

Untangling the Complexity within Oligonucleotide Therapeutics

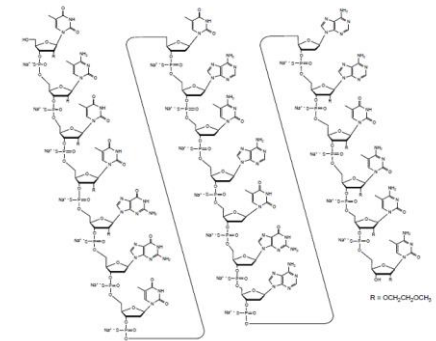
WCBP 2024

25-January-2024

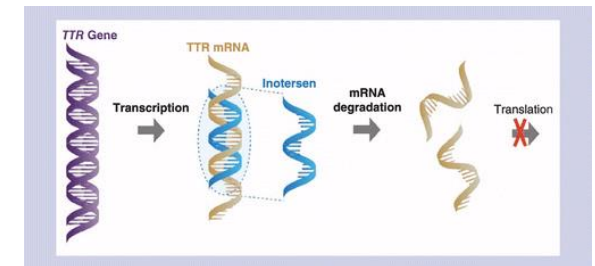
Jace W. Jones, Ph.D.

Department of Pharmaceutical Sciences
School of Pharmacy, University of Maryland

The use of mass spectrometry to determine oligonucleotide structure



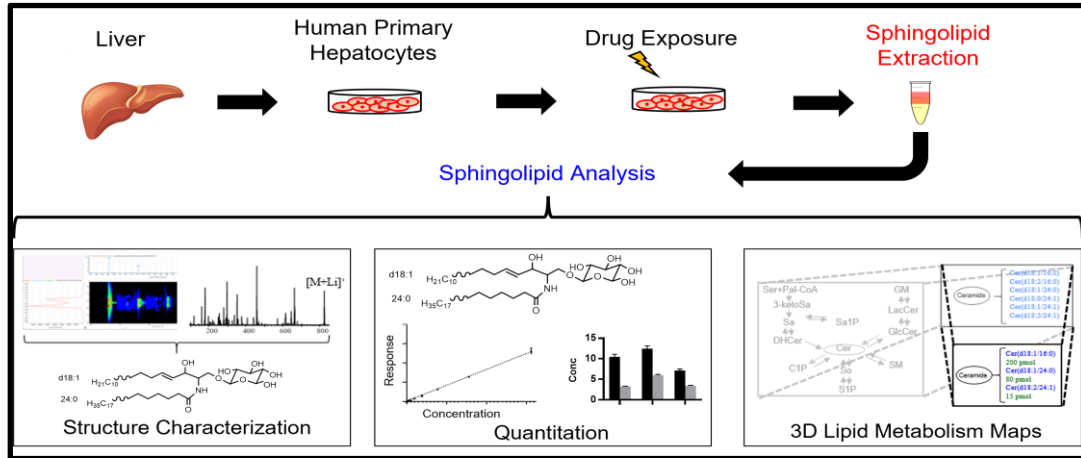
Frederick S. Brundick/cc-2.0/<https://flic.kr/p/29umt8b>



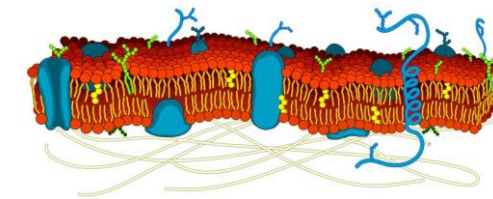
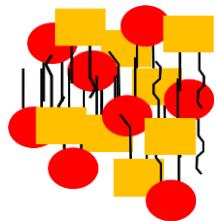
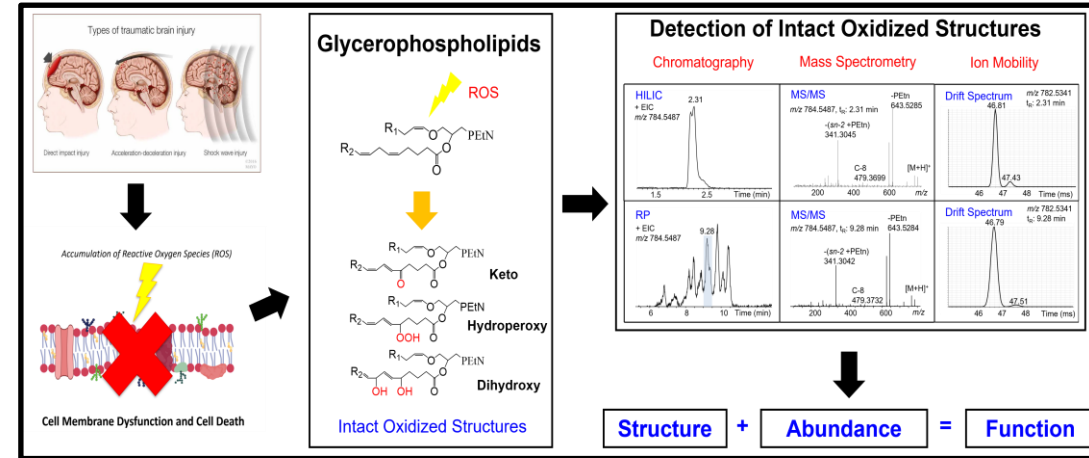
<https://www.futuremedicine.com/doi/10.2217/nmt-2018-0037>

The use of mass spectrometry to determine lipid structure and abundance

Spingolipid Metabolism as a Molecular Marker



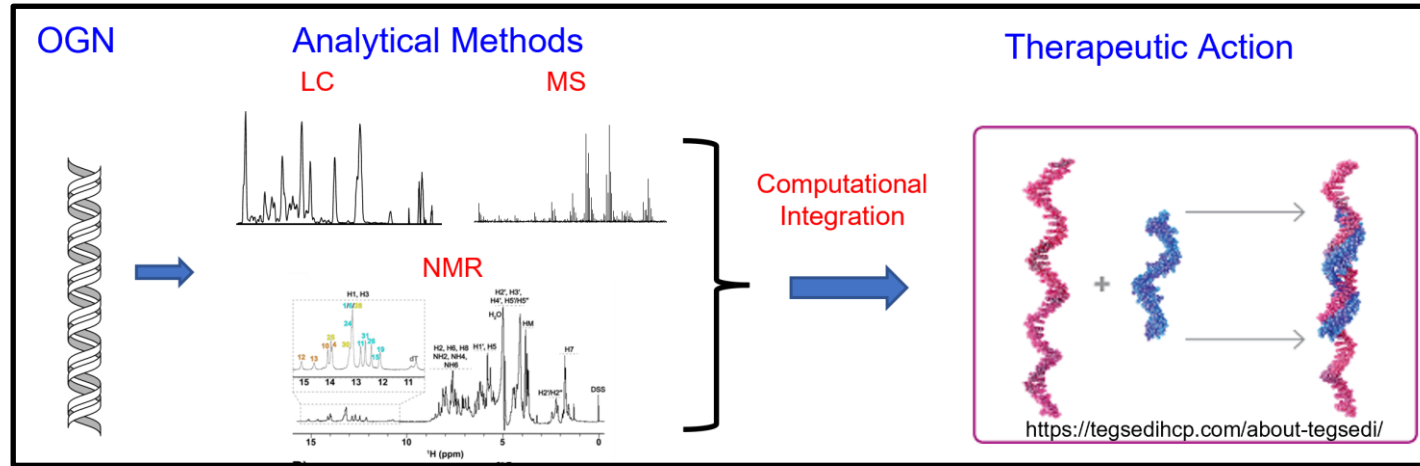
Phospholipid Oxidation Susceptibility Following Lipid Peroxidation



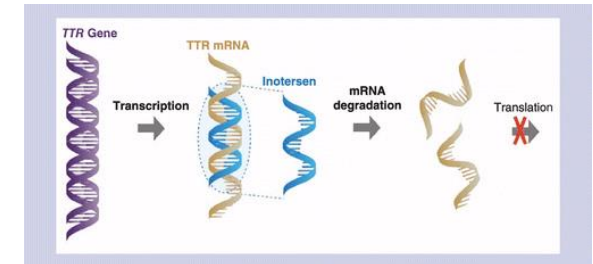
<https://biologydictionary.net/lipid-bilayer/>

The use of mass spectrometry to determine oligonucleotide structure

Oligonucleotide Therapeutics

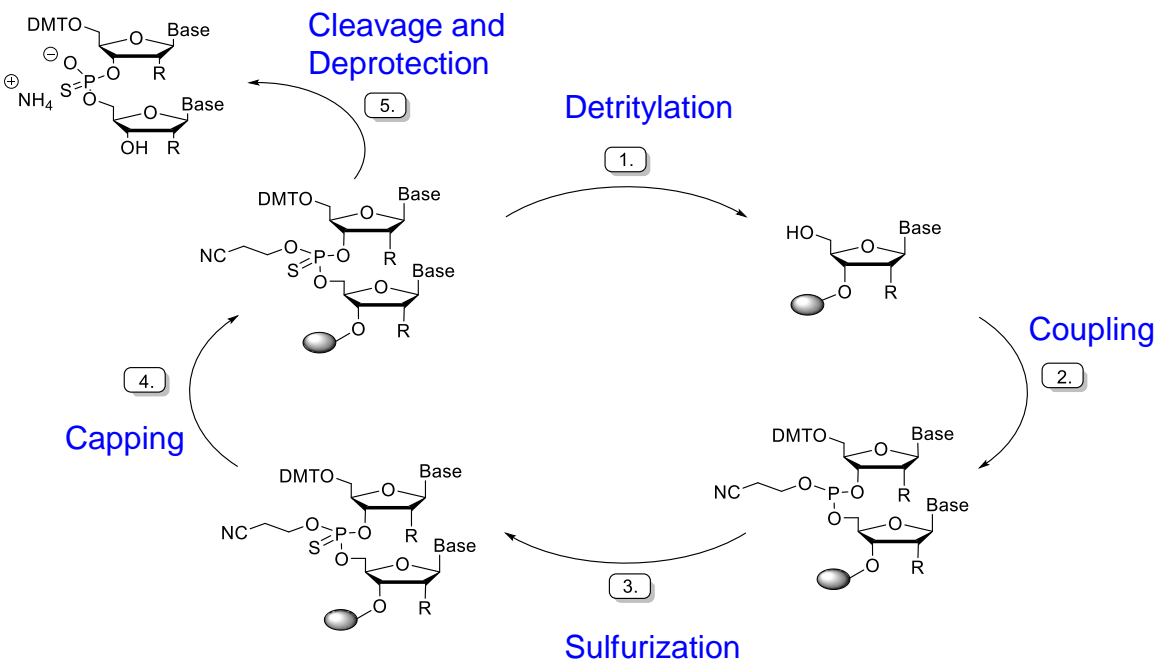


Frederick S. Brundick/cc-2.0/<https://flic.kr/p/29umt8b>



<https://www.futuremedicine.com/doi/10.2217/nmt-2018-0037>

Chemical Synthesis of Oligonucleotides



Chemical Modifications:

- Sugar modifications
 - O-Me, MOE, F
- Base modifications
 - 5-methylcytosine
- Conjugates (GalNAc)
- Backbone modifications
 - Phosphorothioate (PS)

Impurities:

- Acetylation byproducts
- Truncations/Failed Sequences
- Incomplete deprotection
- Incomplete thiolation
- Deamination, Depurination

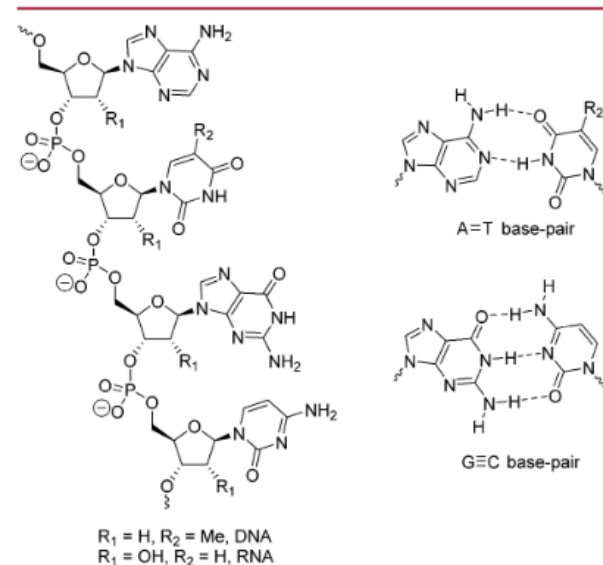


Figure 1. Structure of DNA and RNA and Watson–Crick base pairing.

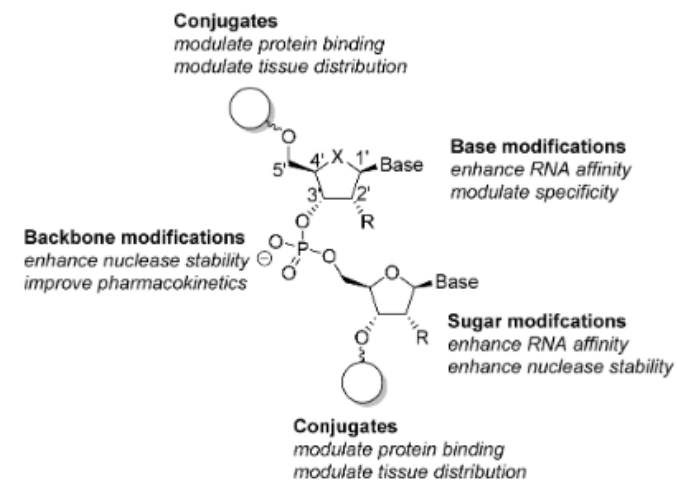


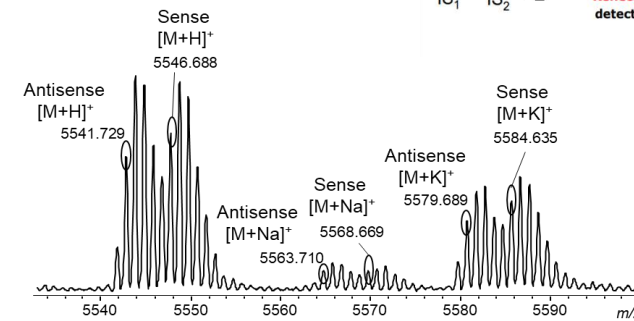
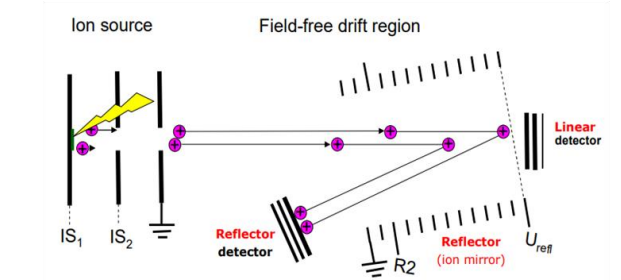
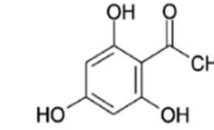
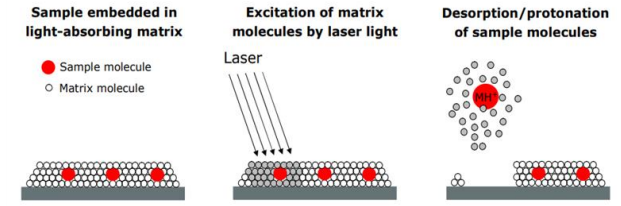
Figure 2. Sites for modification on a dinucleotide subunit.

Use of Mass Spec is Complementary to NMR Structural Fingerprinting

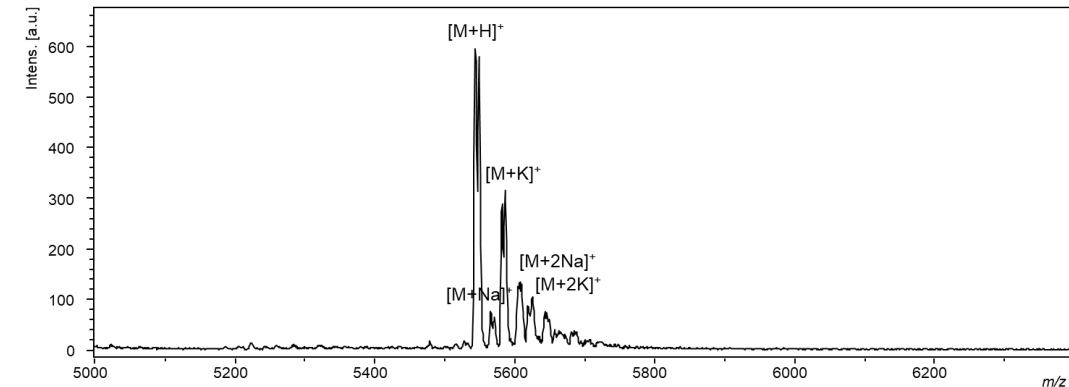
MALDI TOF Mass Spectrometry



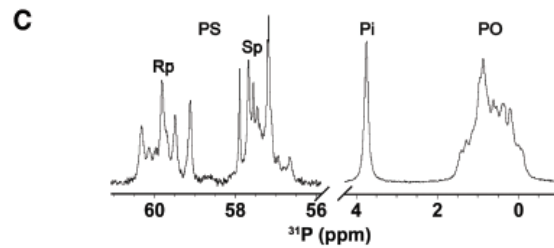
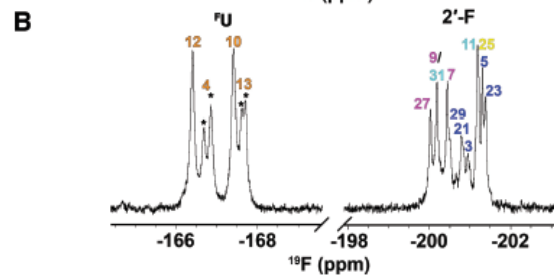
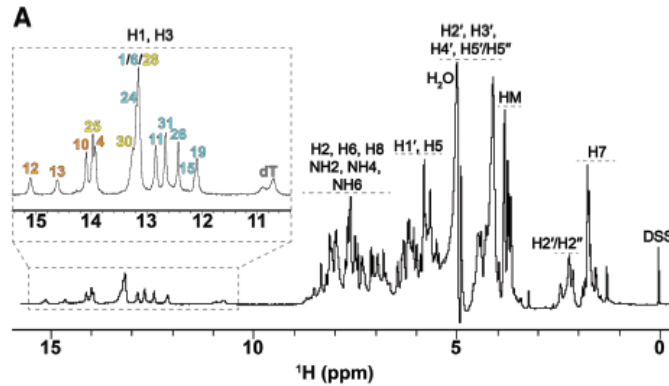
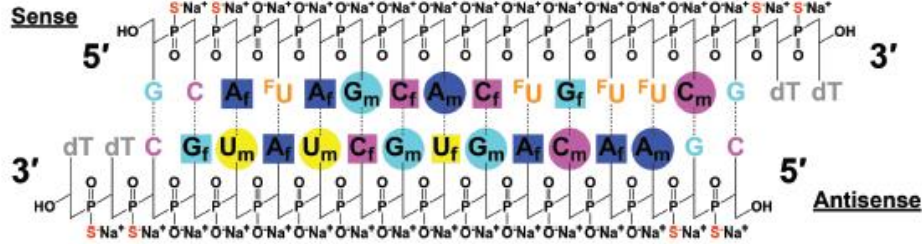
Robert Brinson, Ph.D.
NIST, IBBR



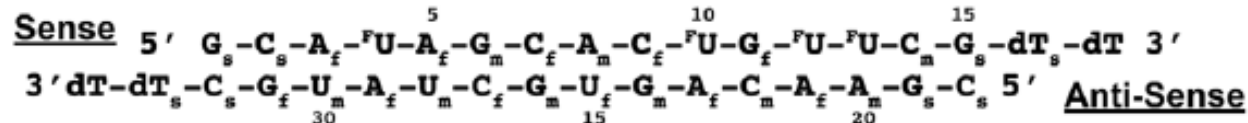
	Adduct	Theoretical m/z	Experimental m/z	mass error (mmu)
Antisense Strand	[M+H] ⁺	5541.761	5541.729	32.0
	[M+Na] ⁺	5563.743	5563.710	32.9
	[M+K] ⁺	5579.717	5579.689	27.8
Sense Strand	[M+H] ⁺	5546.653	5546.688	34.6
	[M+Na] ⁺	5568.635	5568.669	33.6
	[M+K] ⁺	5584.609	5584.635	25.7



