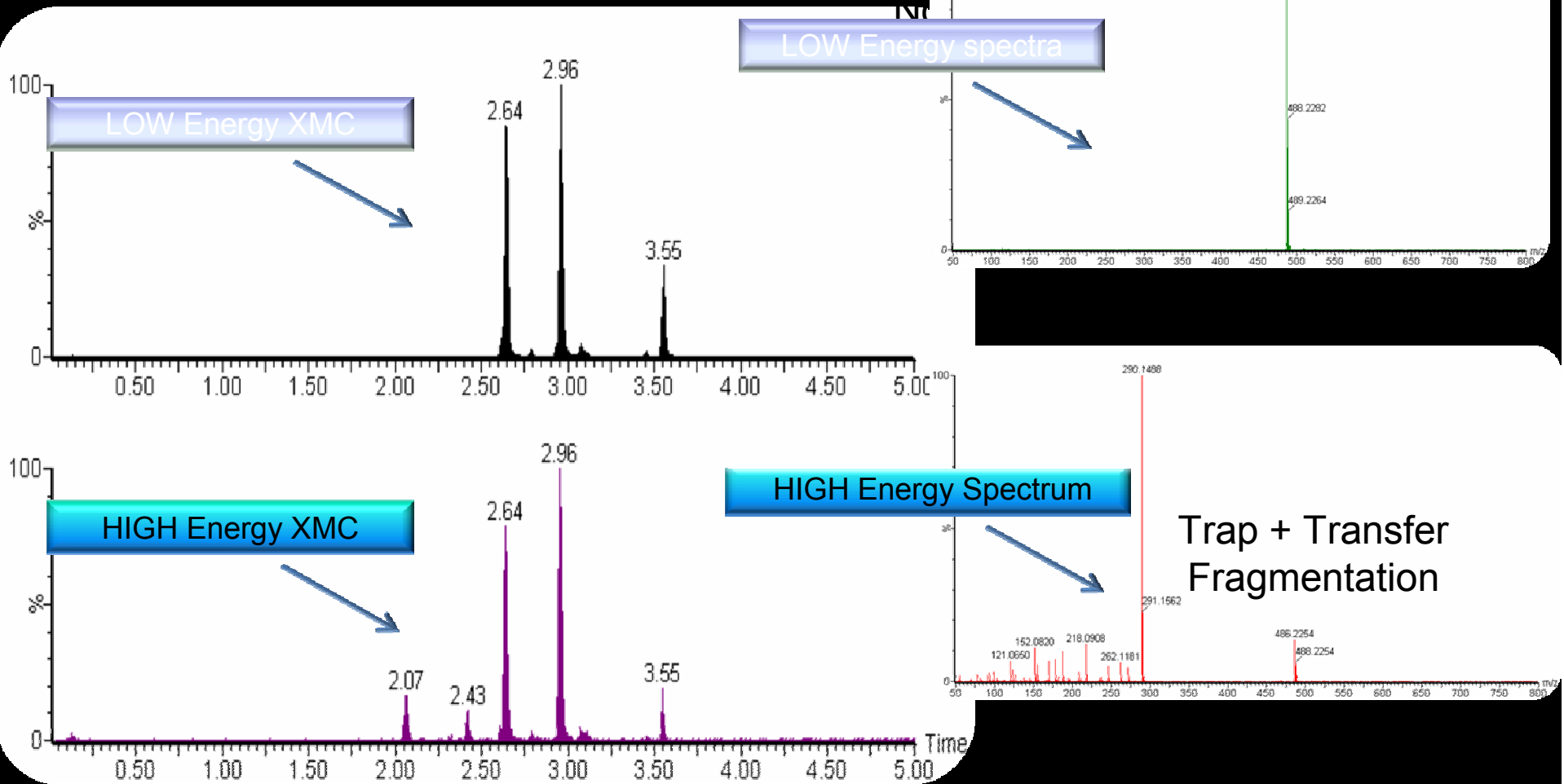
MS<sup>E</sup> is a **PARALLEL** process

High collision energy mode to produce fragment ion data

# MS<sup>E</sup> provides data rich information for Metabolite ID assays- in a single injection

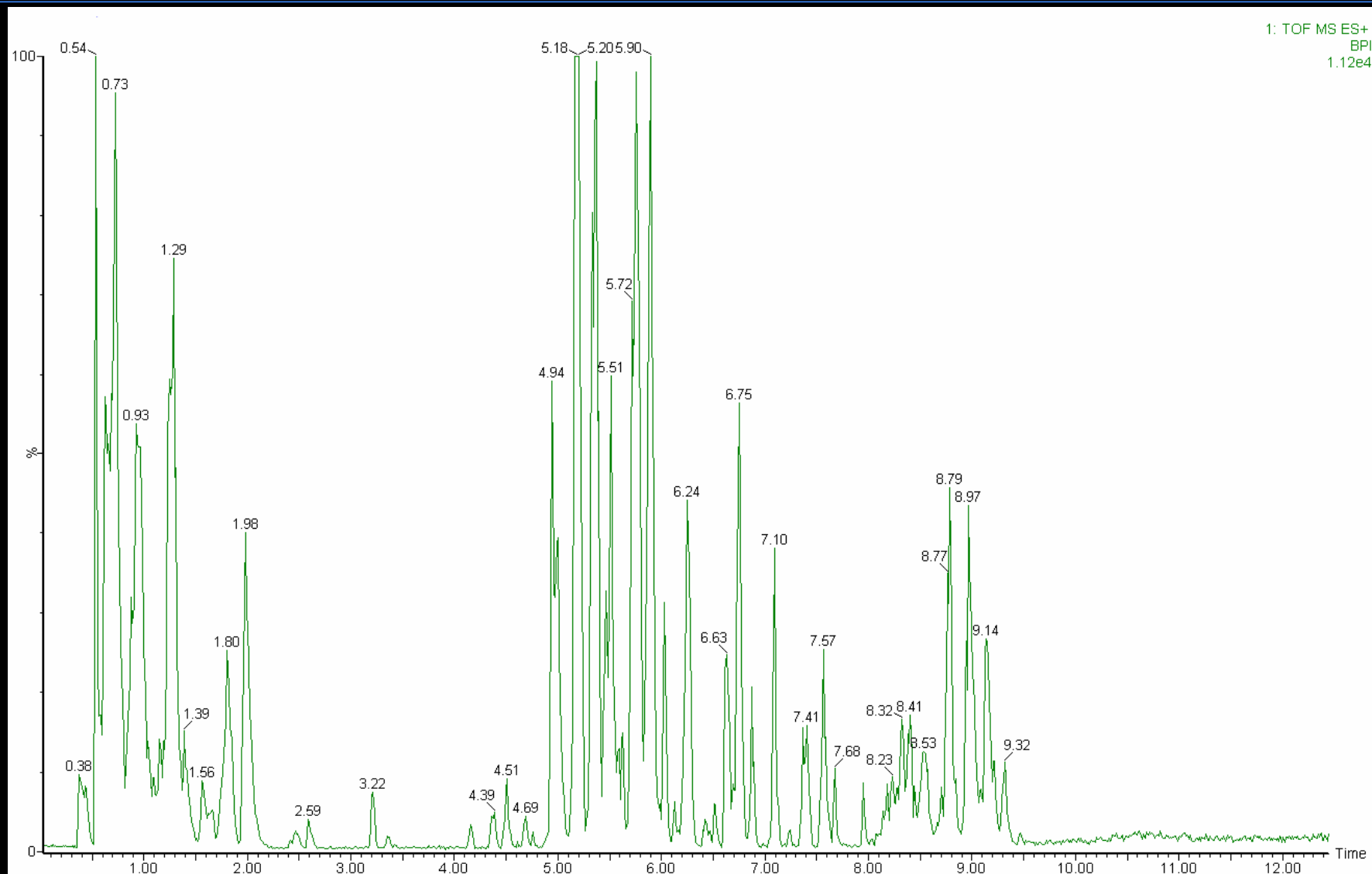
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Nefazadone *in vitro* +OH metabolites



