



High-Resolution Ion Mobility Mass Spectrometry for Oligonucleotide Impurity Analysis

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71st ASMS Conference on Mass Spectrometry and Allied Topics

Houston TX, June 6, 2023

ASMS2023 #312994

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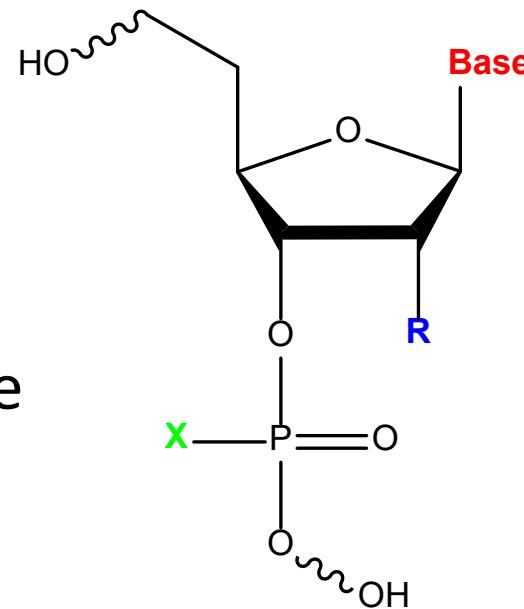
Pharmaceutical quality is

what gives patients confidence in
their *every* dose of medicine.

Oligonucleotide Therapeutics (ONTs)



- An evolving class of drugs that can modulate gene expression or hinder protein function by binding to specific mRNA targets.
- Modification can occur at the **nucleobase**, **sugar**, and **internucleotide linkage**.
- Solid-phase synthesis consists of repetitive synthetic cycles, each cycle including multiple steps. Failure in any step may lead to formation of impurities



Analytical Challenges of ONTs



- Product-related impurities produced during synthesis can be structurally closely related. Examples include:
 - Deletion sequences
 - Addition sequences
 - P=O impurities
 - Deamination impurities
- Separation of impurities from desired product or from each other can be challenging, particularly for LC or MS-inseparable isomeric and isobaric molecules.

Limitations of Current Analytical Approach

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IP-RP LC/UV-MS

- Ion-pair reversed phase (IP-RP) LC involves ion pair reagents that can lead to MS signal suppression.
- Structurally similar impurities may not be fully LC resolved.
- Isobaric and isomeric molecules may be inseparable by either LC or MS dimension.

Recent development of methods free of IP reagents: HILIC-MS

- ASMS poster **#313427** (Rabiul Islam) – method validation
- ASMS WOD pm **#312952** (AM Abdullah) – data processing
- ASMS ThOH am **#313595** (Kui Yang) – MAMO platform

An Orthogonal Dimension to LC/MS

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Ion mobility

- Adds an extra dimension of separation by separating molecules based off size, shape, and charge.
- Potential of separating LC-MS inseparable molecules.
- Provides collision cross section (CCS) of a molecule as a molecular characteristic.

Collision Cross Section (CCS)

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- CCS describes the collision between the ion and the buffer gas, and gives direct information about the conformation of the ion travelling through the drift region.
- Mobility or drift time (**DT**) is measured and converted to CCS using the Mason-Schamp equation for drift tube ion mobility.
- Cyclic-IM requires calibration to extract CCS values.

$$\Omega = \frac{\frac{3}{16} \left(\frac{2\pi}{\mu k_b T} \right)^{\frac{1}{2}} z e}{N_0 K_0}$$

e , charge of an electron

z , ion charge

N₀ , buffer gas density

μ , reduced mass of collision partners

K₀, mobility

T , drift region temperature

k_b , Boltzmann's constant

Materials and Methods

- Instrumentation: Cyclic IMS (Waters)
- Software: MassLynx, DriftScope
- Model molecules: full-length product (FLP), and impurities