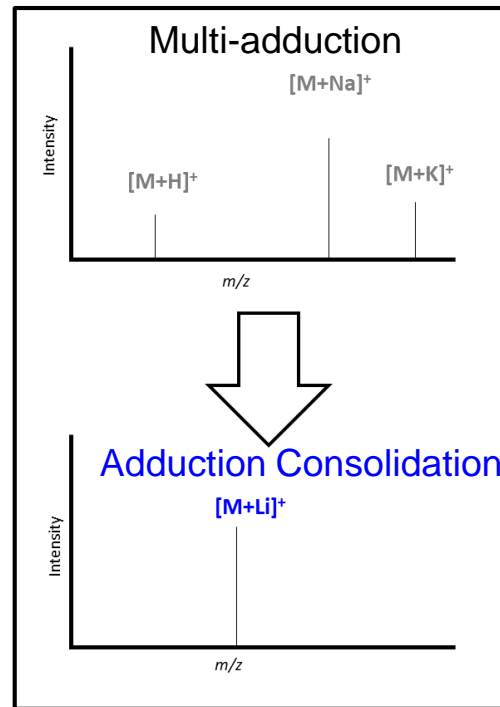
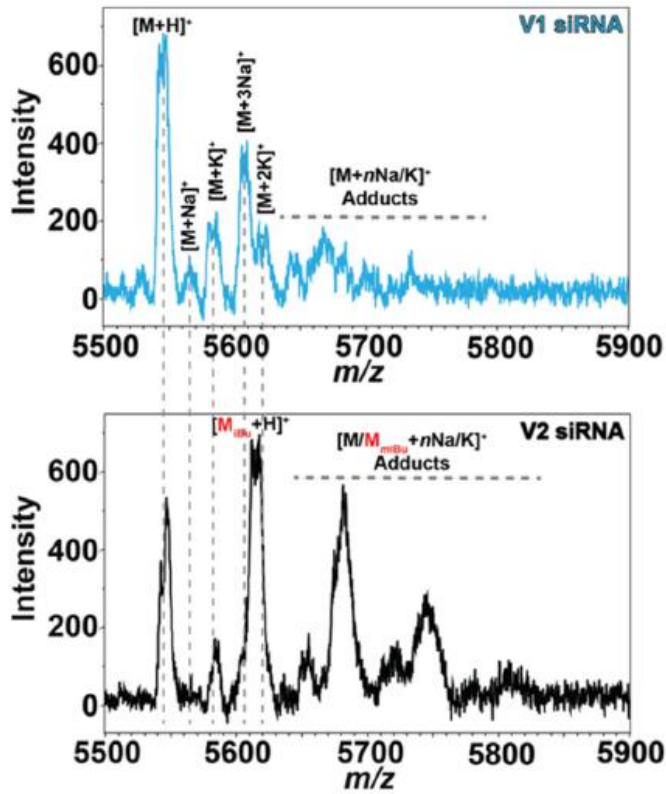
Model siRNA



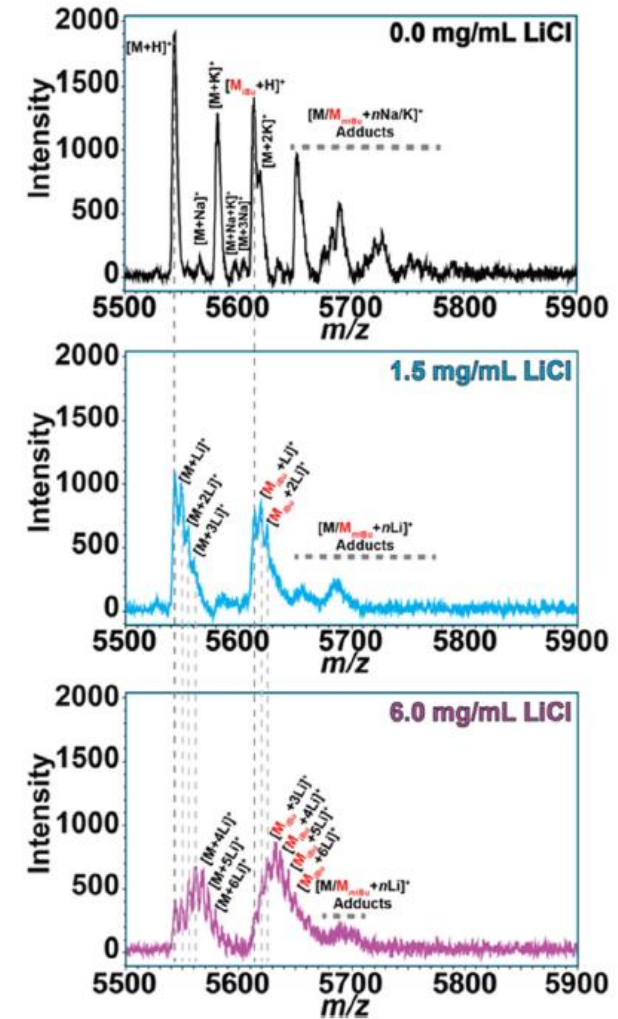
Use of Mass Spec to detect OGN Impurities



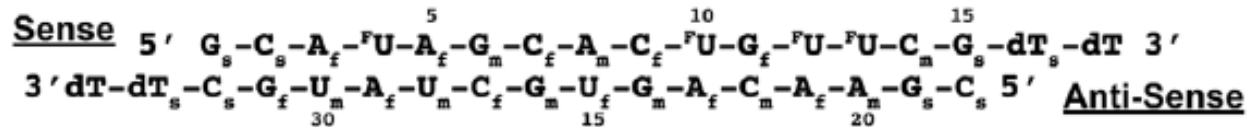
A = adenosine C = cytidine G = guanosine U = uridine dT = deoxythymidine
 s = phosphorothioate linkage f = 2'-fluoro m = 2'-O-methyl F = 5-fluoro



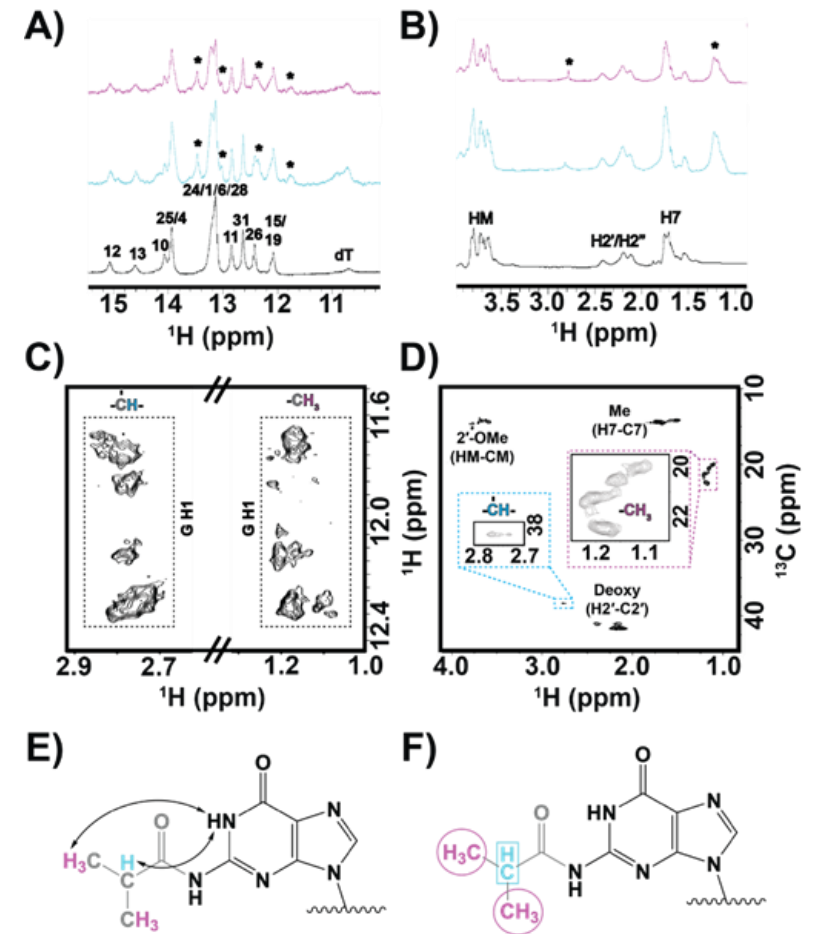
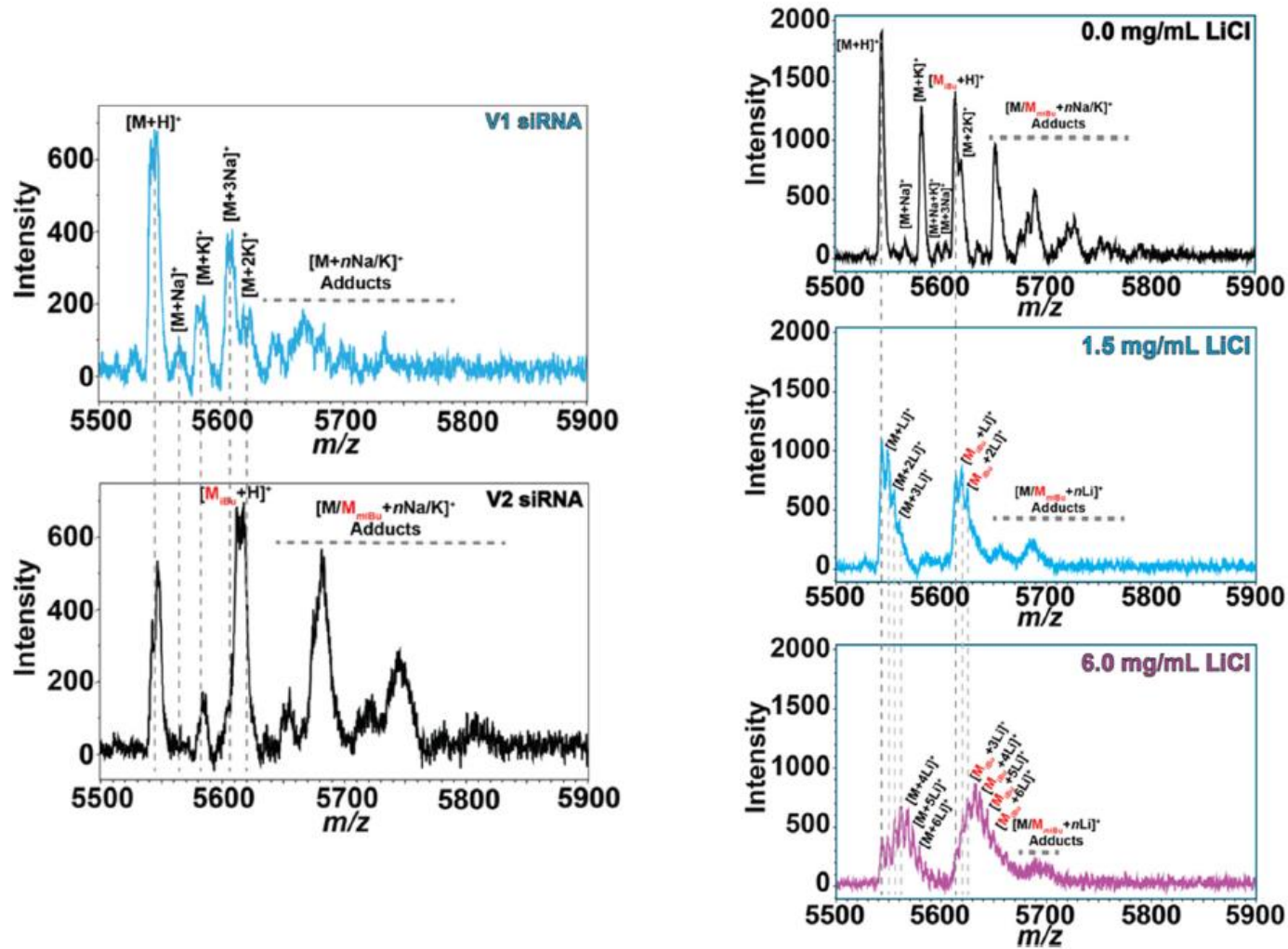
A Tran et al *JASMS*. 2021 Sep 1;32(9):2322-2333.
 A Tran et al *JASMS*. 2021 Jan 6;32(1):289-300.



Use of Mass Spec to detect OGN Impurities

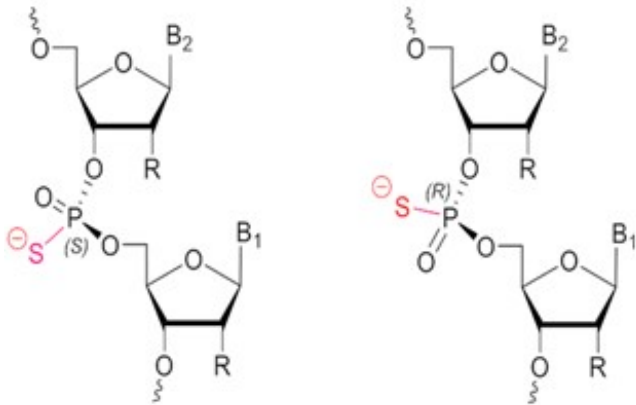
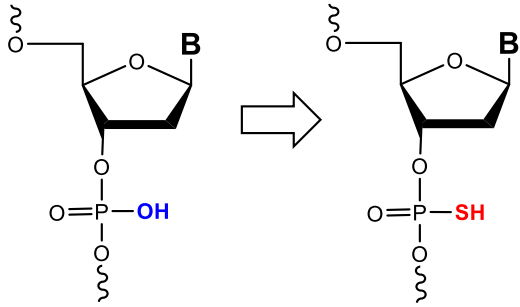


A = adenosine C = cytidine G = guanosine U = uridine dT = deoxythymidine
 s = phosphorothioate linkage f = 2'-fluoro m = 2'-O-methyl F = 5-fluoro



Multidimensional Approach to Characterize the Diastereomers of OGN

Phosphorothioate (PS) linkages



- PS linkage confers nuclease resistance and enhances protein binding
- PS linkage introduces chiral center
- Creates 2ⁿ diastereomers (n is the number of PS linkages)
- A 20-mer potentially yields 2¹⁹ (524,288) possible stereoisomers
- PS stereoisomer mixtures potentially alter the pharmacological effects
- Adversely impact active ingredient sameness and bioequivalence

Reference Listed Drug (RLD)

- TEGSEDI (inotersen)
 - Used to treat polyneuropathy (nerve disease) of hereditary transthyretin-mediated amyloidosis
 - 20-mer Antisense Oligonucleotide (ASO)
 - FDA approved 2018 (first-in-class medication)

Key Objective:

- To develop a high-resolution analytical method for sensitive and robust determination of diastereomer composition in PS OGNs

Approach

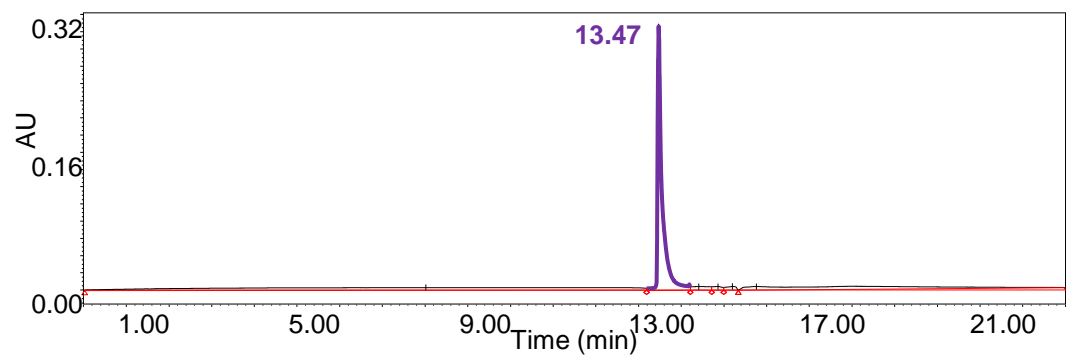
- Chemical synthesis of inotersen using different chemistries and computational integration of LC, MS, and NMR data
- Chemical synthesis (Fletcher Lab)
- Analytical Chemistry (LC, MS, NMR) (Jones and Brinson Labs)
- Computational Integration (Cummings Lab)

Outcome

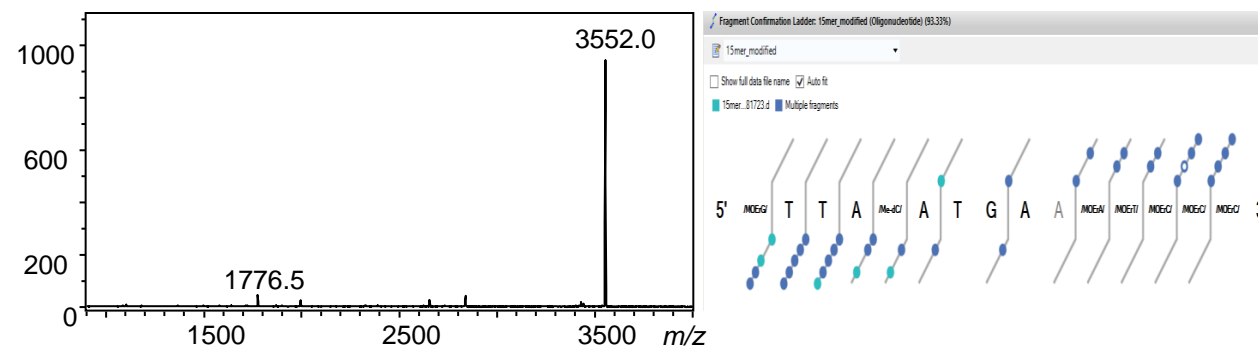
- Establish PS diastereomer composition as a well-defined chemical marker for ASO quality control

Synthesis and Product Characterization

Liquid Chromatography

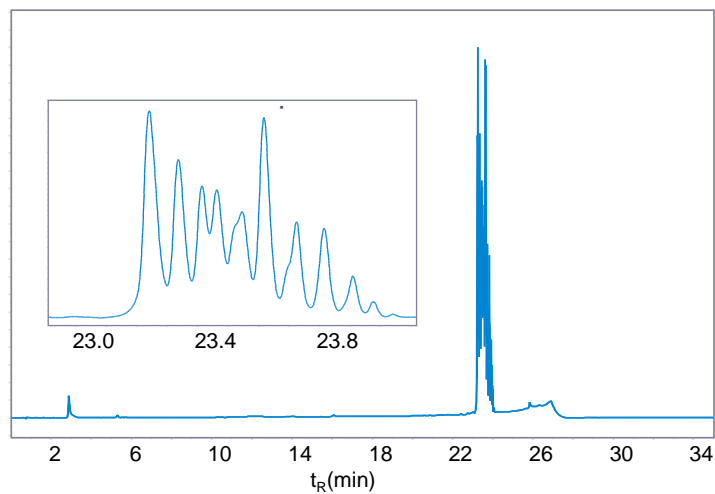


Mass Spectrometry

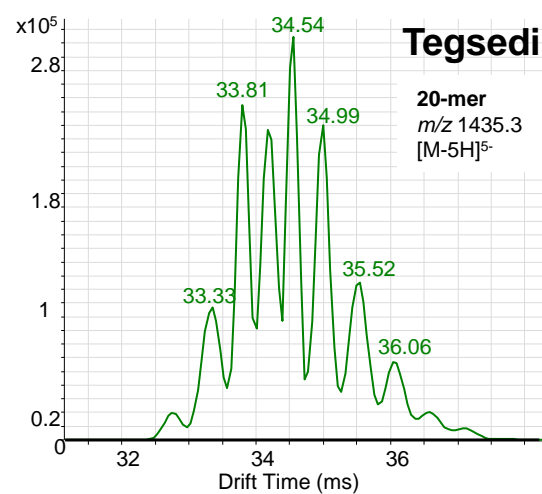


Diastereomer Composition Characterization

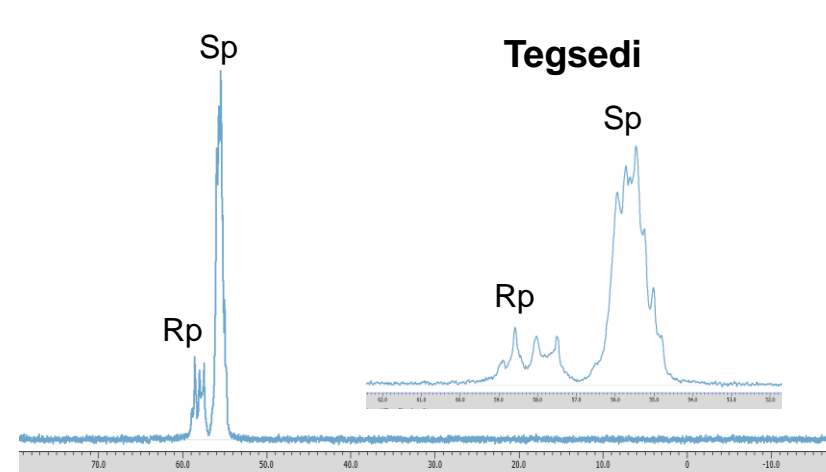
Liquid Chromatography



Ion Mobility



^{31}P NMR



Synthesis and Product Characterization

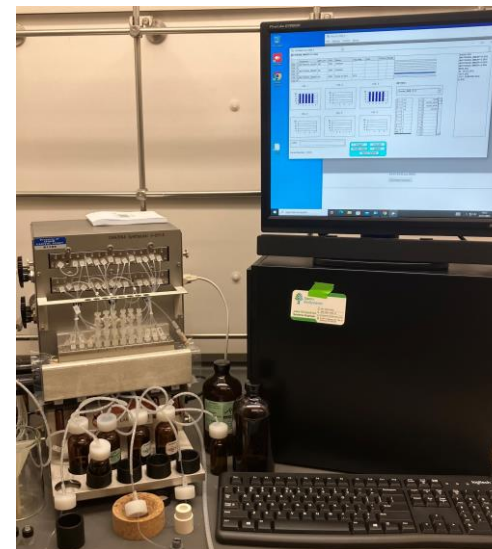
Inotersen:

- Synthetic 20-mer ASO, all PS linkages (19)
- 2'-MOE modifications at positions 1–5 and 15–20
- All C modified with 5-methyl group
- T*MC*T*T*G*G*T*T*A*MC*A*T*G*A*A*A*T*MC*MC*MC
- Synthesize in-house to control chemistry (choice of activator)
- n=3 per sequence

Sequence #	Oligo length	Activator	# of PS linkages	# of potential Diastereomers
Sequence 1	2-mer	DCI	1	2
	5-mer		4	16
	10-mer		9	512
	15-mer		14	16384
	20-mer		19	524288
Sequence 2	2-mer	ETT	1	2
	5-mer		4	16
	10-mer		9	512
	15-mer		14	16384
	20-mer		19	524288

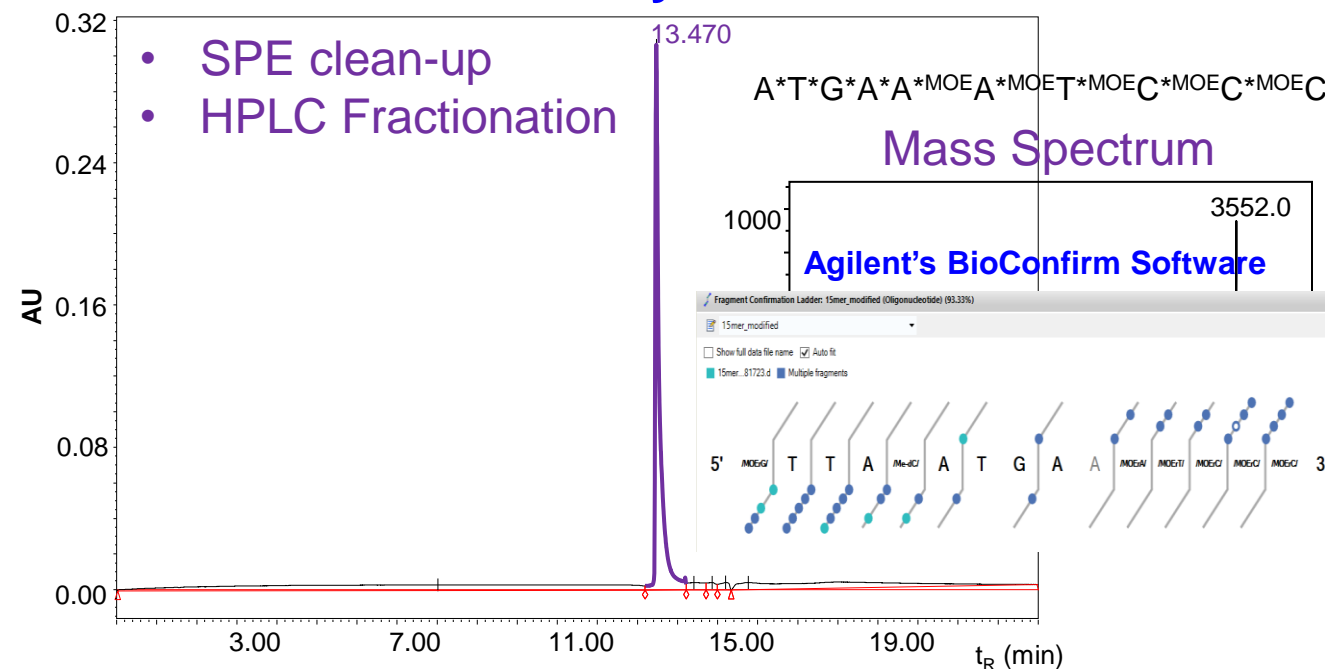
Note, additional sequences including RLD and other sequences were purchased from vendors.

DCI: 4,5-dicyanoimidazole
ETT: 5-(ethylthio)-1H-tetrazole



Steven Fletcher, Ph.D.
UMB SOP

In-house Synthesis



Liquid Chromatography: Analytical Separations

Collaboration with Agilent (Graham Robinett)

- 1290 Infinity Bio LC System



Triethyl:

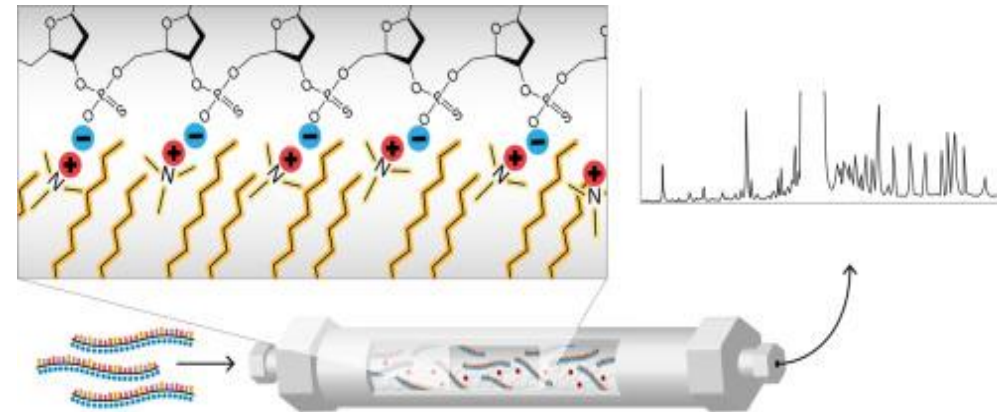
CC)

graphy (HILIC)

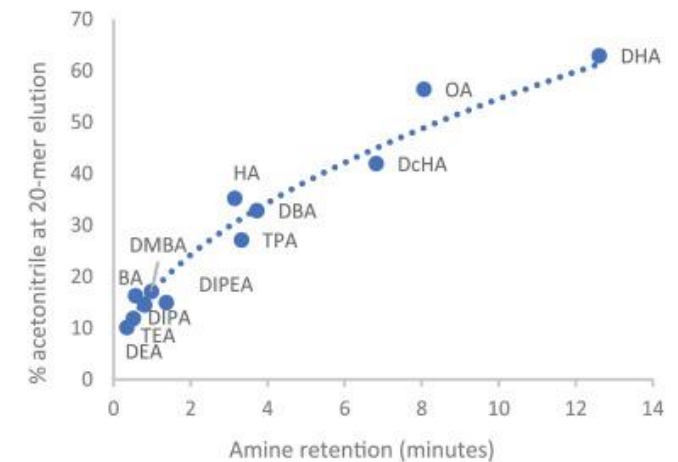
g reagent,
c OGNs to

resolution
adjusted to

such as
tion when



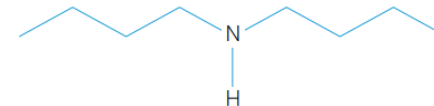
OGNs interact with the stationary phase on which ion-pairing reagents are adsorbed and result is chromatographic separation



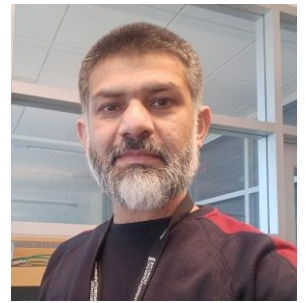
Correlation between alkyl amine retention time and the concentration of acetonitrile (20-mer)

amine (HA)

Dibutylamine (DBA)



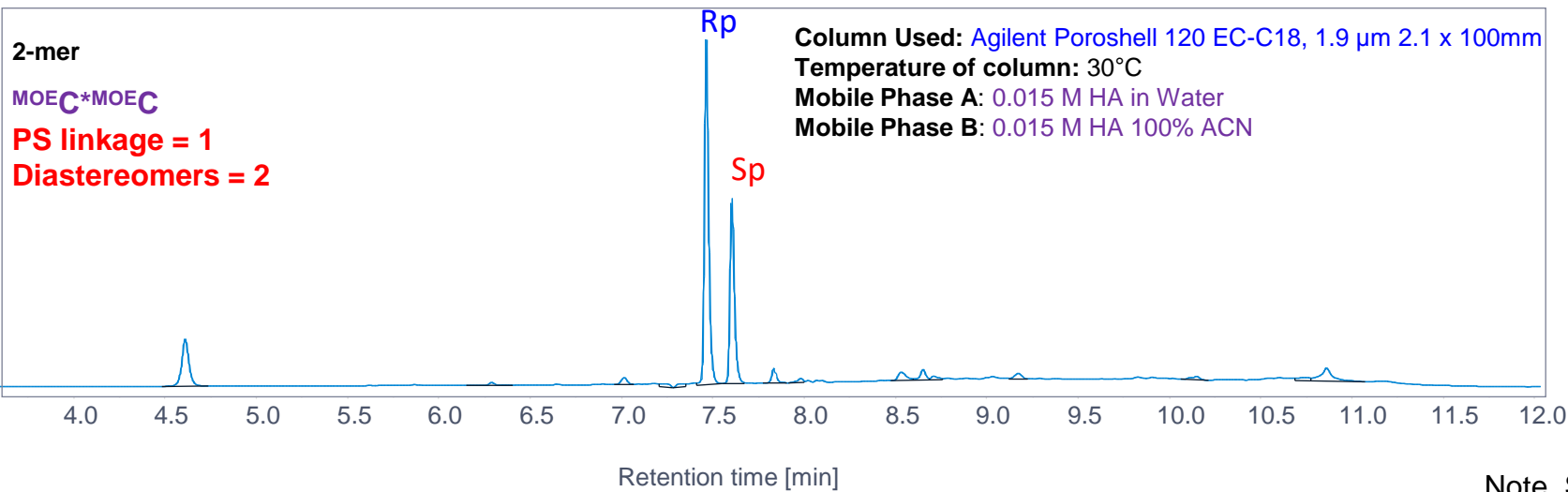
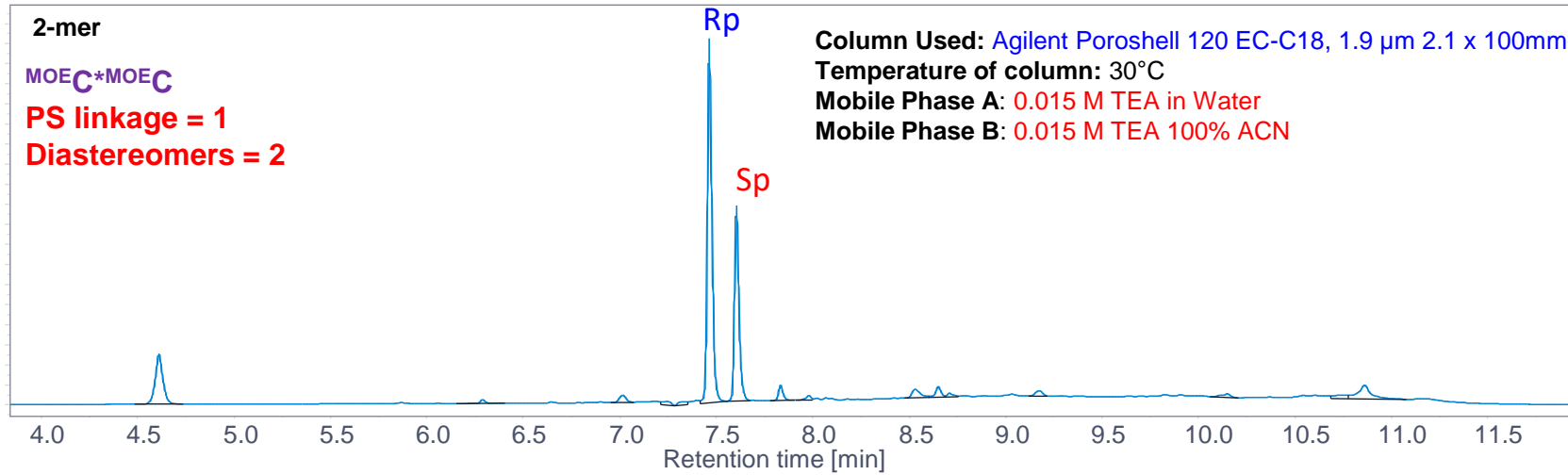
In-house 2-mer IP-RP chromatography



Mohsin Ali, Ph.D.



Padmapriya Sridhar



Time [min]	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00	95.00	5.00	0.400	1300.00
2.00	95.00	5.00	0.400	---
7.00	75.00	25.00	0.400	---
10.00	60.00	40.00	0.400	---
11.00	95.00	5.00	0.400	---
13.00	95.00	5.00	0.400	---

Note, SPE clean-up includes TFA to cleave DMT group

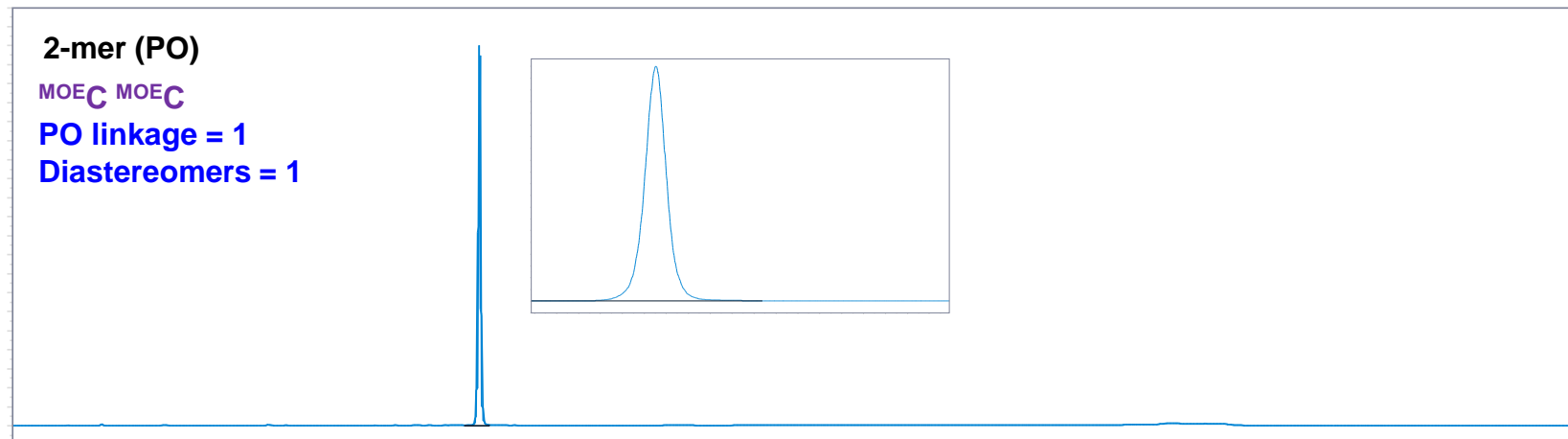
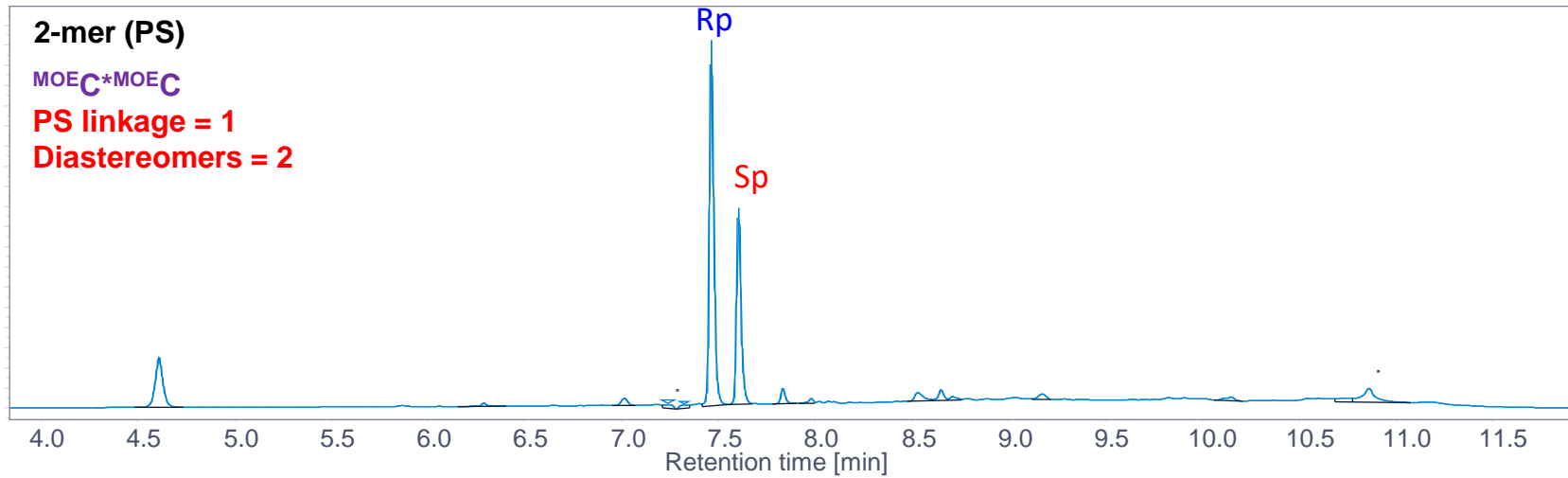
In-house 2-mer IP-RP chromatography: Comparison of PO and PS linkages