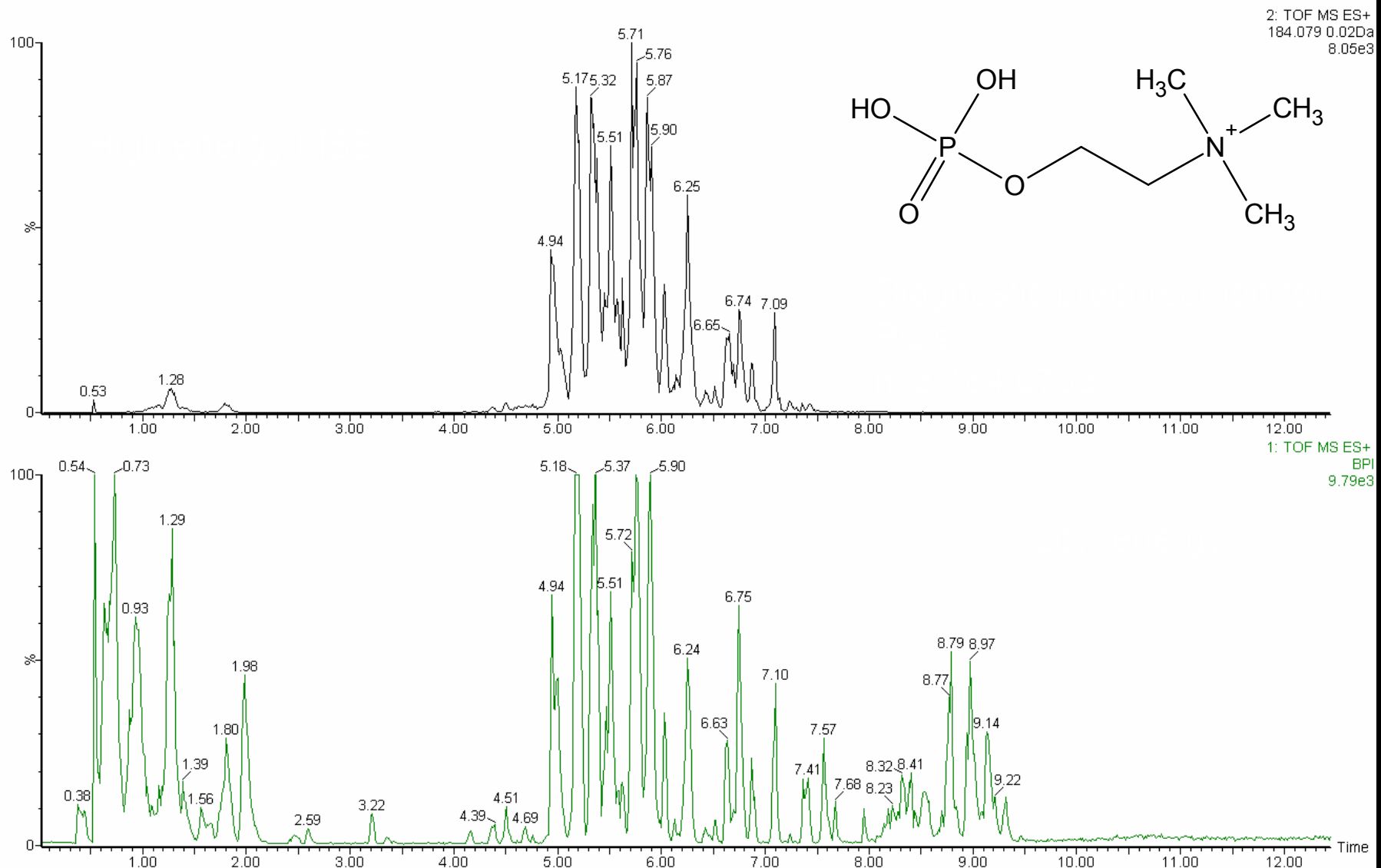
# UPLC-TOF MS Analysis for Lipids and TAG's

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# MS<sup>E</sup> analysis for Lipids and TAG's showing polar head group for PC's

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# Phosphocholine Structures

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Molecular Weight: 786.130

Molecular Weight (Exact Mass): 785.593

Molecular Formula:  $C_{44}H_{84}NO_8P$

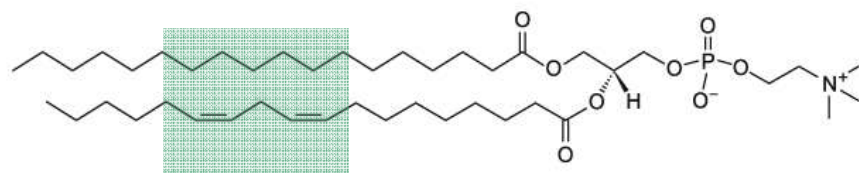
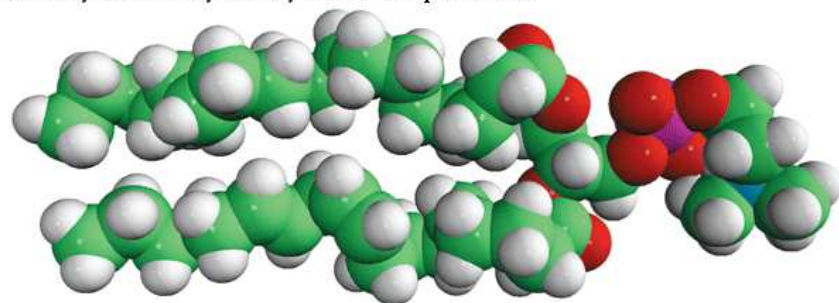
Molecular Weight: 786.130

Molecular Weight (Exact Mass): 785.593

Molecular Formula:  $C_{44}H_{84}NO_8P$

18:0-18:2 PC

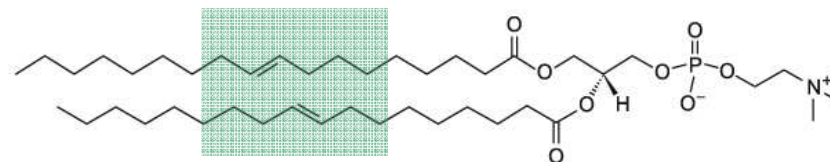
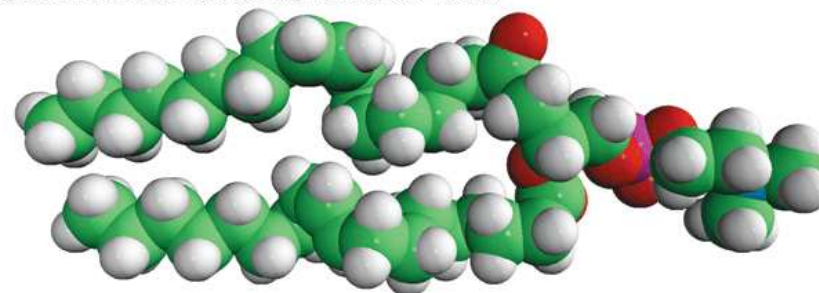
1-Stearoyl-2-Linoleoyl-*sn*-Glycero-3-Phosphocholine