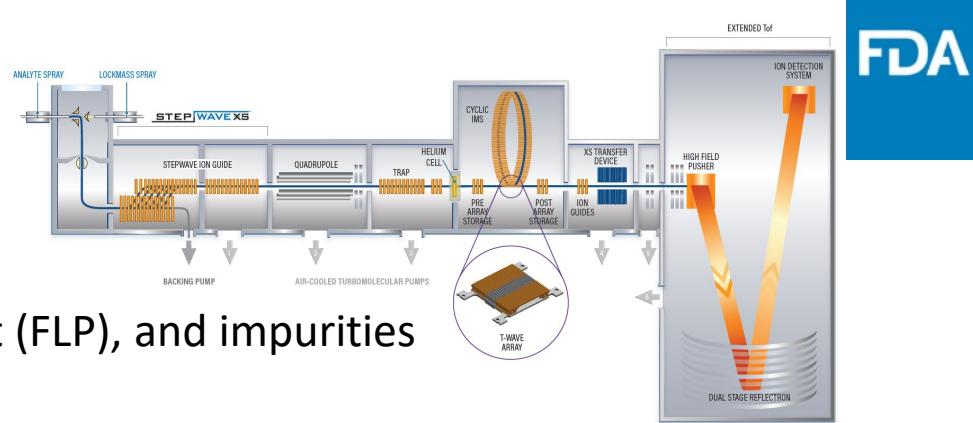
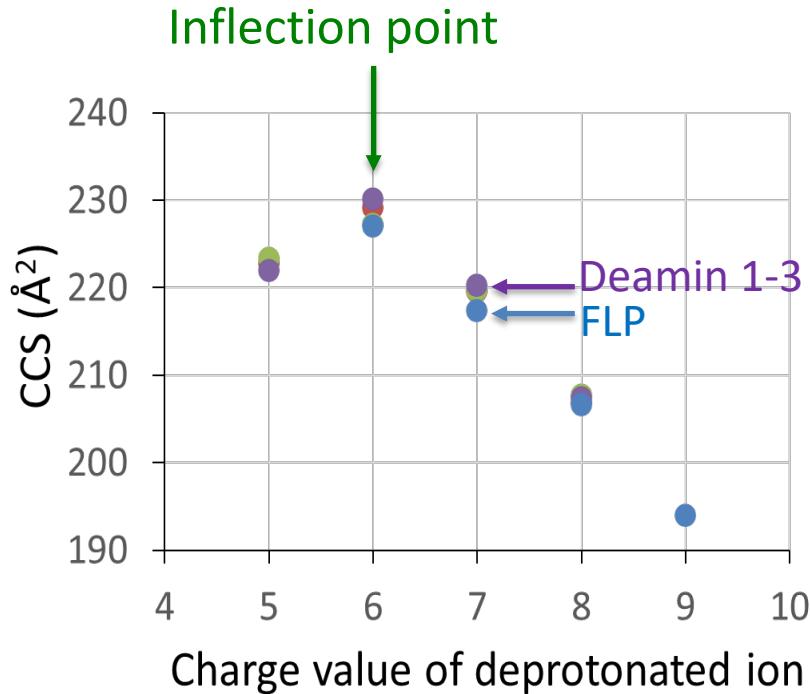


Table 1. Custom-synthesized FLP and isomeric or isobaric impurities

Name	Sequence	Theoretical Molecular Weight (g/mol)
FLP*	UCACUUUCAUAAUGCUGG (nusinersen)	7126.2
Deamin_1	UUACUUUCAUAAUGCUGG	
Deamin_2	UCAU UUU CAUAAUGCUGG	7127.2
Deamin_3	UCACUUU U AUAAUGCUGG	
n-G_1	UCACUUUCAUAA G CUGG	
n-G_2	UCACUUUCAUAAUGCUG G	6706.9
n-U_1	U CACUUUCAUAAUGCUGG	
n-U_2	UCAC U UUCAUAAUGCUGG	
n-U_3	UCACUUUCA U AUAAUGCUGG	6732.0
n-U_4	UCACUUUCAUAA U GCUGG	
n-U_5	UCACUUUCAUAAUGC U GG	

*FLP has the same sequence and modifications as nusinersen.

FLP and Deamination Products: CCS



FLP*	UCACUUUCAUAAUGCUGG
Deamin_1	UUACUUUCAUAAUGCUGG
Deamin_2	UCAUUUUCAUAAUGCUGG
Deamin_3	UCACUUUUUAUAAUGCUGG

- Deamin 1
- Deamin 2
- Deamin 3
- FLP

FLP is separated slightly from the deamination products.

FLP and Deamination Products: Relative DT shift



	RSD (%) of DT		
Reference:	-6	-7	-8
FLP	0.79	0.64	0.66

	% Relative DT shift		
	-6	-7	-8
Deamin_1	0.71	0.86	0.08
Deamin_2	0.33	0.92	0.13
Deamin_3	1.10	1.09	0.07