Column Used: Agilent Poroshell 120 EC-C18, 1.9 μ m 2.1 x 100mm

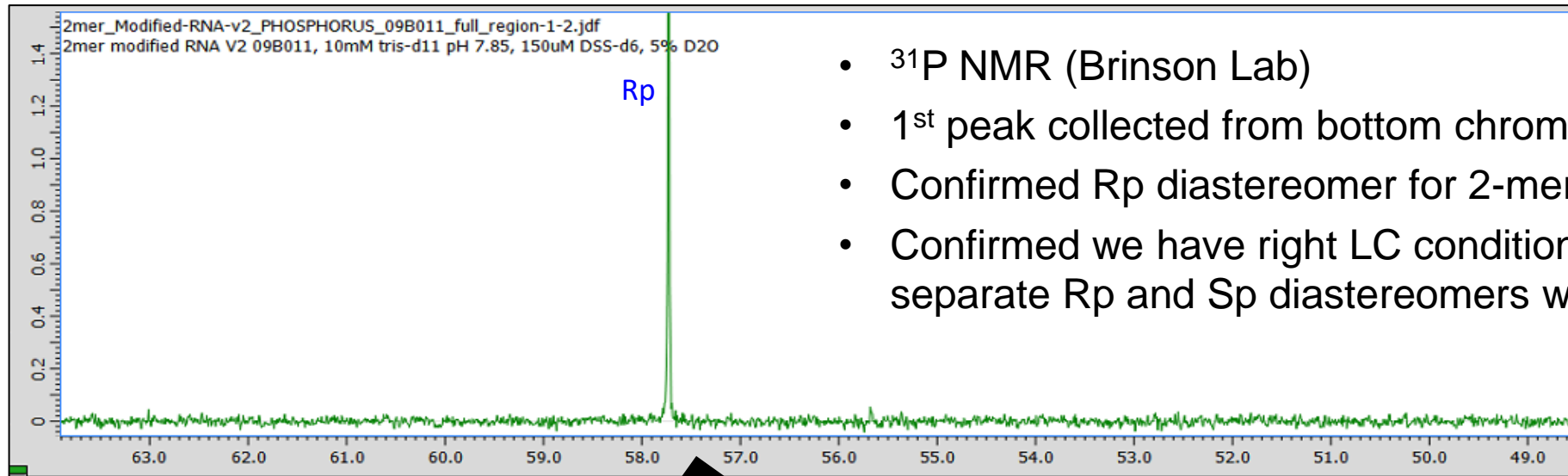
Temperature of column: 30°C

Mobile Phase A: 0.015 M TEA in Water

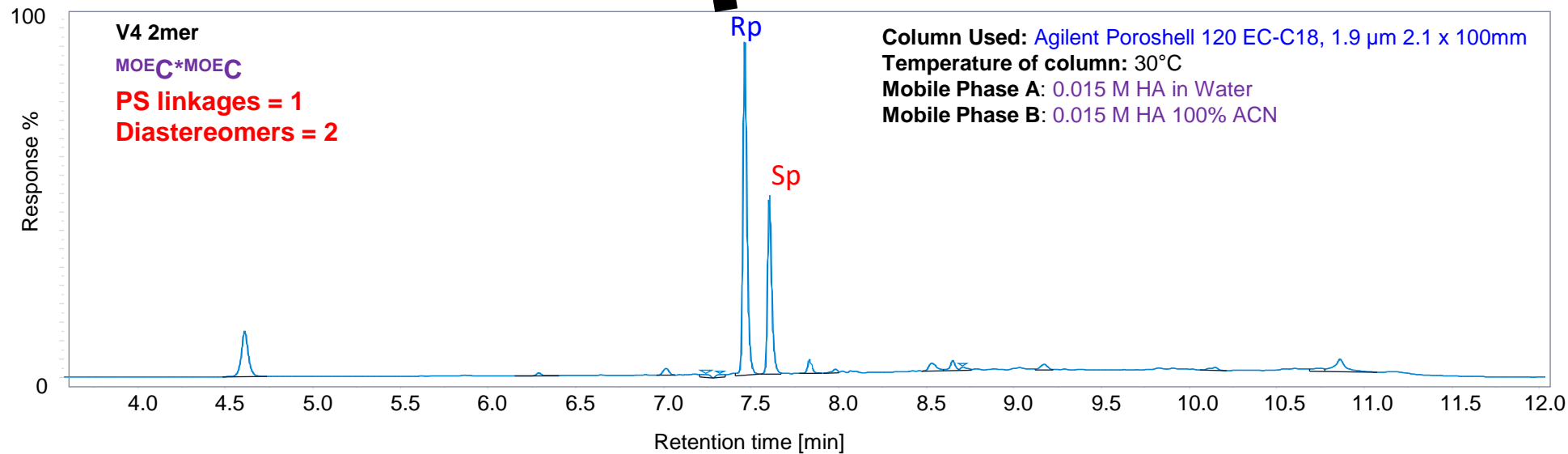
Mobile Phase B: 0.015 M TEA 100% ACN



IP-RP Diastereomer Separation and NMR Confirmation

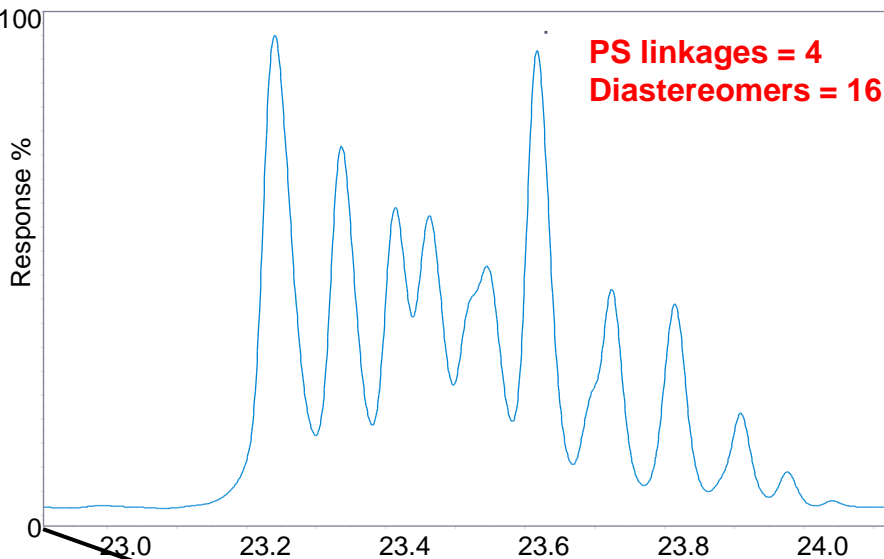


- ^{31}P NMR (Brinson Lab)
- 1st peak collected from bottom chromatogram
- Confirmed Rp diastereomer for 2-mer
- Confirmed we have right LC conditions to separate Rp and Sp diastereomers without DMT

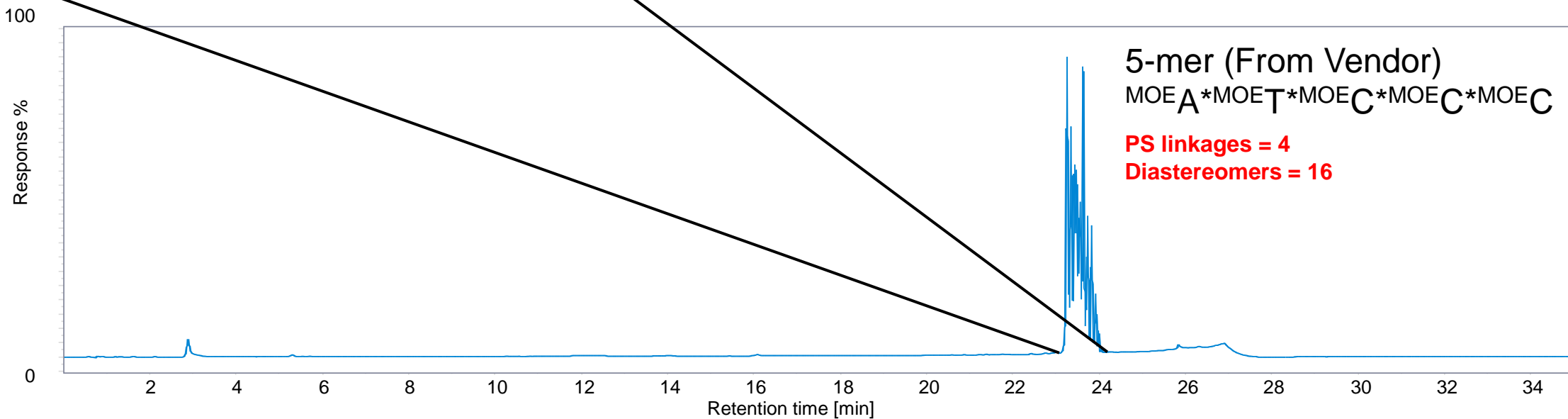


IP-RP separation of 5-mer

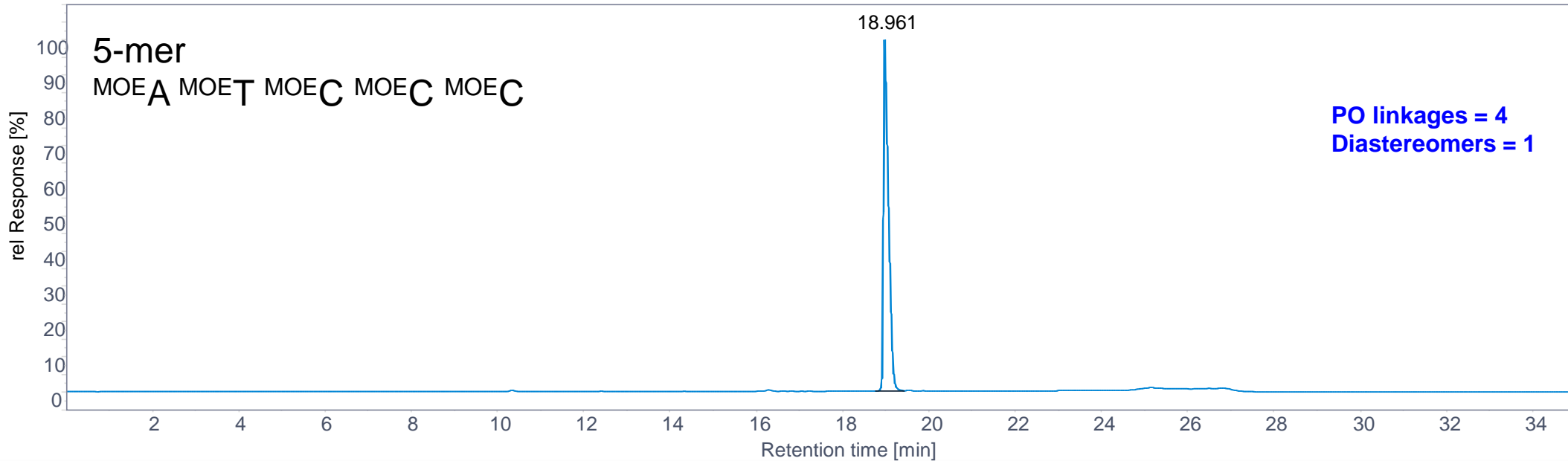
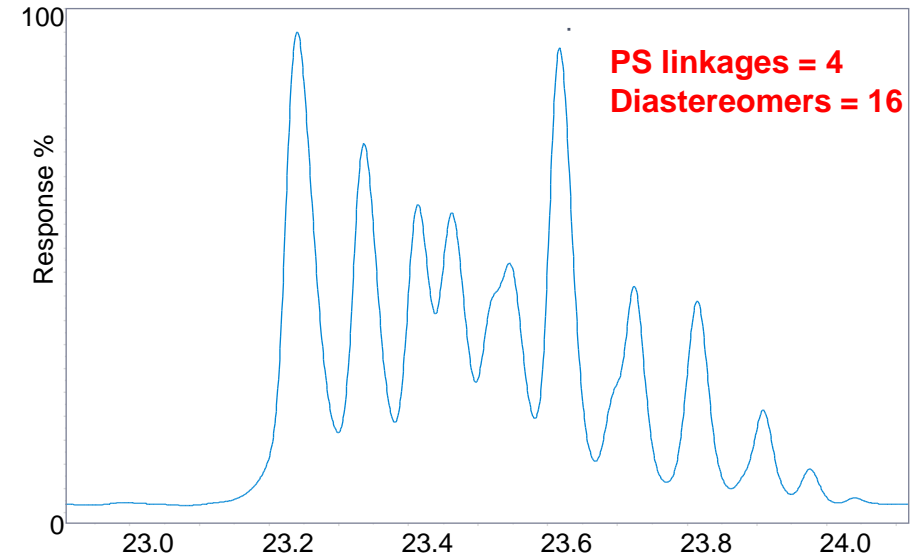
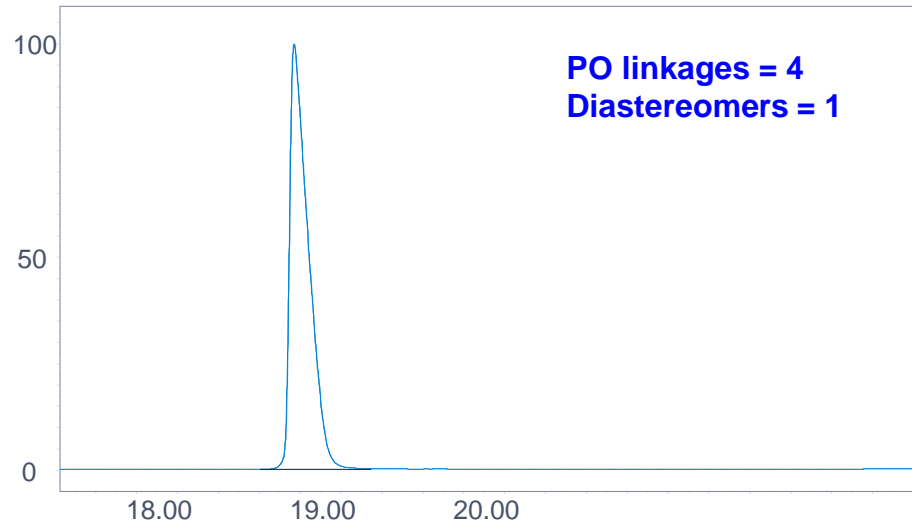
Time [min]	Δ	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00		95.00	5.00	0.400	1300.00
2.00		95.00	5.00	0.400	---
22.00		75.00	25.00	0.400	---
26.00		60.00	40.00	0.400	---
27.00		95.00	5.00	0.400	---
35.00		95.00	5.00	0.400	---



Column: Agilent Poroshell 120 EC-C18, 1.9 μ m 2.1 x 100mm
Temperature = 30°C
Mobile Phase A = 0.015 M HA in Water
Mobile Phase B = 0.015 M HA in ACN



IP-RP chromatography of 5-mer: comparison of PO and PS



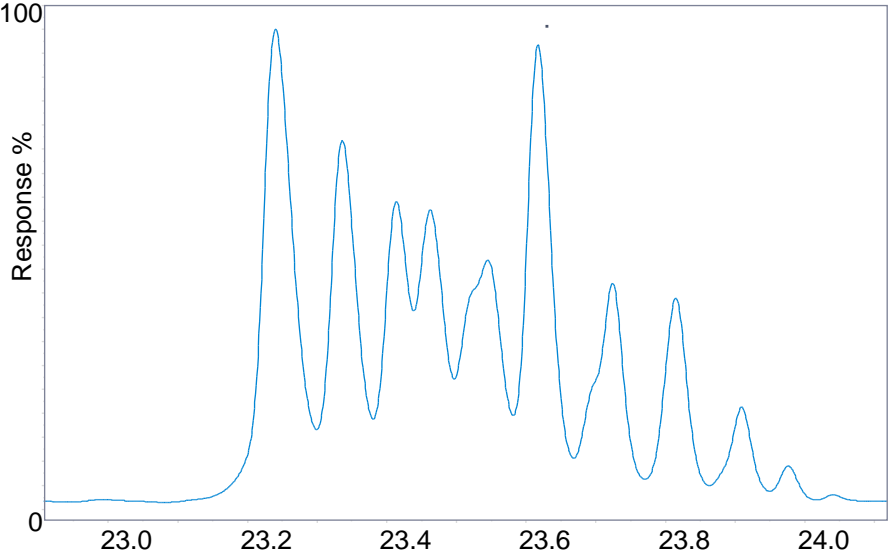
5-mer: Diastereomer Evaluation via IP-RP and NMR



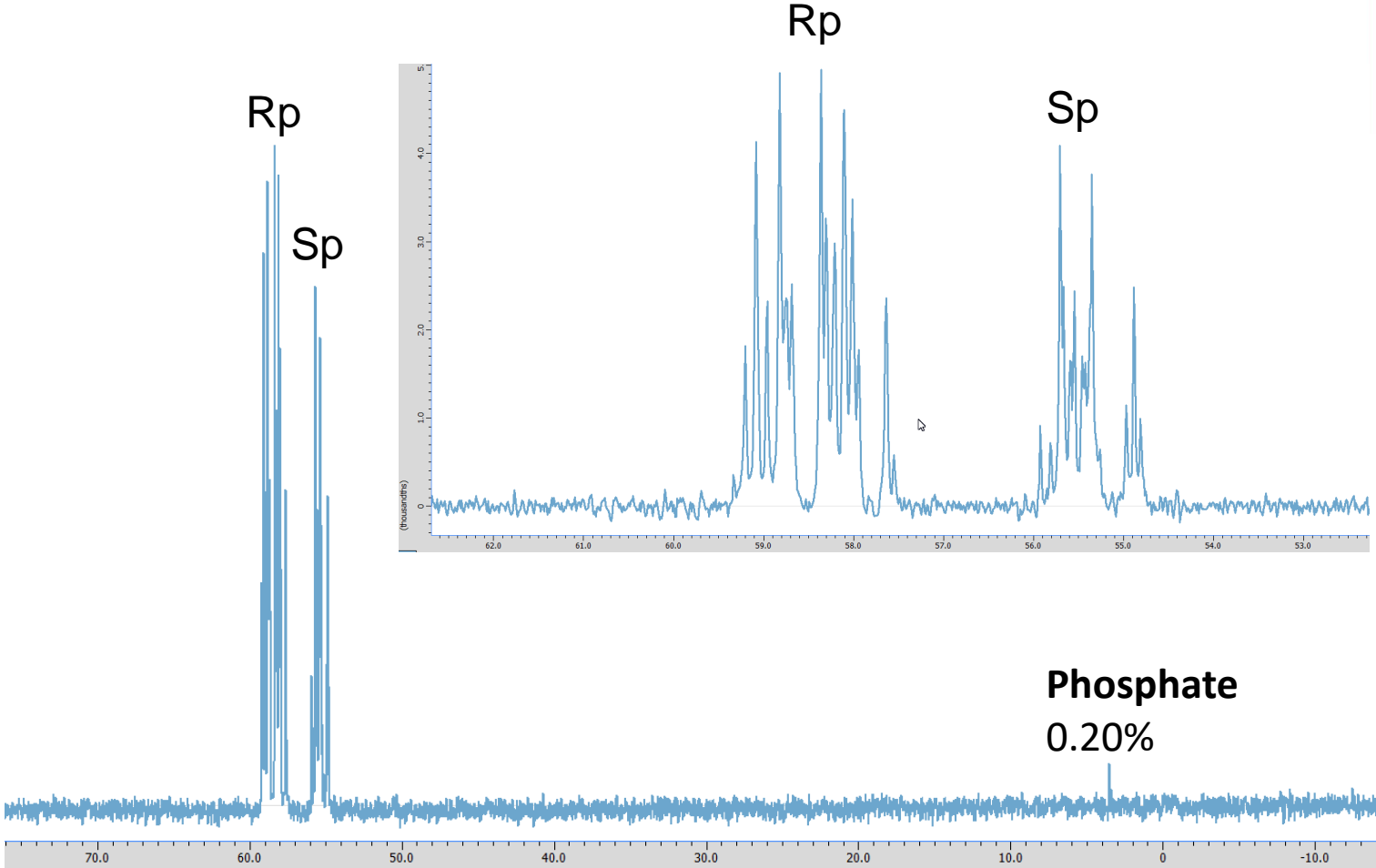
Robert Brinson, Ph.D.
NIST, IBBR

5-mer (From Vendor)
MOE_A*MOE_T*MOE_C*MOE_C*MOE_C
PS linkages = 4
Diastereomers = 16