18:0/18:2

18:1 Trans PC

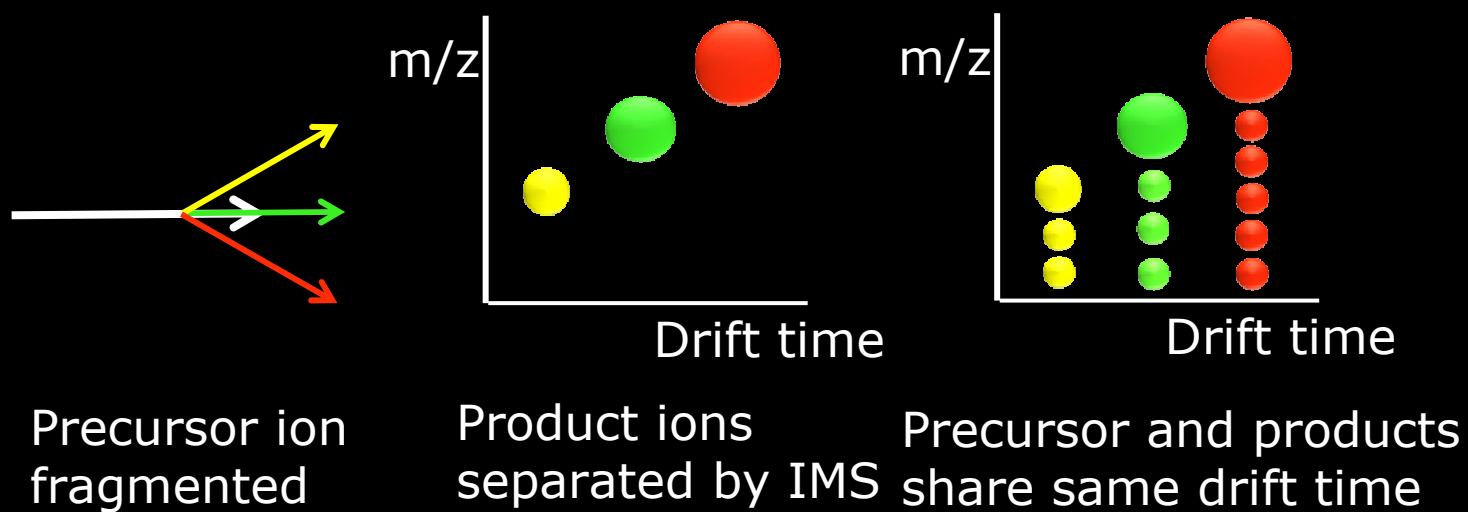
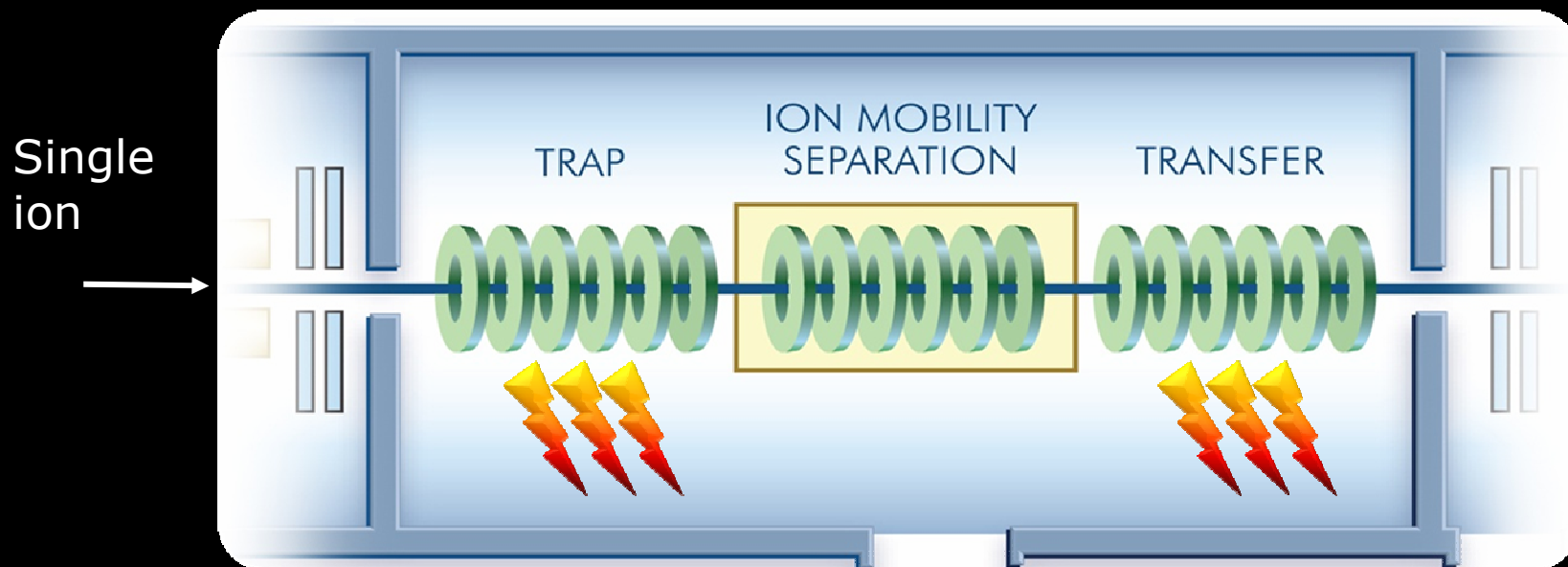
1,2-Dielaidoyl-*sn*-Glycero-3-Phosphocholine (Formerly 85T375)  
HYGROSCOPIC AS LYOPHILIZED POWDER



18:1/18:1

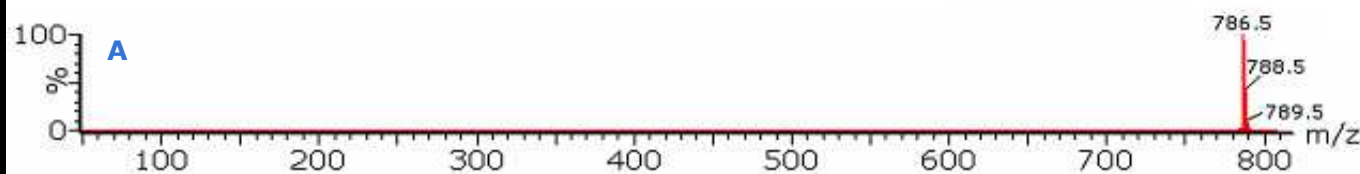
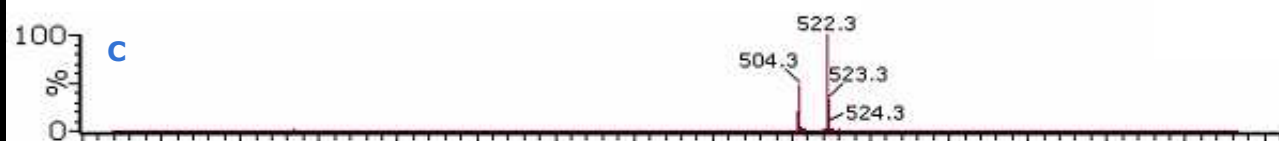
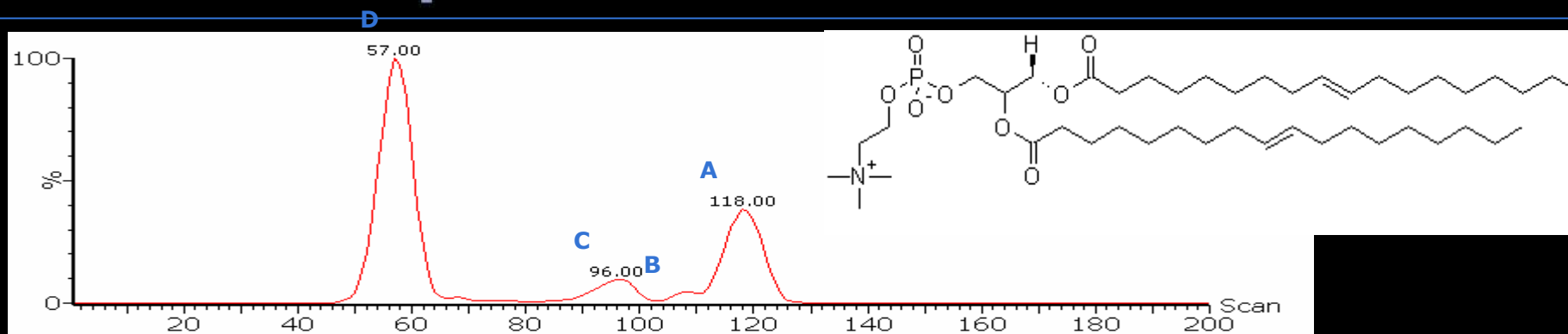
# Time Aligned Parallel Fragmentation (TAP) CID-IMS-CID