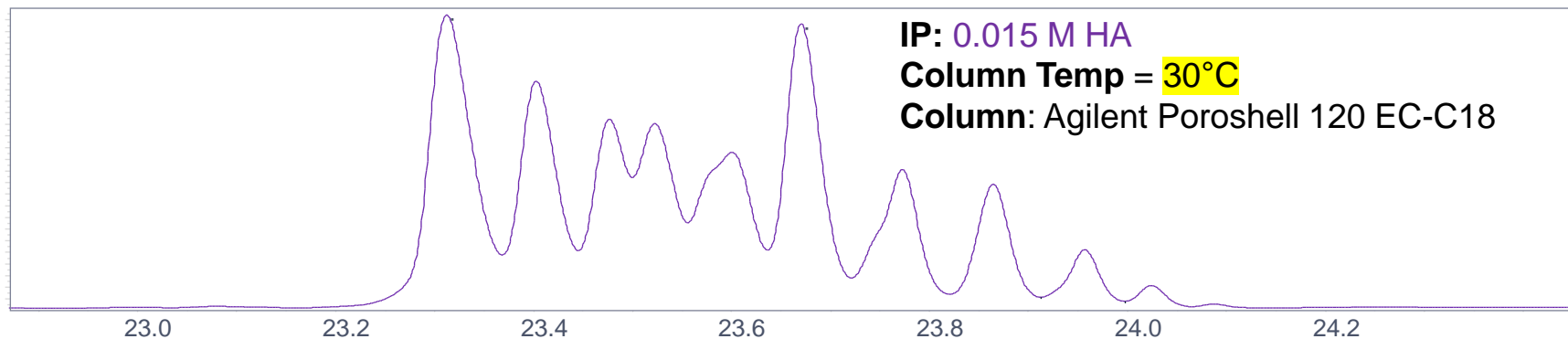
IP-RP Chromatogram



³¹P NMR

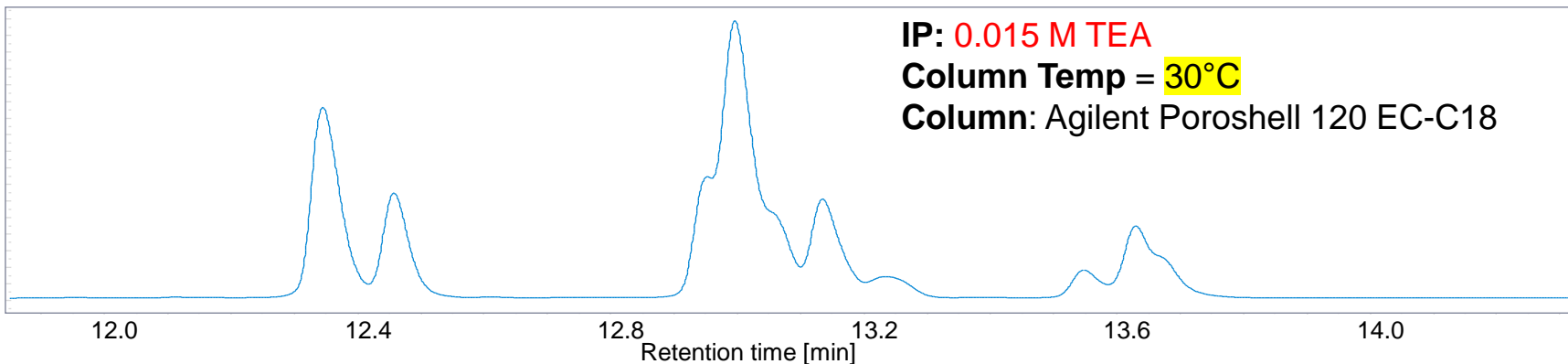
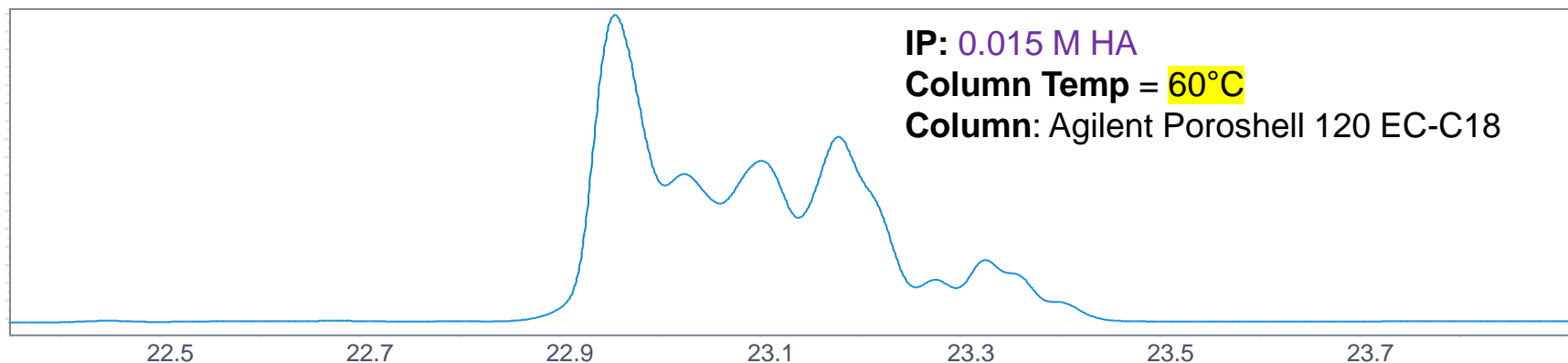


Ion Pair Reagent and Temperature Effect Chromatographic Separation



5-mer (Vendor)
MOE_A*MOE_T*MOE_C*MOE_C*MOE_C

PS linkages = 4
Diastereomers = 16

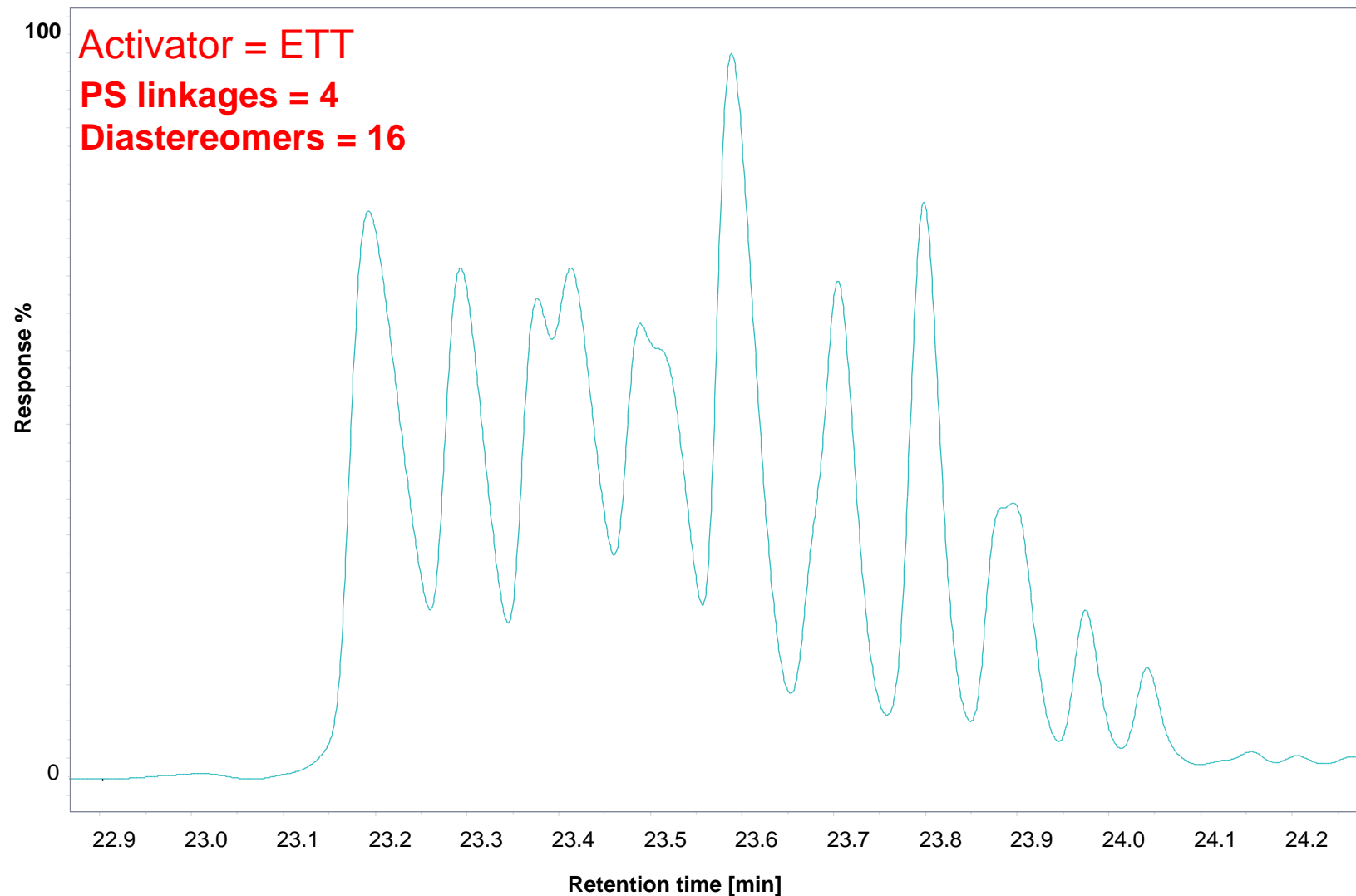


IP RP of 5-mer (In-house synthesis, ETT)

5-mer (in-house ETT)

MOE_A*MOE_T*MOE_C*MOE_C*MOE_C

Activator = ETT
PS linkages = 4
Diastereomers = 16



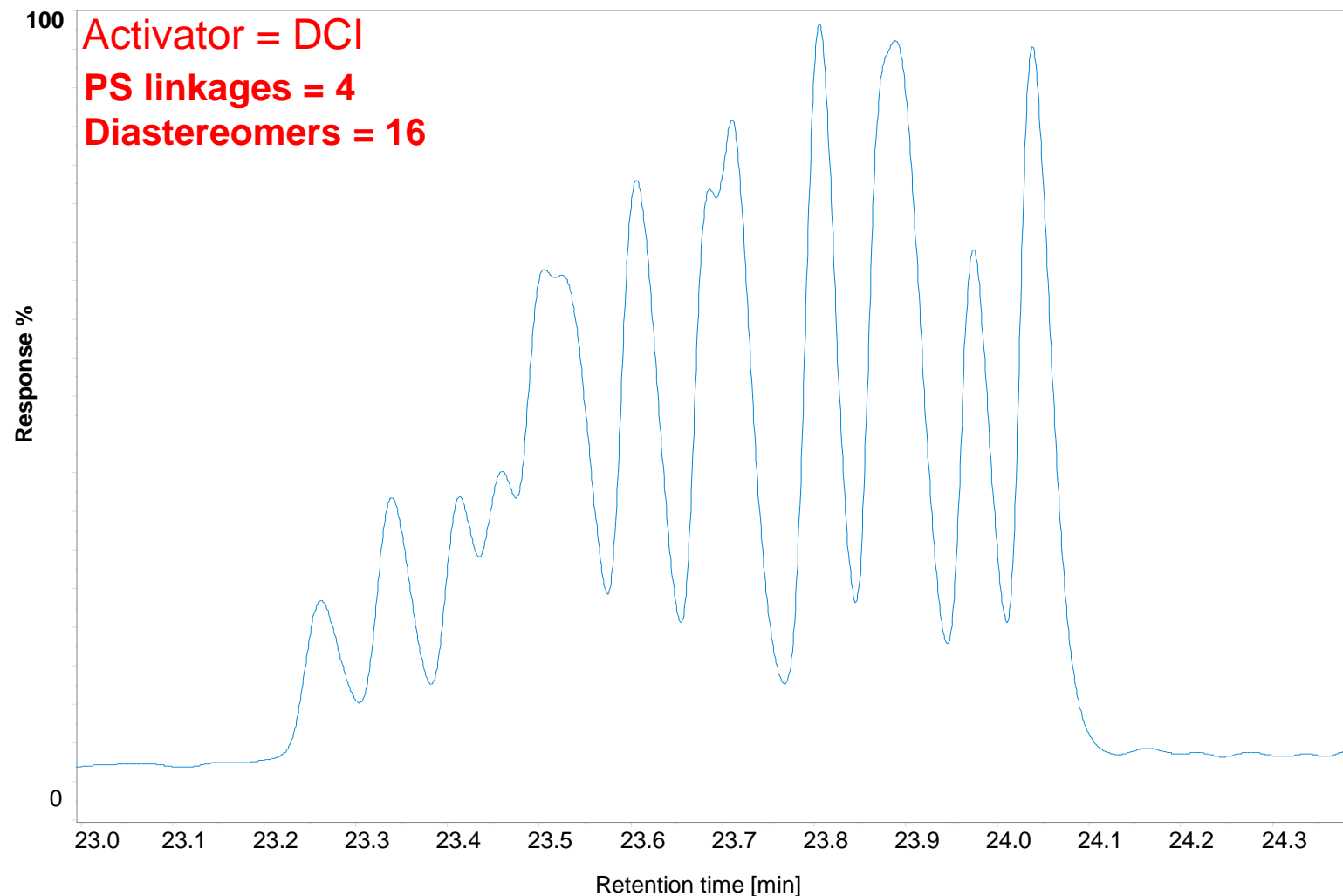
Column: Agilent Poroshell 120 EC-C18
1.9 μ m 2.1 x 100mm
Temperature = 30°C
Mobile Phase A = 0.015 M HA in Water
Mobile Phase B = 0.015 M HA in ACN

Time [min]	Δ	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00		95.00	5.00	0.400	1300.00
2.00		95.00	5.00	0.400	---
22.00		75.00	25.00	0.400	---
26.00		60.00	40.00	0.400	---
27.00		95.00	5.00	0.400	---
35.00		95.00	5.00	0.400	---

IP RP of 5-mer (In-house synthesis, DCI)

5-mer (in-house DCI)

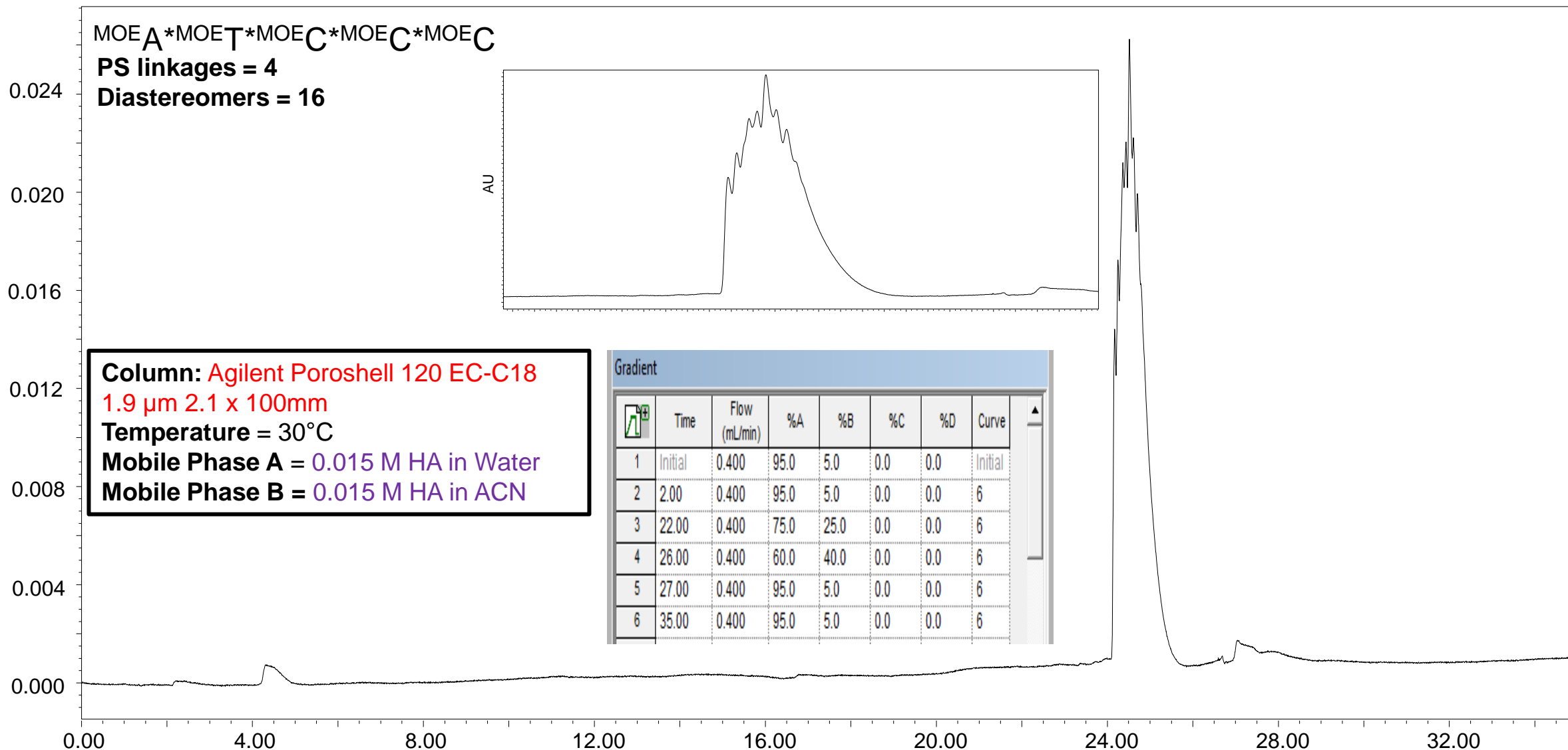
MOE_A*MOE_T*MOE_C*MOE_C*MOE_C



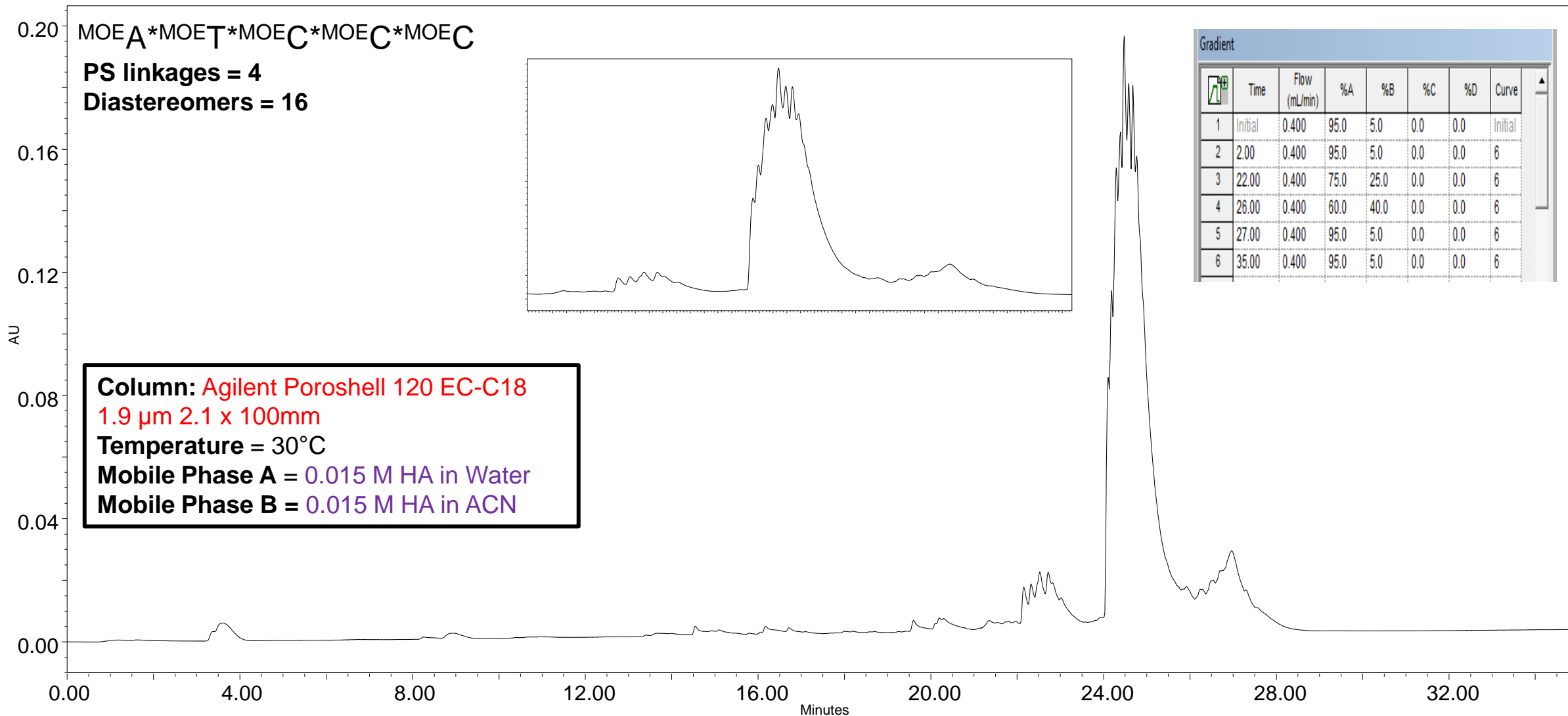
Column: Agilent Poroshell 120 EC-C18
1.9 μ m 2.1 x 100mm
Temperature = 30°C
Mobile Phase A = 0.015 M HA in Water
Mobile Phase B = 0.015 M HA in ACN

Time [min]	Δ	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00		95.00	5.00	0.400	1300.00
2.00		95.00	5.00	0.400	---
22.00		75.00	25.00	0.400	---
26.00		60.00	40.00	0.400	---
27.00		95.00	5.00	0.400	---
35.00		95.00	5.00	0.400	---

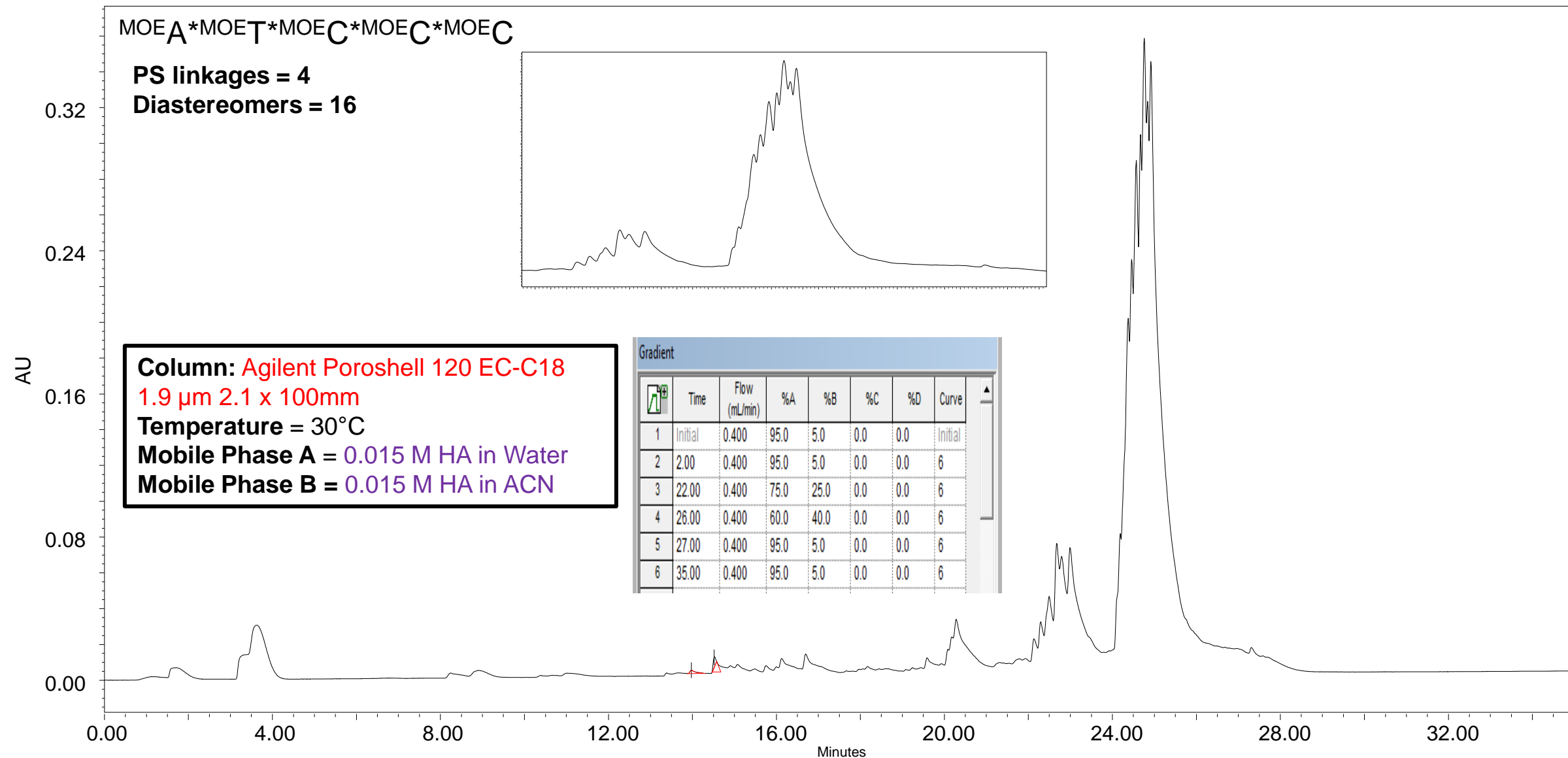
IP-RP separation of 5-mer on different UHPLC under same conditions



IP-RP separation of 5-mer (ETT) on different UHPLC under same conditions



IP-RP separation of 5-mer (DCI) on different UHPLC under same conditions



5-mer comparison using Agilent 1290 Bio-LC vs Another LC

MOEA*MOET*MOEC*MOEC*MOEC

PS linkages = 4

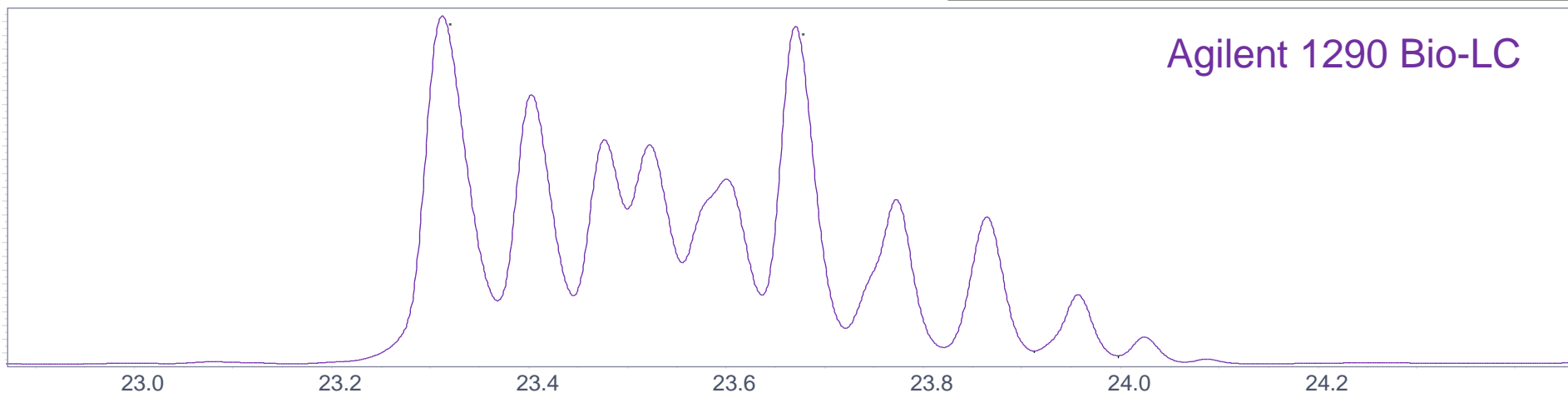
Diastereomers = 16

Column: Agilent Poroshell 120 EC-C18

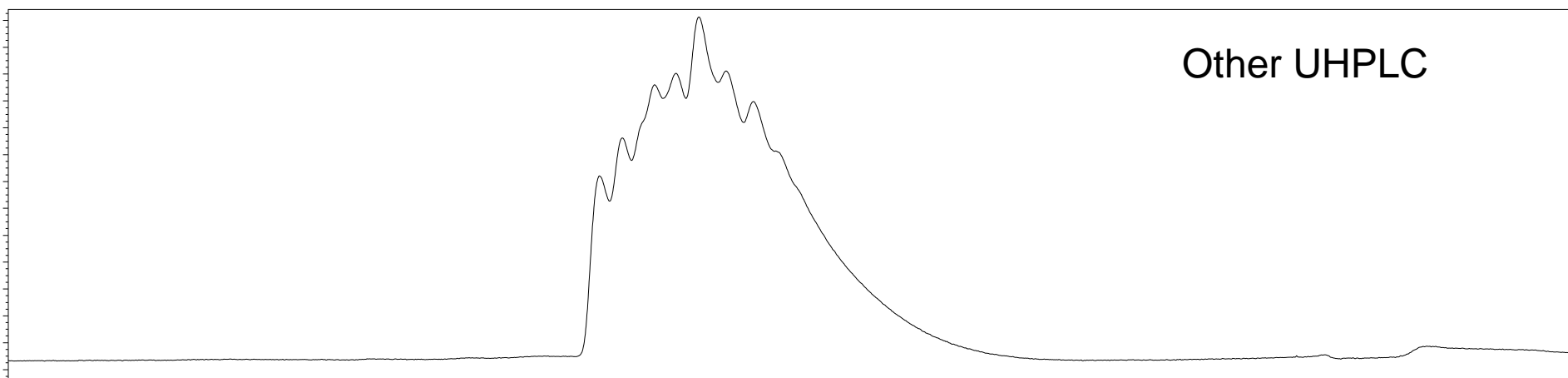
Temperature = 30°C

Mobile Phase A = 0.015 M HA in Water

Mobile Phase B = 0.015 M HA in ACN



Time [min]	A [%]	B [%]	Flow [mL/min]	Max. Pressure Limit [bar]
0.00	95.00	5.00	0.400	1300.00
2.00	95.00	5.00	0.400	---
22.00	75.00	25.00	0.400	---
26.00	60.00	40.00	0.400	---
27.00	95.00	5.00	0.400	---
35.00	95.00	5.00	0.400	---



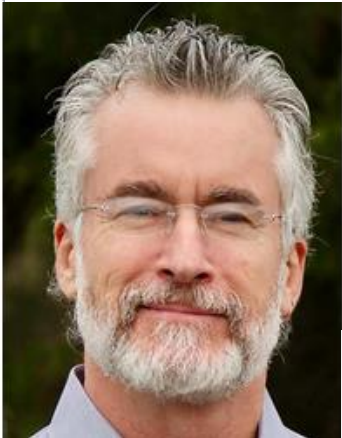
Time	Flow (mL/min)	%A	%B	%C	%D	Curve
1 Initial	0.400	95.0	5.0	0.0	0.0	Initial
2 2.00	0.400	95.0	5.0	0.0	0.0	6
3 22.00	0.400	75.0	25.0	0.0	0.0	6
4 26.00	0.400	60.0	40.0	0.0	0.0	6
5 27.00	0.400	95.0	5.0	0.0	0.0	6
6 35.00	0.400	95.0	5.0	0.0	0.0	6

IP RP Had Unique Chromatographic Profiles for Different Activators

In-house synthesized 5-mer (ETT)
Activator = ETT

Next steps:

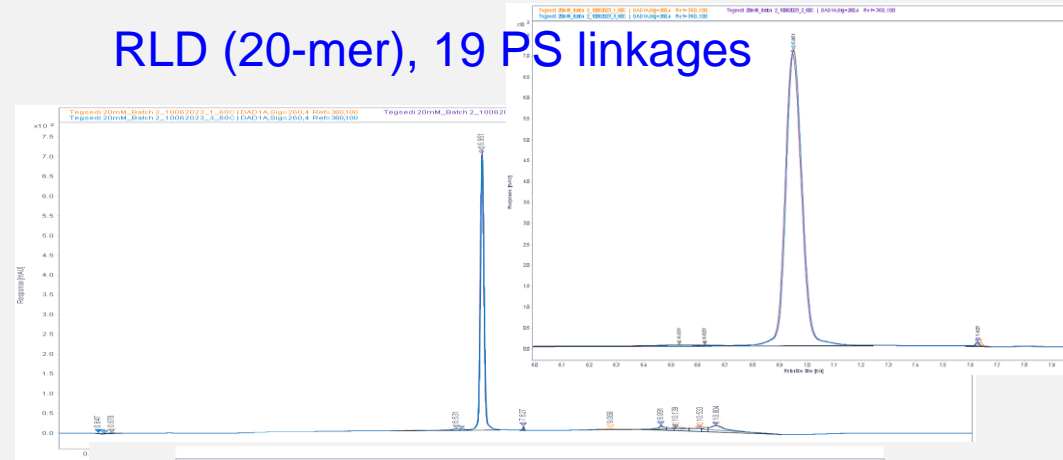
- Continued IP-RP separation of other length oligos and RLD
- Use of other LC separations (MICC, SAX, HILIC)
- Work with the Cummings Lab to develop statistical/computational models to comprehensively evaluate and visualize diastereomer composition



Michael P. Cummings, Ph.D.
 University of Maryland

23.0 23.2 23.4 23.6

RLD (20-mer), 19 PS linkages



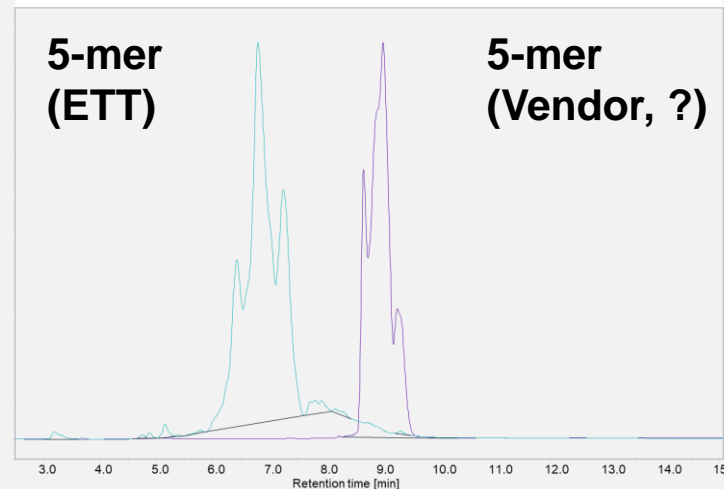
OEC

EC-C18

AA in Water
 AA in ACN

5-mer
 (ETT)

5-mer
 (Vendor, ?)



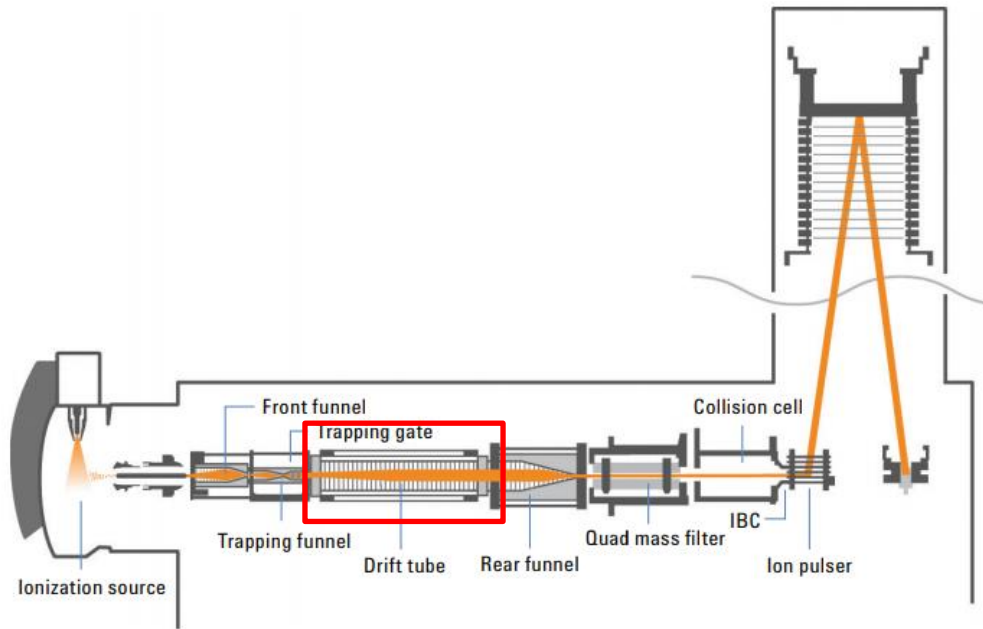
- MICC:** Agilent ZORBAX SB-C18 (150 x 2.1mm, 3.5µm)
- Temperature: 35°C
- Mobile Phase A: 10 mM NH₄PO₄ + 20 ppm Potassium Acetate, pH 6.8 – 6.9
- Mobile Phase B: 100% ACN

	Max. Pressure Limit [bar]
100	1300.00
100	---
100	---
100	---
100	---
100	---

23.0 24.0

Use of Ion Mobility to characterize OGN structure

- Gas phase separation
- Based on shape, size and charge
- Allows direct collisional cross section (CCS) calculation

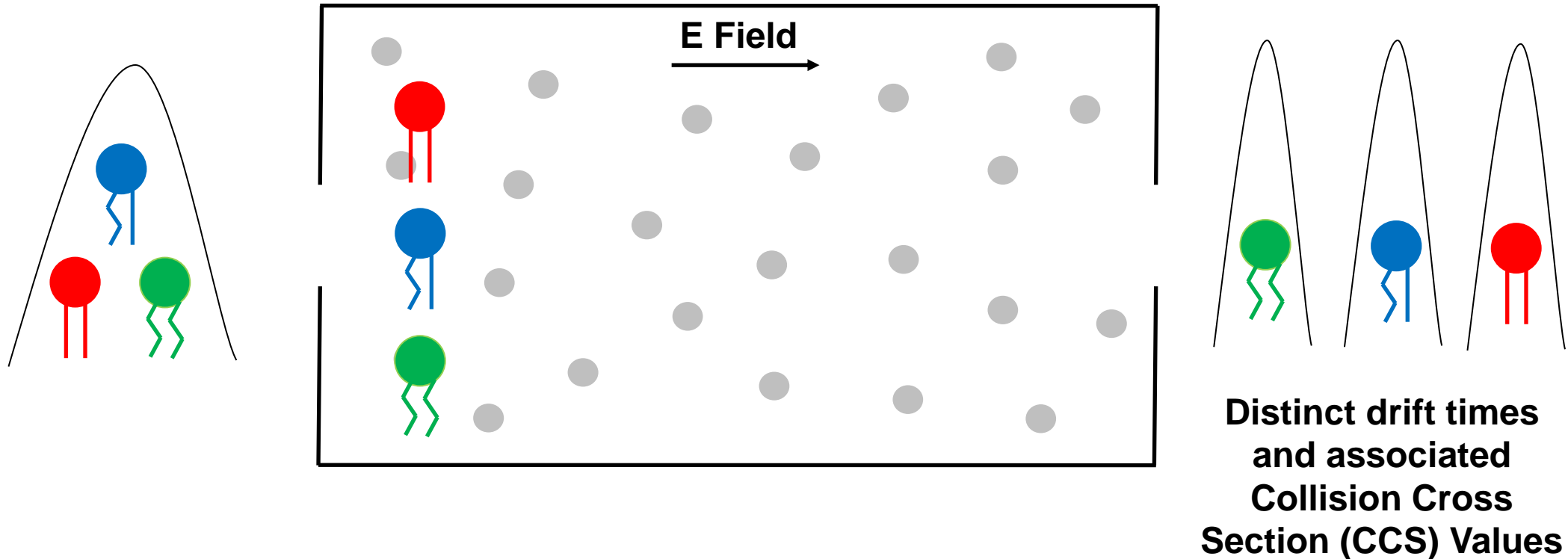


Agilent DT-IM-QTOF 6560



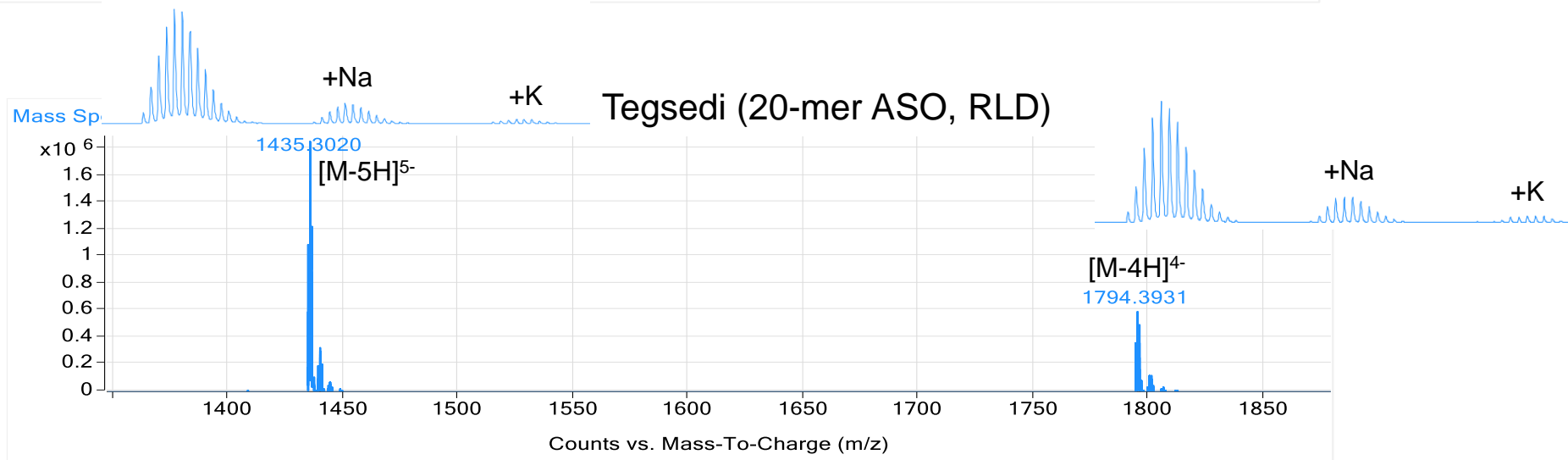
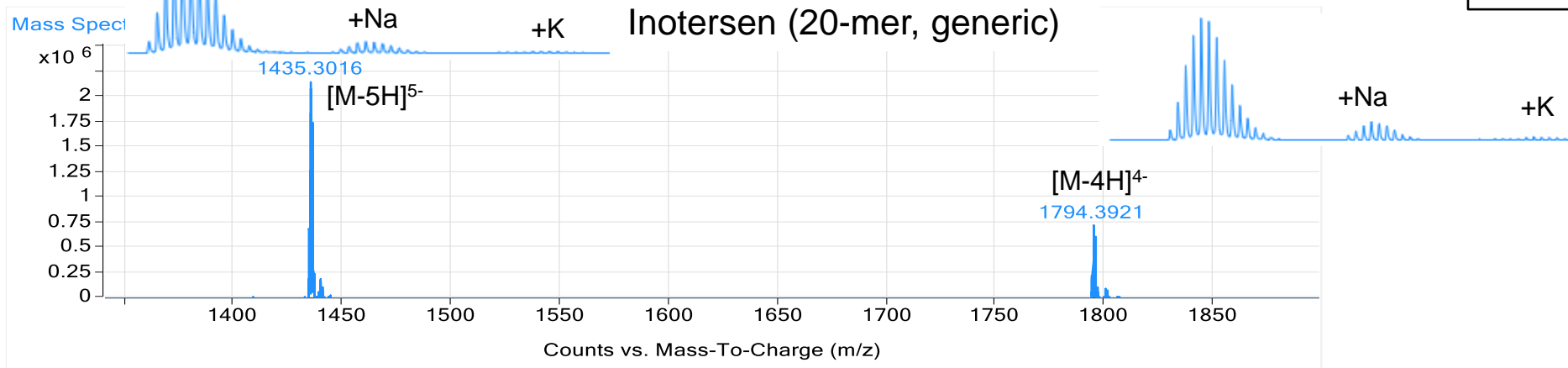
Drift Tube Ion Mobility

Another dimension of separation to effectively isolate isobaric and isomeric structures that may not be resolved through LC-MS.