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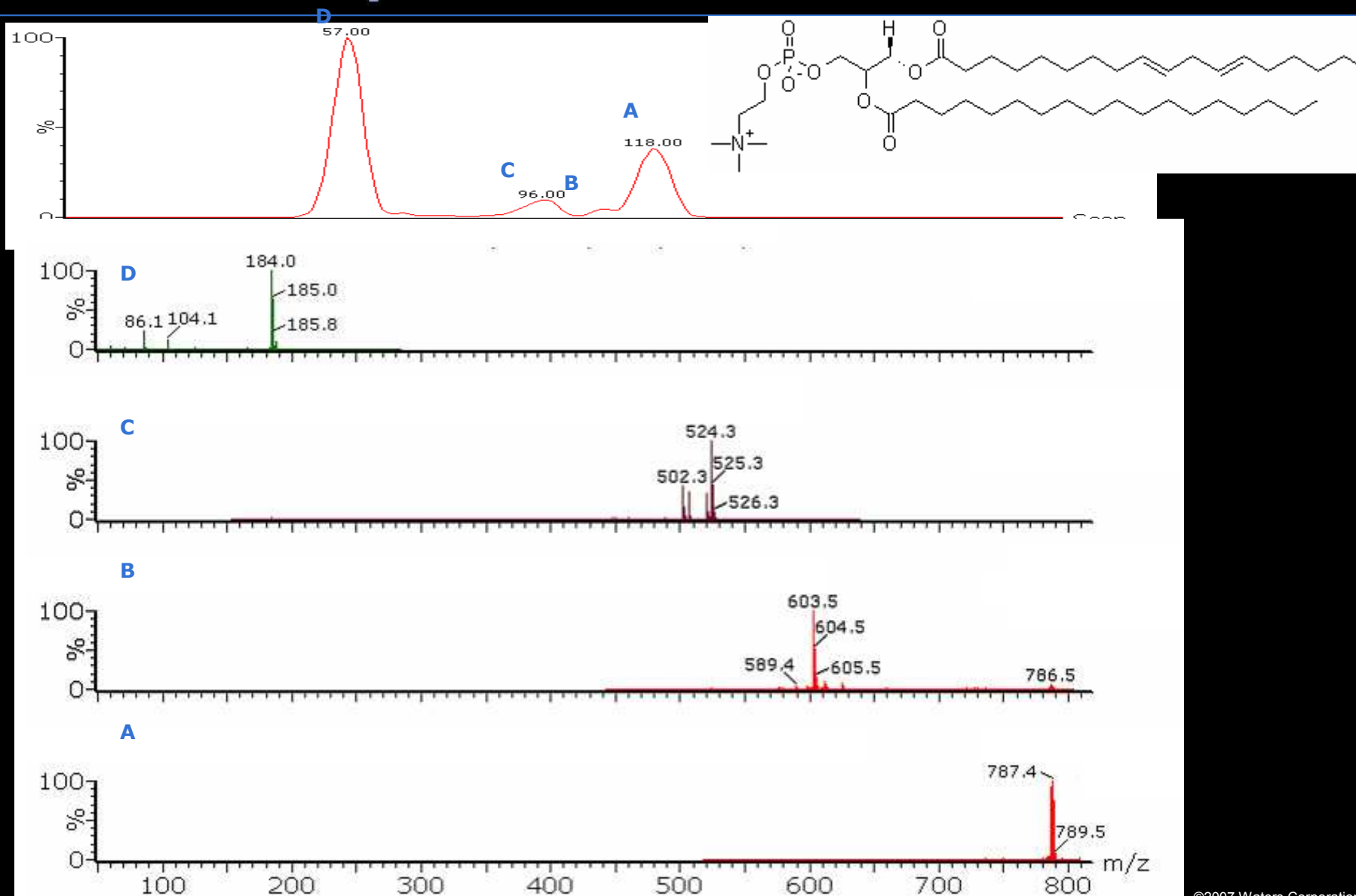
# Individual drift time spectra PC 18:1/18:1

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# Individual Drift time traces PC 18:0/18:2

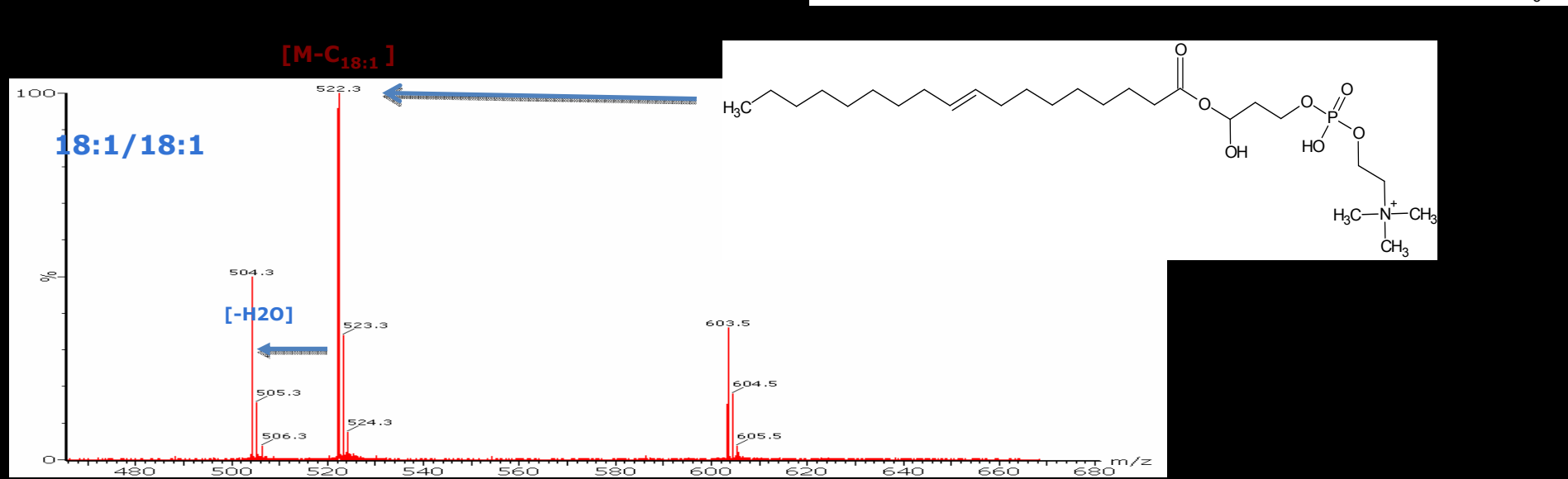
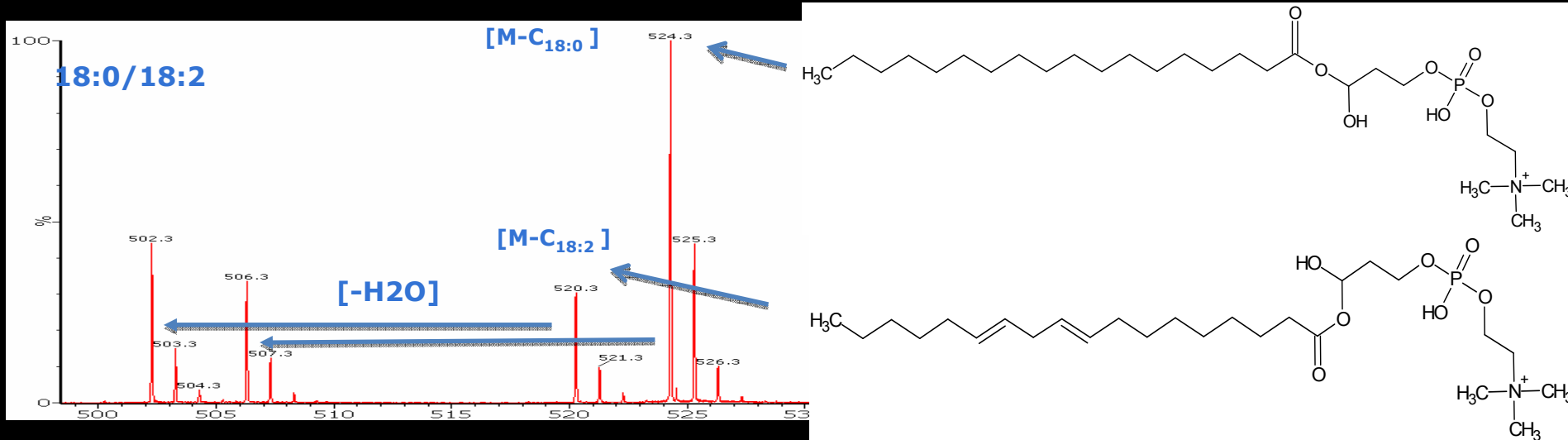
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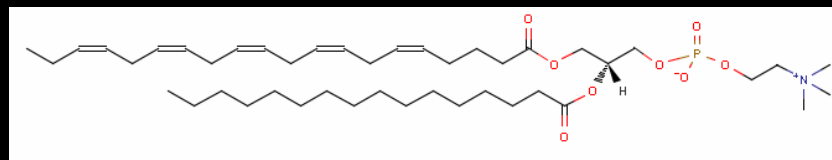
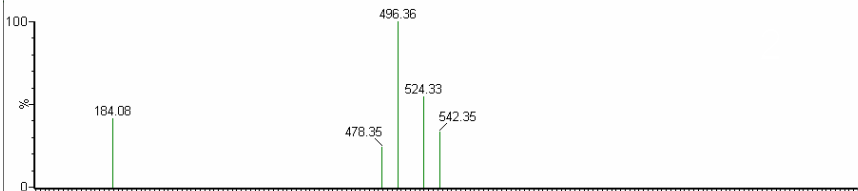
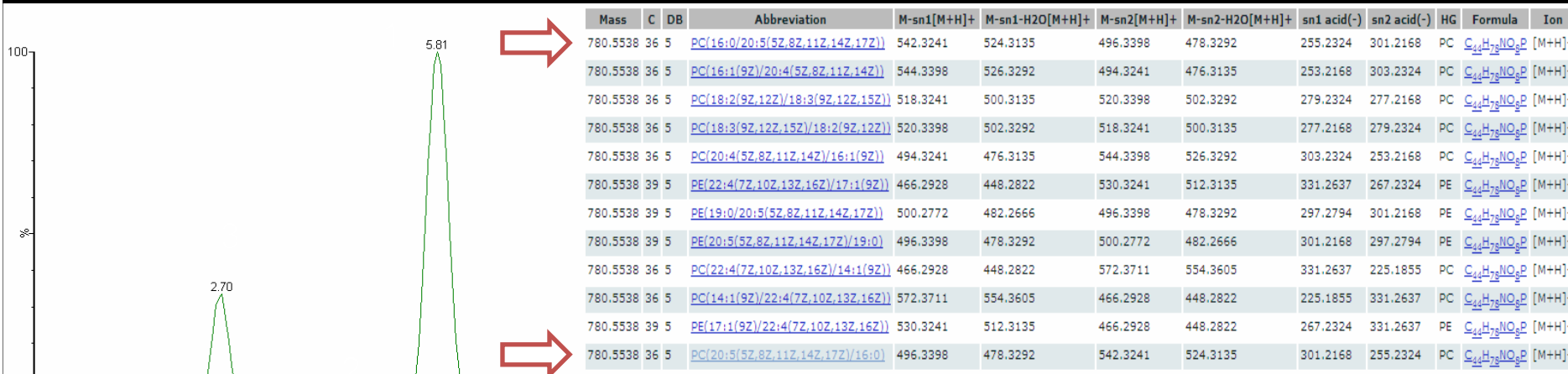
# PC 18:0/18:2 vs. PC 18:1/18:1 Fragmentation Differences

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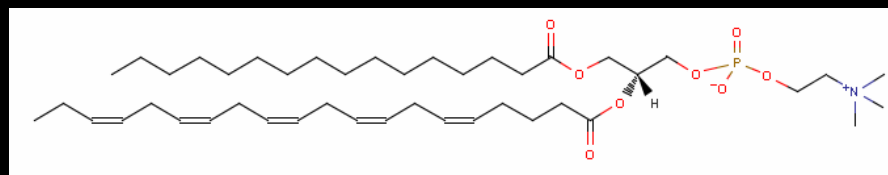


# TAP fragmentation results for m/z 780.5 (16:0/20:5)

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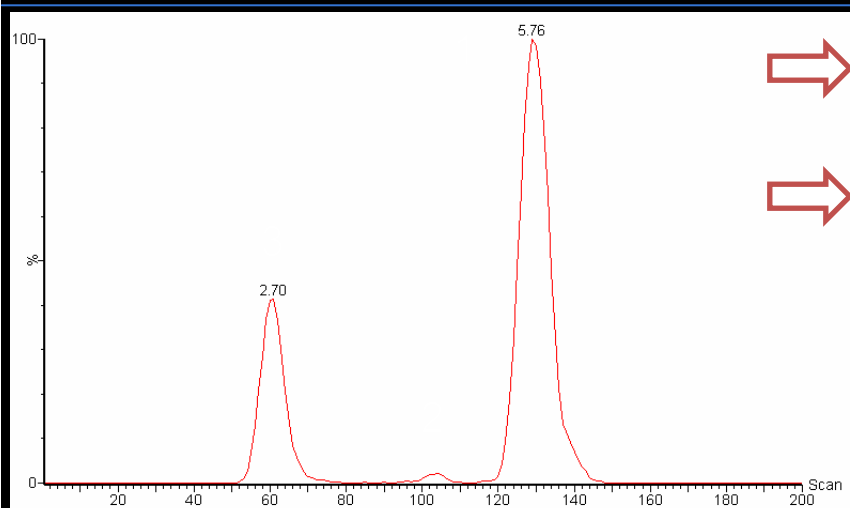


or

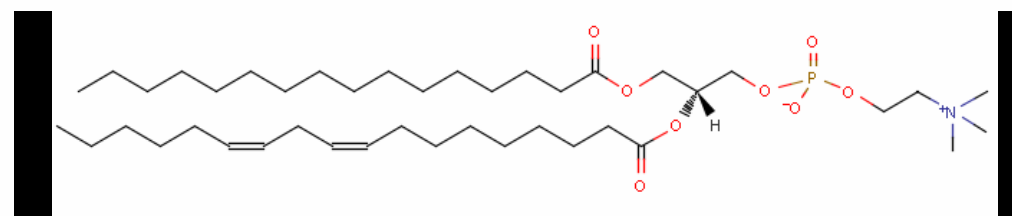
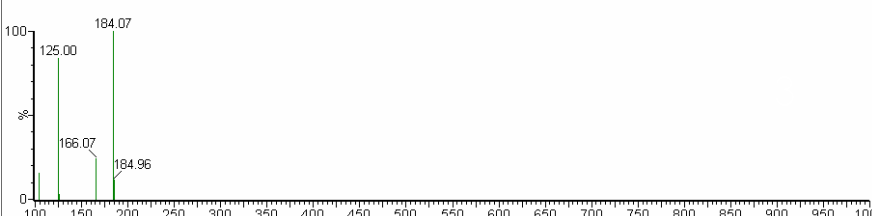