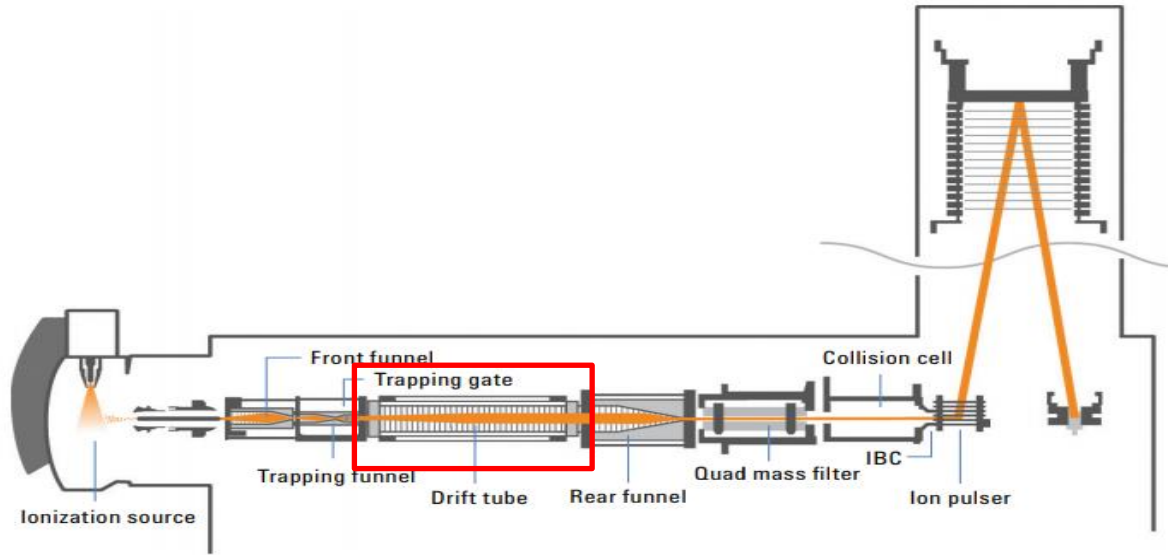


High Resolution Mass Spectrometry

- Accurate Mass
- Charge State Distribution
- Adduct distribution (deprotonation with various Na and/or K)
- Isotopic Envelope

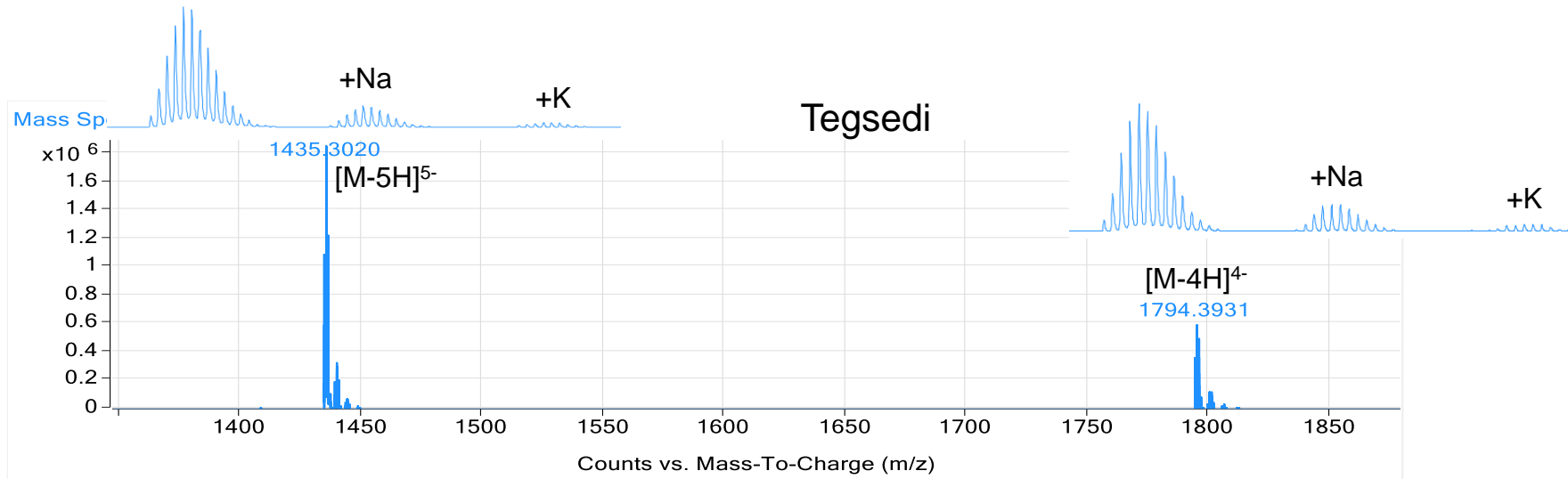


Drift Tube Ion Mobility (DT-IM)

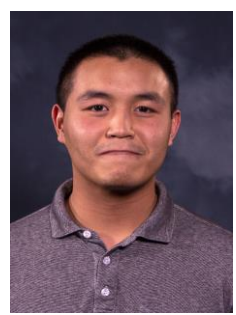


DT-IM

- Charge State
- Adduct
- Isotopic Envelope or individual peak



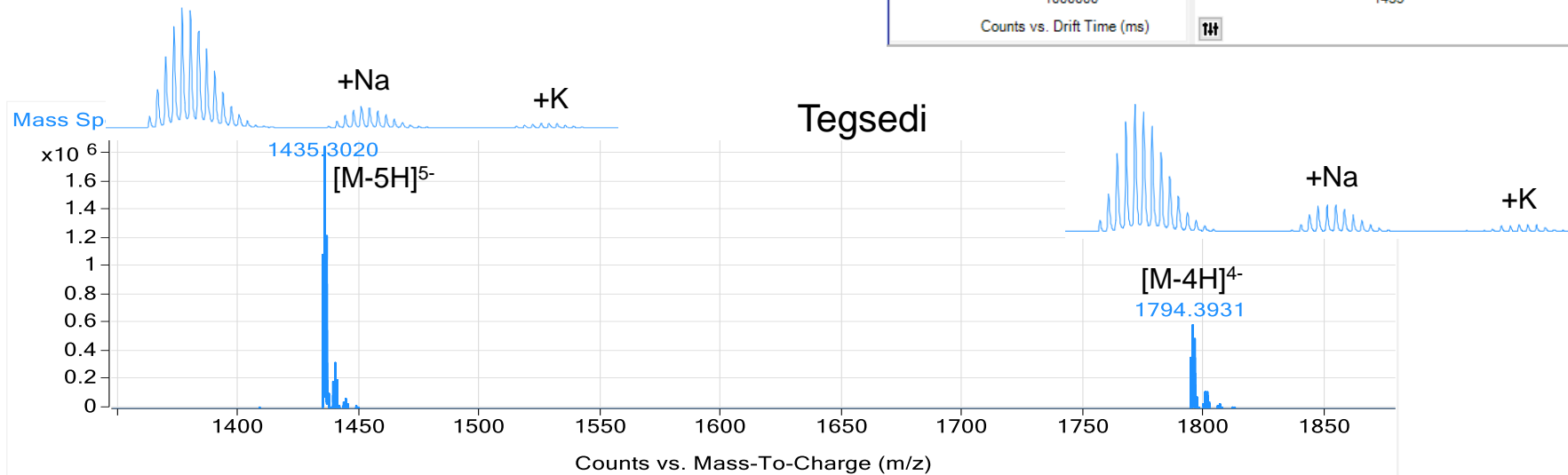
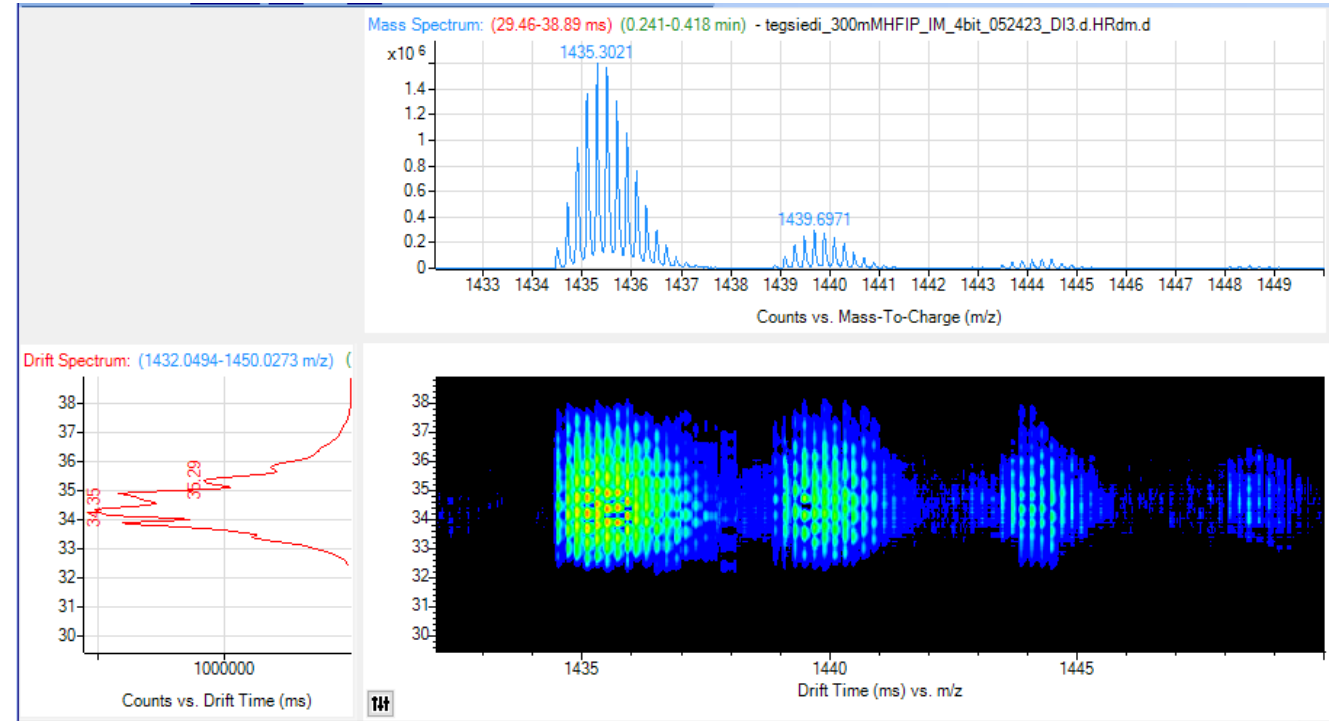
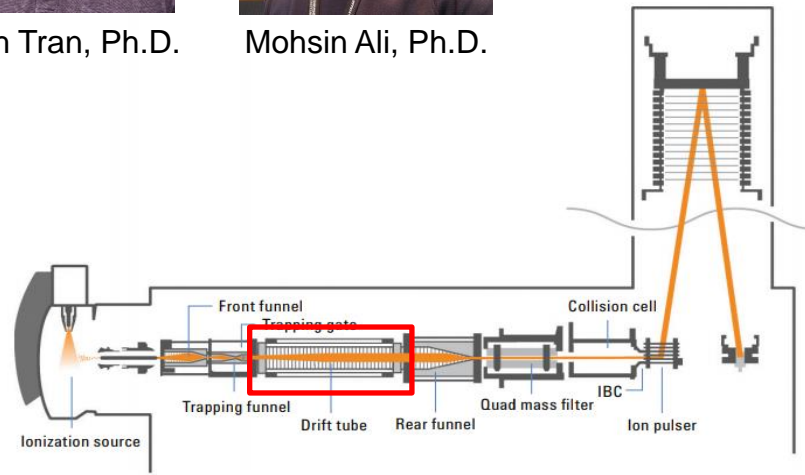
Drift Tube Ion Mobility (DT-IM)



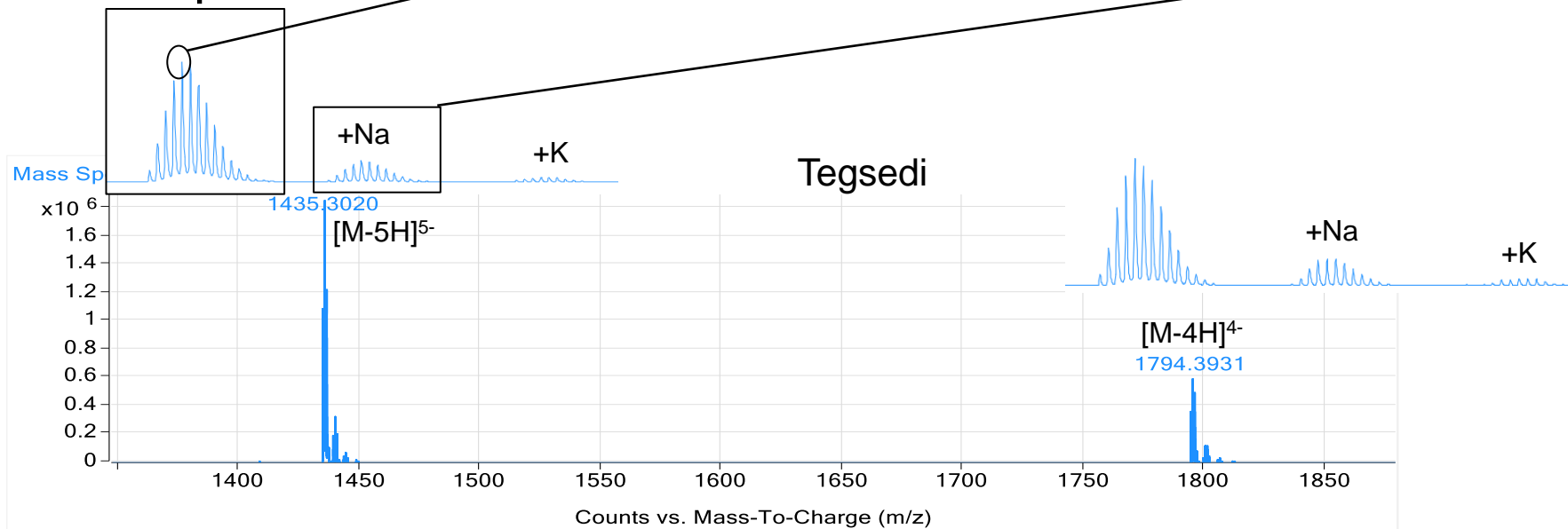
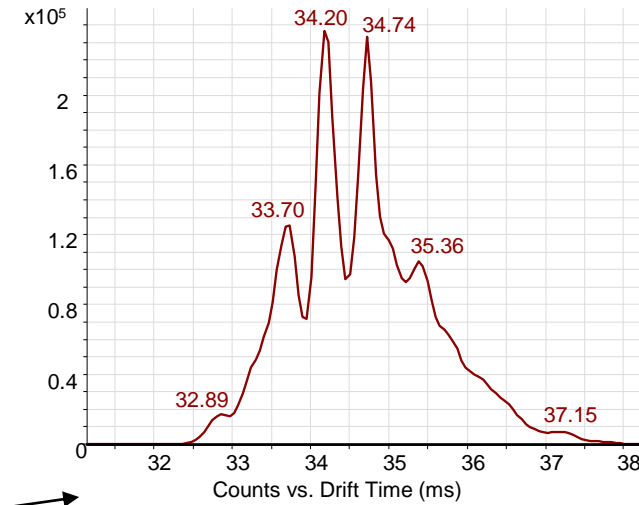
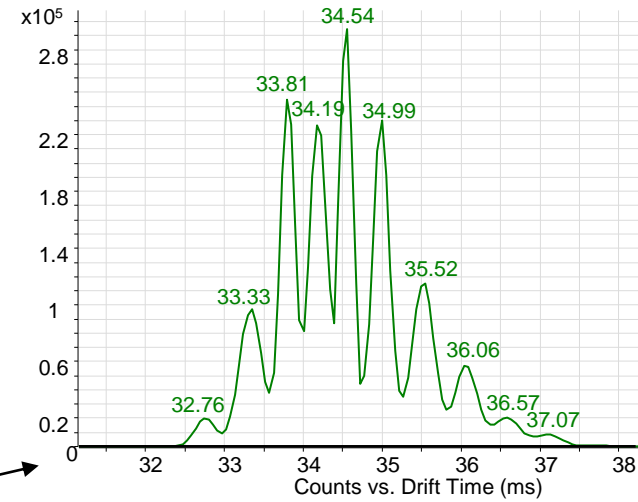
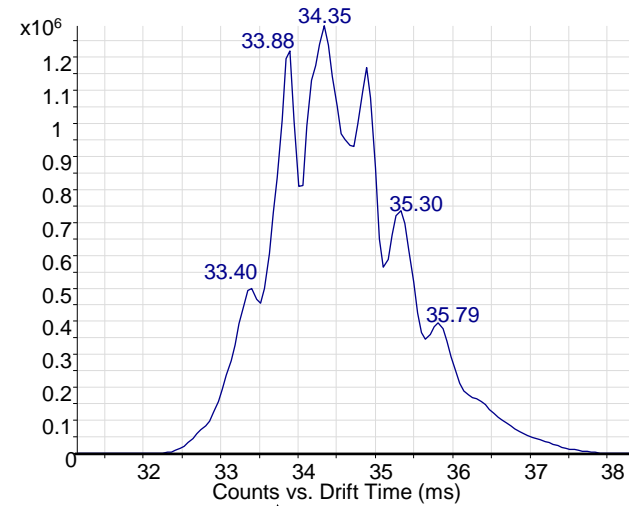
Anh Tran, Ph.D.



Mohsin Ali, Ph.D.