# TAP fragmentation results for m/z 758.5 PC(18:2/16:0)

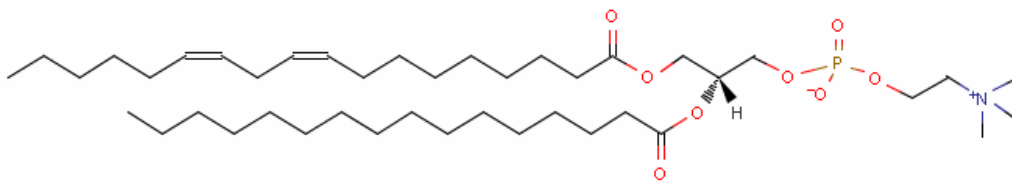
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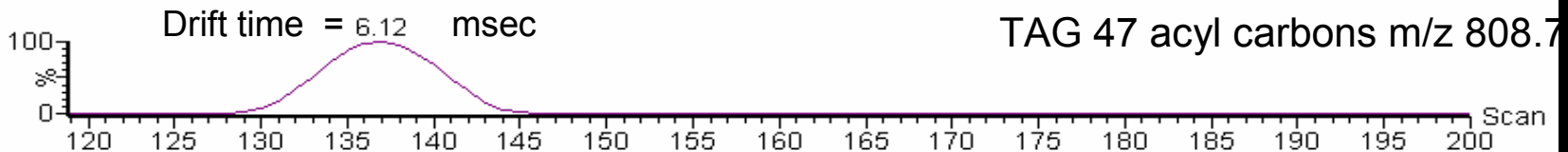
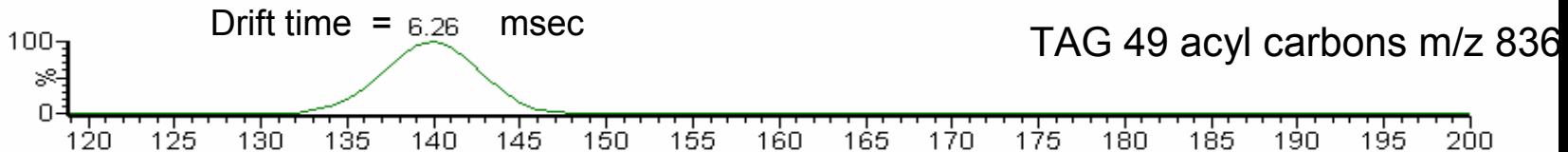
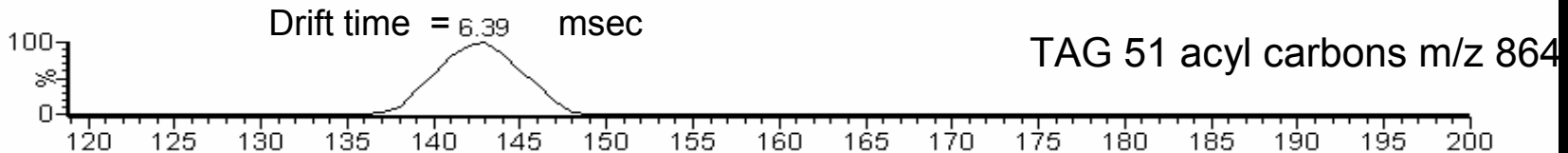
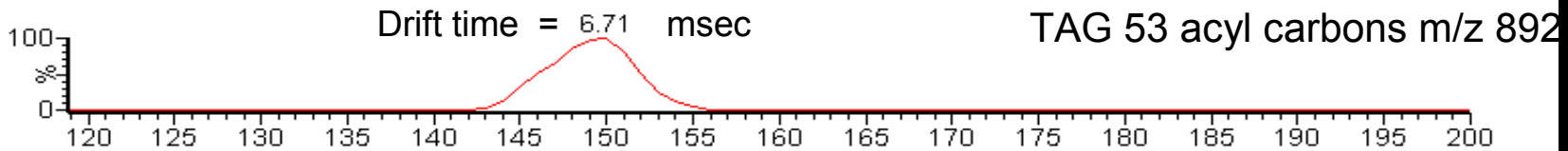
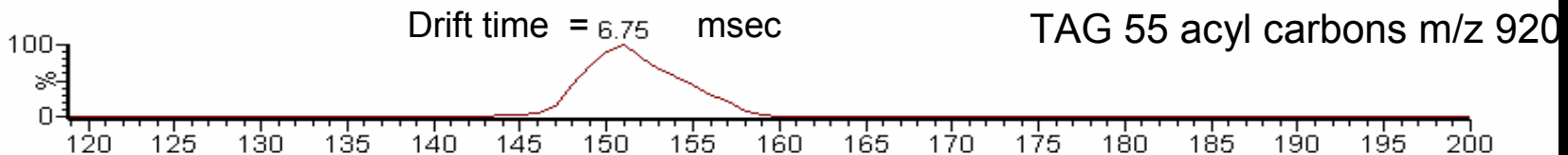
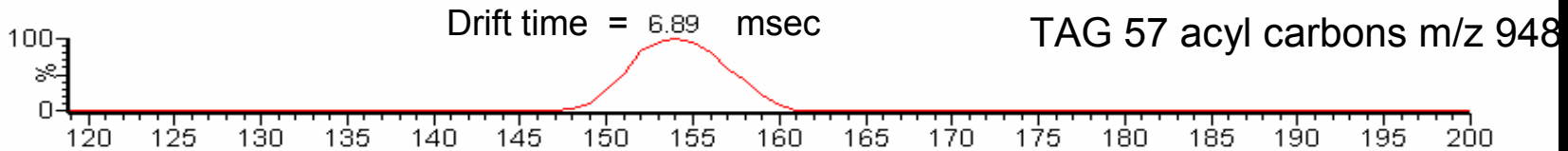
Mass	C	DB	Abbreviation	M-sn1[M+H] <sup>+</sup>	M-sn1-H2O[M+H] <sup>+</sup>	M-sn2[M+H] <sup>+</sup>	M-sn2-H2O[M+H] <sup>+</sup>	sn1 acid(-)	sn2 acid(-)	HG	Formula	Ion
758.5695	34	2	PC(12:0/22:2(13Z,16Z))	576.4024	558.3918	440.2772	422.2666	199.1698	335.295	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(20:1(11Z)/17:1(9Z))	466.2929	448.2823	508.3398	490.3292	309.2794	267.2324	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(16:0/18:2(9Z,12Z))	520.3398	502.3292	496.3398	478.3292	255.2324	279.2324	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(16:1(9Z)/18:1(9Z))	522.3555	504.3449	494.3242	476.3136	253.2168	281.2481	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(17:0/17:2(9Z,12Z))	506.3242	488.3136	510.3555	492.3449	269.2481	265.2168	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(17:2(9Z,12Z)/17:0)	510.3555	492.3449	506.3242	488.3136	265.2168	269.2481	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(18:1(9Z)/16:1(9Z))	494.3242	476.3136	522.3555	504.3449	281.2481	253.2168	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(18:2(9Z,12Z)/16:0)	496.3398	478.3292	520.3398	502.3292	279.2324	255.2324	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(20:2(11Z,14Z)/14:0)	468.3085	450.2979	548.3711	530.3605	307.2637	227.2011	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(22:2(19Z,16Z)/12:0)	440.2772	422.2666	576.4024	558.3918	335.295	199.1698	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(15:0/22:2(13Z,16Z))	534.3555	516.3449	440.2772	422.2666	241.2168	335.295	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(17:0/20:2(11Z,14Z))	506.3242	488.3136	468.3085	450.2979	269.2481	307.2637	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(17:2(9Z,12Z)/20:0)	510.3555	492.3449	464.2772	446.2666	265.2168	311.295	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(18:2(9Z,12Z)/19:0)	496.3398	478.3292	478.2929	460.2823	279.2324	297.2794	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(19:0/18:2(9Z,12Z))	478.2929	460.2823	496.3398	478.3292	297.2794	279.2324	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(20:0/17:2(9Z,12Z))	464.2772	446.2666	510.3555	492.3449	311.295	265.2168	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(22:2(19Z,16Z)/15:0)	440.2772	422.2666	534.3555	516.3449	335.295	241.2168	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(20:1(11Z)/14:1(9Z))	466.2929	448.2823	550.3868	532.3762	309.2794	225.1855	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(14:1(9Z)/20:1(11Z))	550.3868	532.3762	466.2929	448.2823	225.1855	309.2794	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(17:1(9Z)/17:1(9Z))	508.3398	490.3292	508.3398	490.3292	267.2324	267.2324	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	37	2	PE(17:1(9Z)/20:1(11Z))	508.3398	490.3292	466.2929	448.2823	267.2324	309.2794	PE	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(17:1(9Z)/17:1(9Z))	508.3398	490.3292	508.3398	490.3292	267.2324	267.2324	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>
758.5695	34	2	PC(14:0/20:2(11Z,14Z))	548.3711	530.3605	468.3085	450.2979	227.2011	307.2637	PC	C <sub>32</sub> H <sub>58</sub> NO <sub>6</sub> P	[M+H] <sup>+</sup>



or

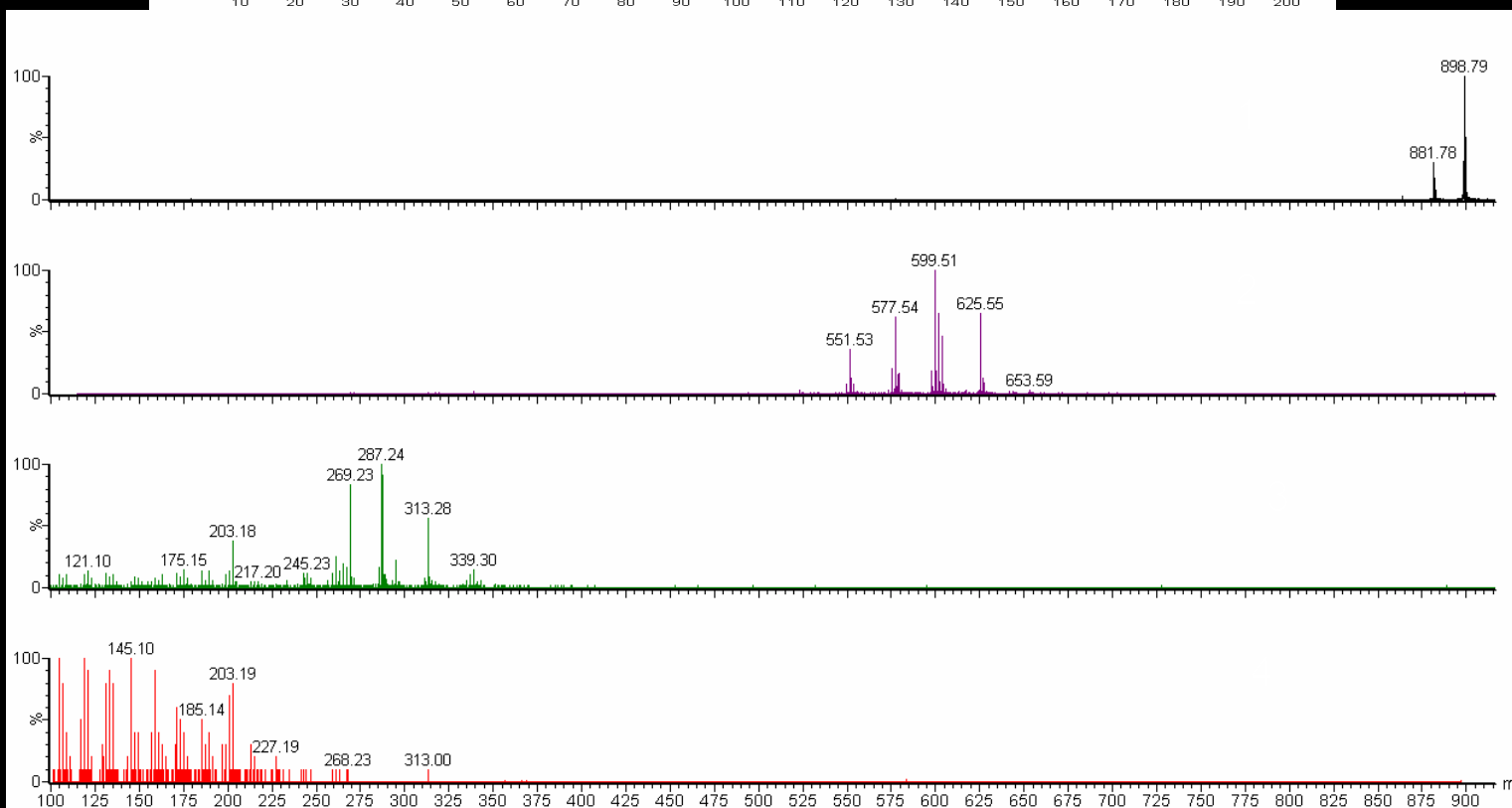
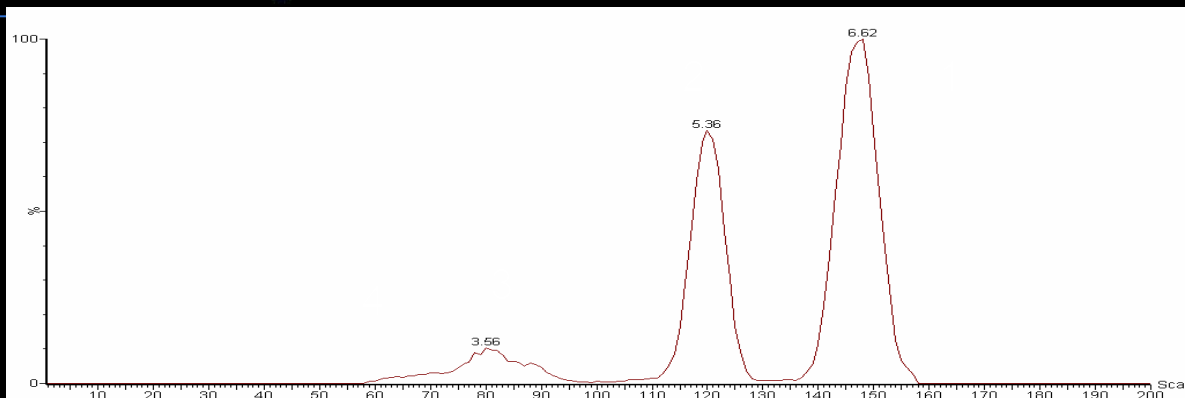


# Drift times for different TAG acyl carbon numbers



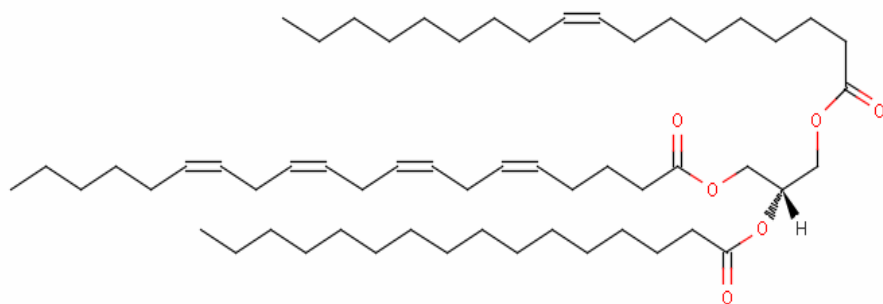
# TAP fragmentation results for m/z 898.8 TAG(54:5)