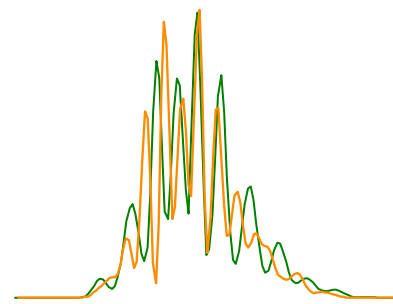
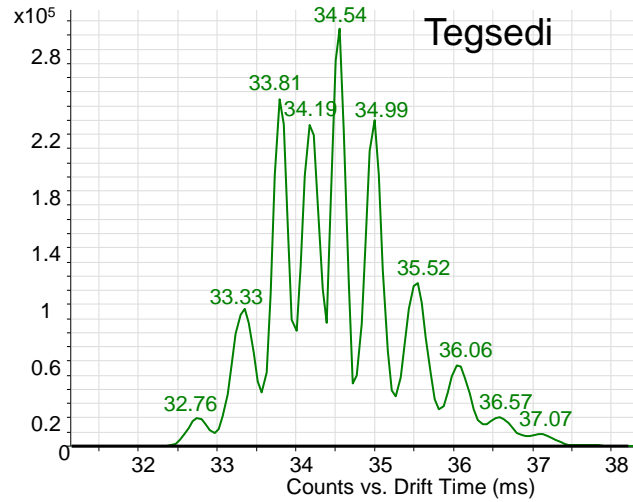


Generation of Drift Spectra to Profile OGN Structure

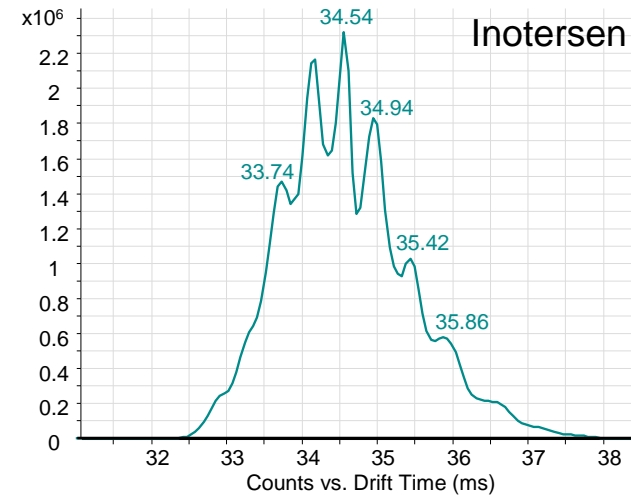
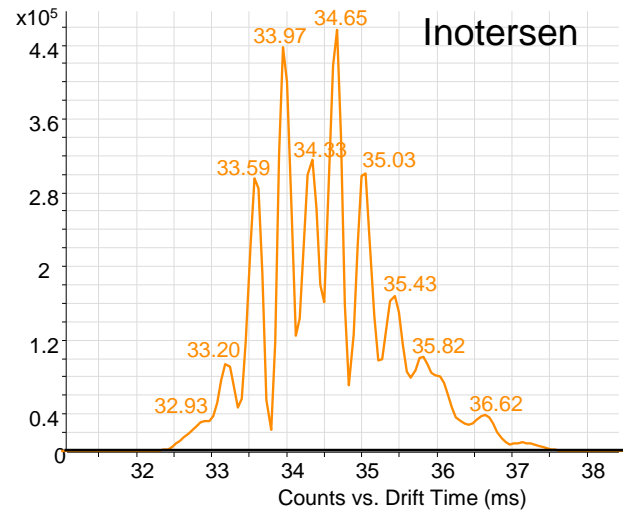
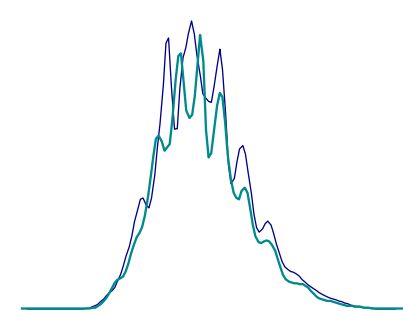
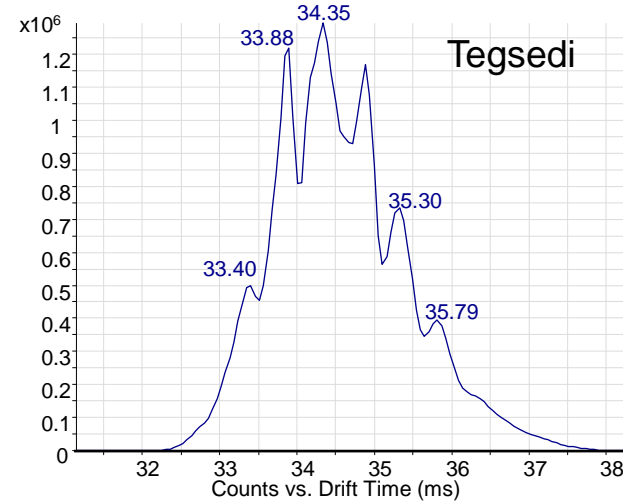


Drift Time Mobiliograms: OGN fingerprints

$[M-5H]^{5-}$, m/z 1435.3; monoisotopic peak



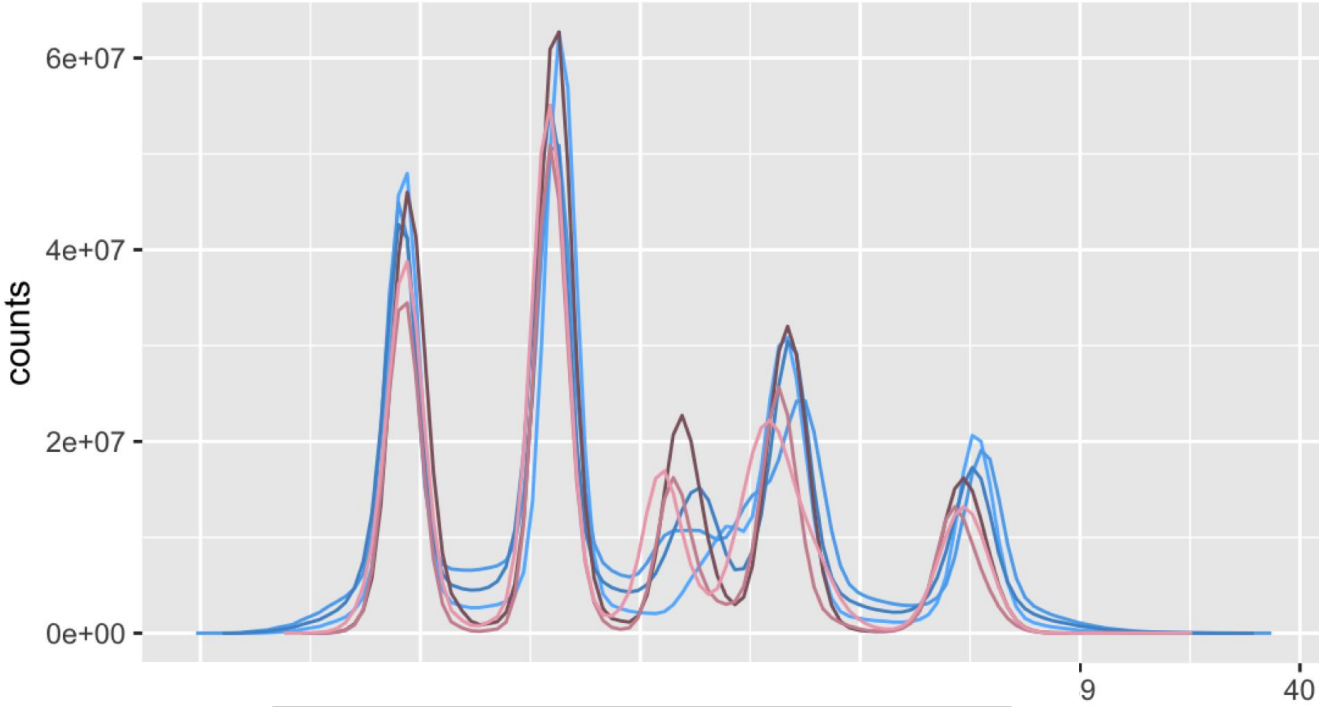
$[M-5H]^{5-}$, m/z 1434-1438; isotopic envelope



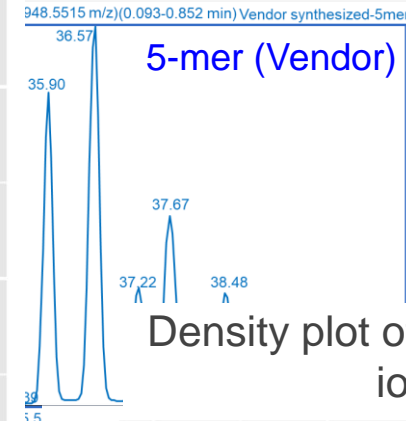
Drift Time Mobiliograms: OGN fingerprints



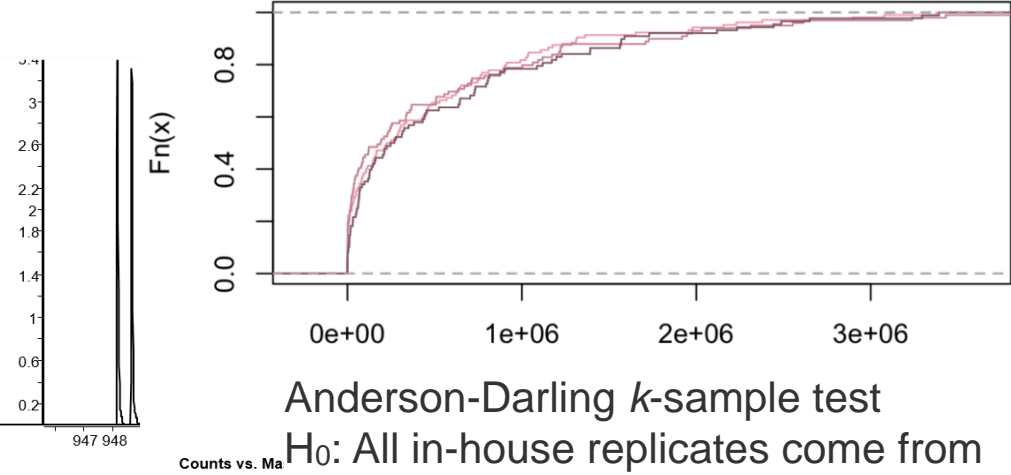
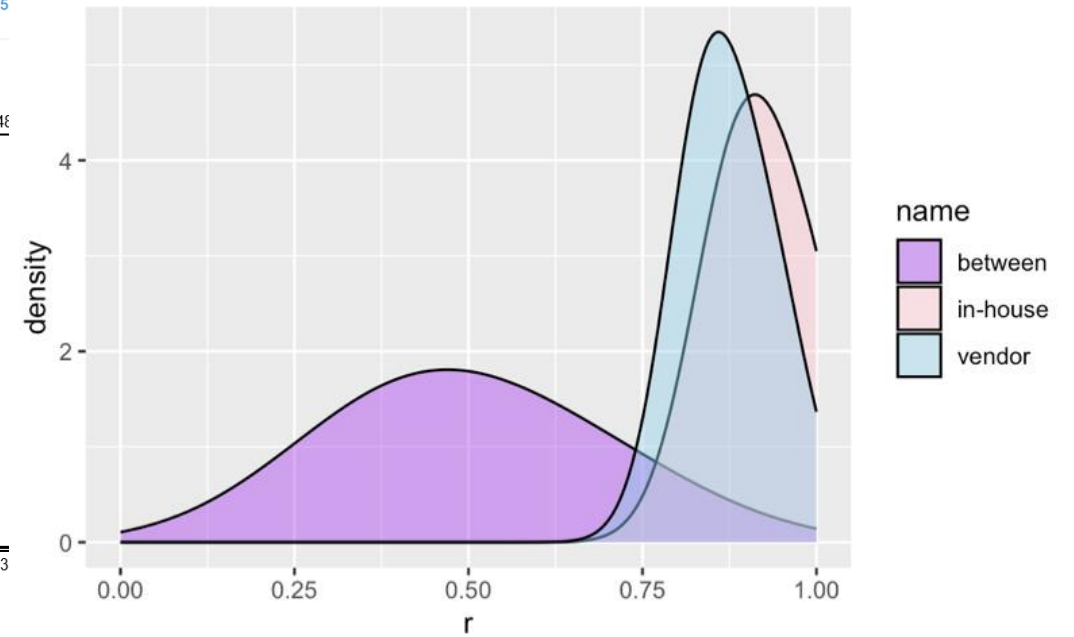
Michael P. Cummings, Ph.D.
University of Maryland



Spectrum (Monoisotopic Peak)



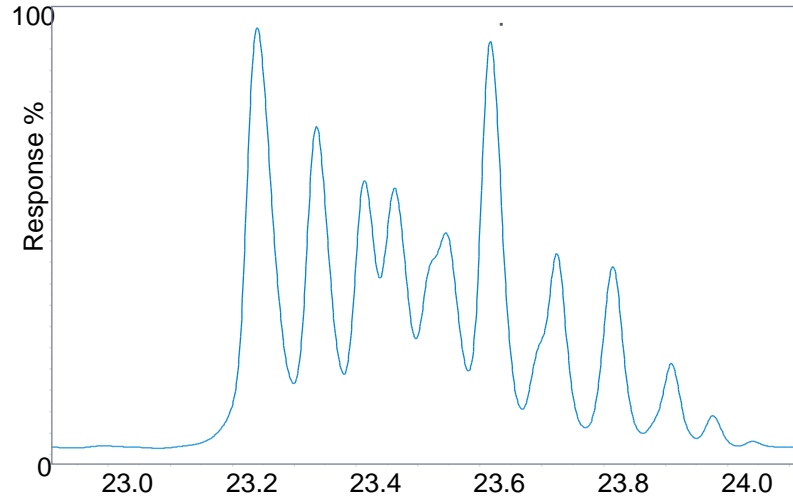
Density plot of correlation coefficients for ion-mobility data



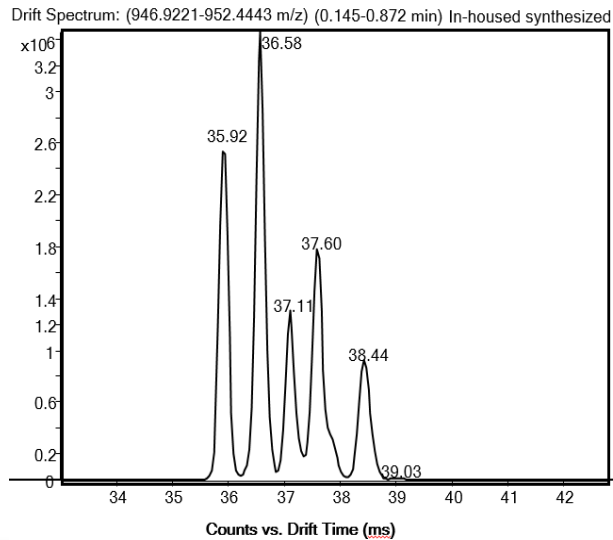
Anderson-Darling k -sample test
 H_0 : All in-house replicates come from a common population

Diastereomer Characterization via IP-RP, IM, and NMR

IP-RP Chromatography



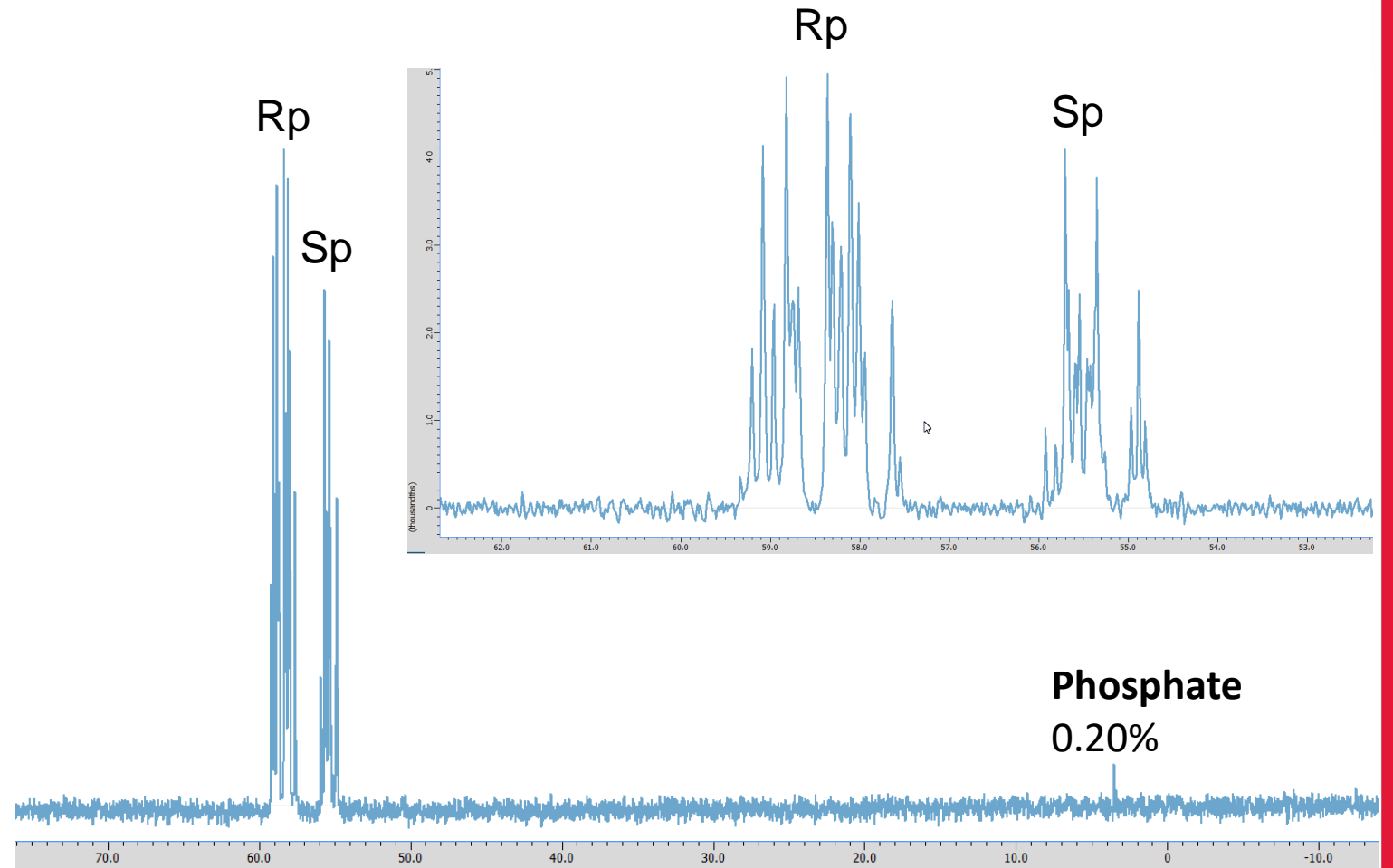
Ion Mobility



5-mer (From Vendor)
MOE_A*MOE_T*MOE_C*MOE_C*MOE_C

PS linkages = 4
Diastereomers = 16

³¹P NMR



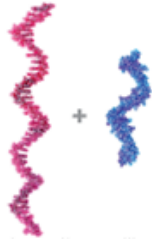
Mass Spec/Ion Mobility

Chromatography

NMR

Chemical Synthesis

Stats/Computation



OGN Structure



Frederick S. Brundick/cc-2.0/<https://flic.kr/p/29umt8b>

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Sazia Kachi

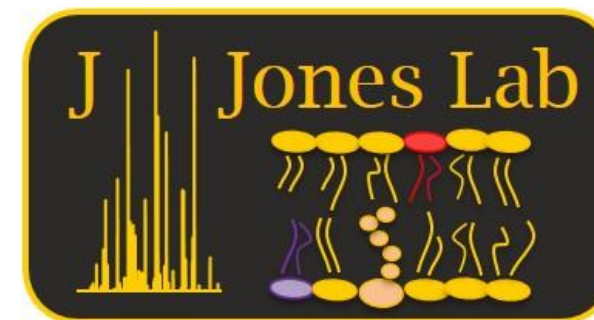
Former Members:

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Yulemni Morel, PhD

Padmapriya Sridhar, MS

Mayur Shete, MS



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Cummings Lab (U. Maryland College Park)

Brinson Lab (IBBR, NIST)

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