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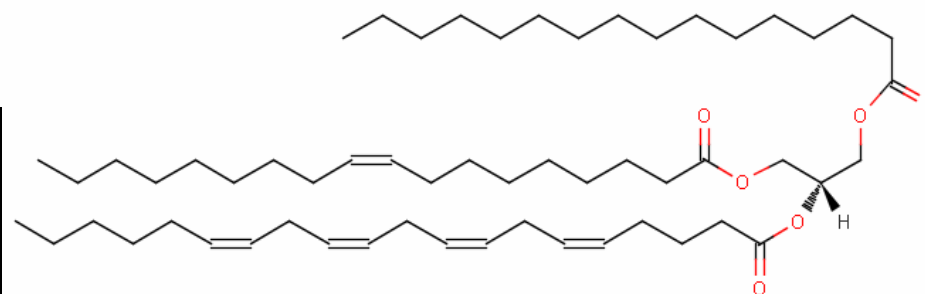


# 3 Possible structures for the TAG (54:5) 16:0/18:1/20:4

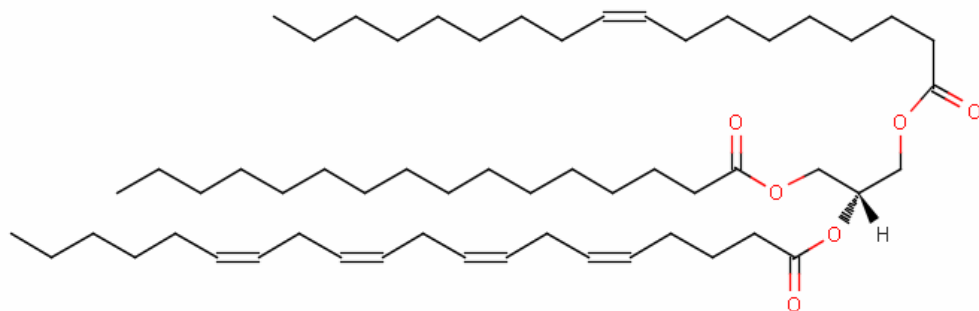
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**Abbreviation** TG(20:4(5Z,8Z,11Z,14Z)/16:0/18:1(9Z))  
**Systematic Name** 1-(5Z,8Z,11Z,14Z-eicosatetraenoyl)-2-hexadecanoyl-3-(9Z-octadecenoyl)-sn-glycerol  
**Formula (Neutral)** C<sub>57</sub>H<sub>100</sub>O<sub>6</sub>  
**m/z** 881.7593  
**Ion** M+H



**Abbreviation** TG(18:1(9Z)/20:4(5Z,8Z,11Z,14Z)/16:0)  
**Systematic Name** 1-(9Z-octadecenoyl)-2-(5Z,8Z,11Z,14Z-eicosatetraenoyl)-3-hexadecanoyl-sn-glycerol  
**Formula (Neutral)** C<sub>57</sub>H<sub>100</sub>O<sub>6</sub>  
**m/z** 881.7593  
**Ion** M+H

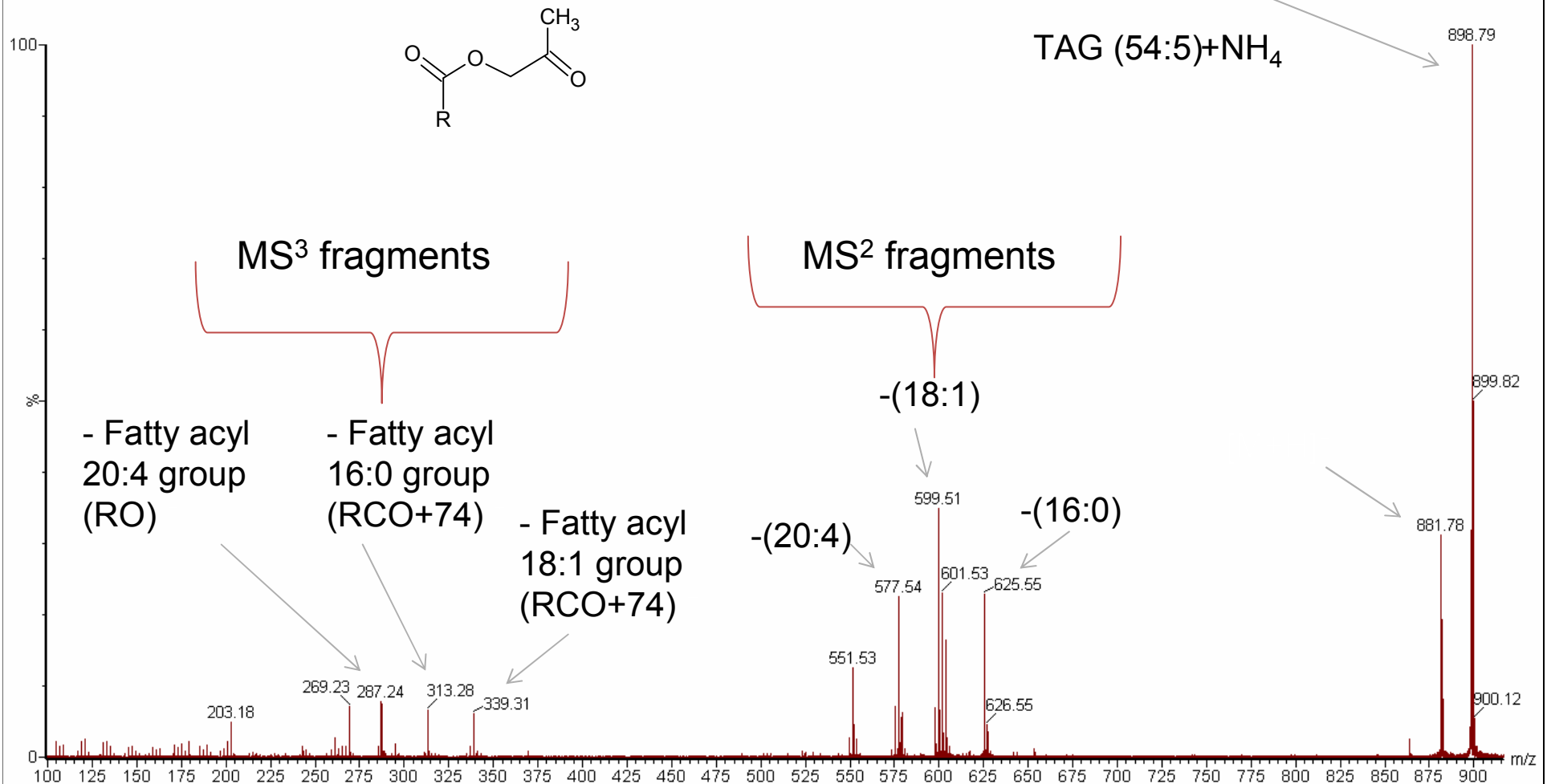


**Abbreviation** TG(16:0/20:4(5Z,8Z,11Z,14Z)/18:1(9Z))  
**Systematic Name** 1-hexadecanoyl-2-(5Z,8Z,11Z,14Z-eicosatetraenoyl)-3-(9Z-octadecenoyl)-sn-glycerol  
**Formula (Neutral)** C<sub>57</sub>H<sub>100</sub>O<sub>6</sub>  
**m/z** 881.7593  
**Ion** M+H

# TAP fragmentation results for m/z 898.8 TAG(54:5)

(RCO+74)<sup>+</sup> MS<sup>3</sup> fragment ion

[M+NH<sub>4</sub>]<sup>+</sup>



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- Kathie Knights Flinders U.
- John Miners Flinders U.
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