	-6	-7	-8
Deamin_all	0.40	0.9366	0.02



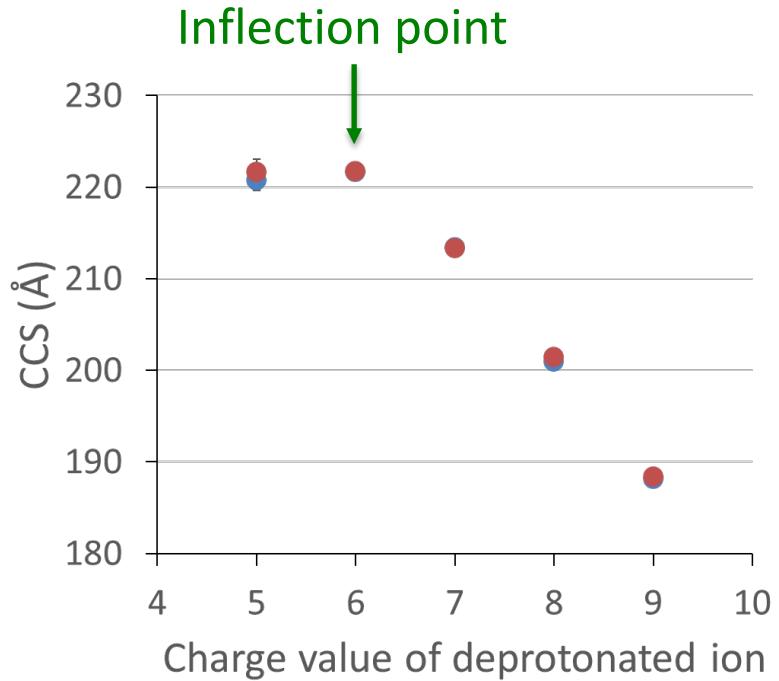
$$n = \% \text{ Relative DT shift} / \text{RSD (\%)} \text{ of DT of reference}$$

* $n > 1$ or above indicates a detected difference in mobility between a tested compound vs reference.

% Relative DT shift of all deamination products for $[M - 7H]^{7-}$ exceeds the DT RSD (%) of the FLP, i.e., yellow coded for $n > 1$.

n-G Impurities (Isomers): CCS

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n-G_1	UCACUUUCAUAAUGCUGG
n-G_2	UCACUUUCAUAAUGCUGG

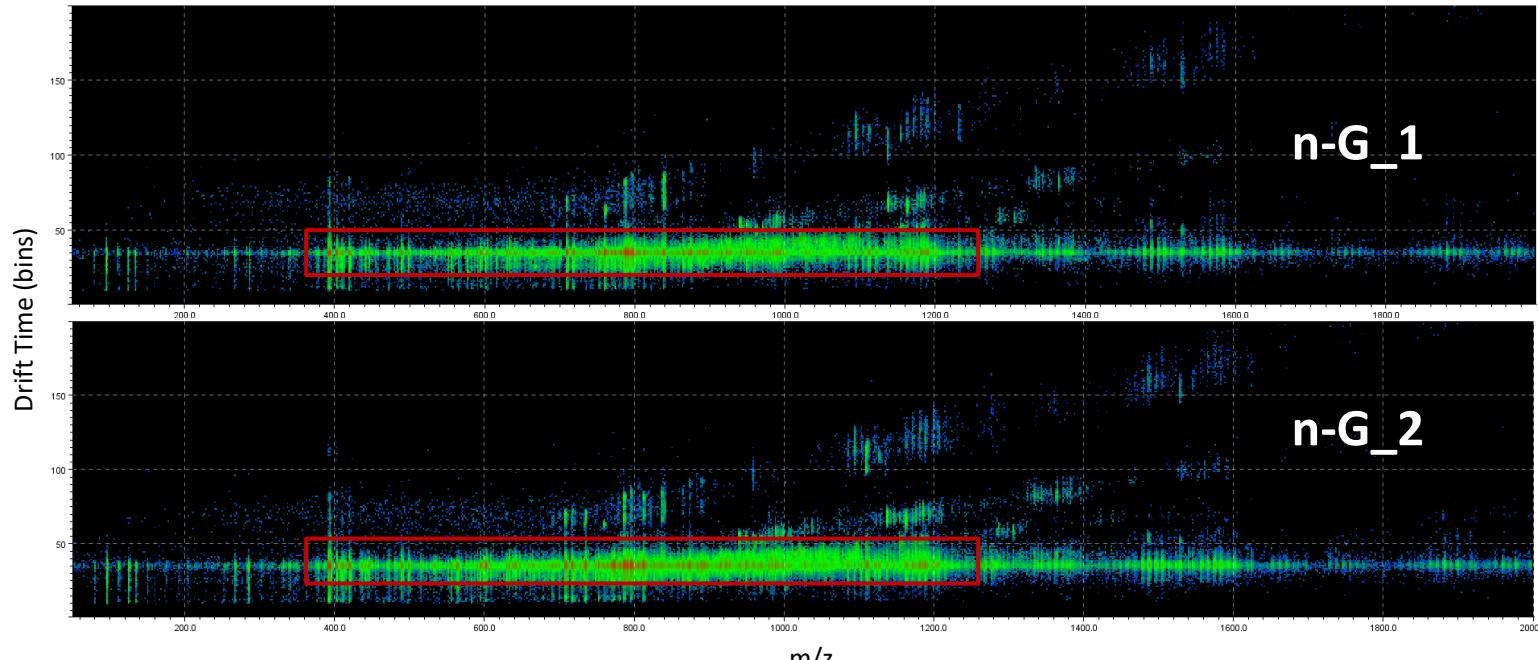
- n-G_1
- n-G_2

Indistinguishable by IM
regardless of charge state.

n-G Impurities (Isomers): MS/MS After IM Separation



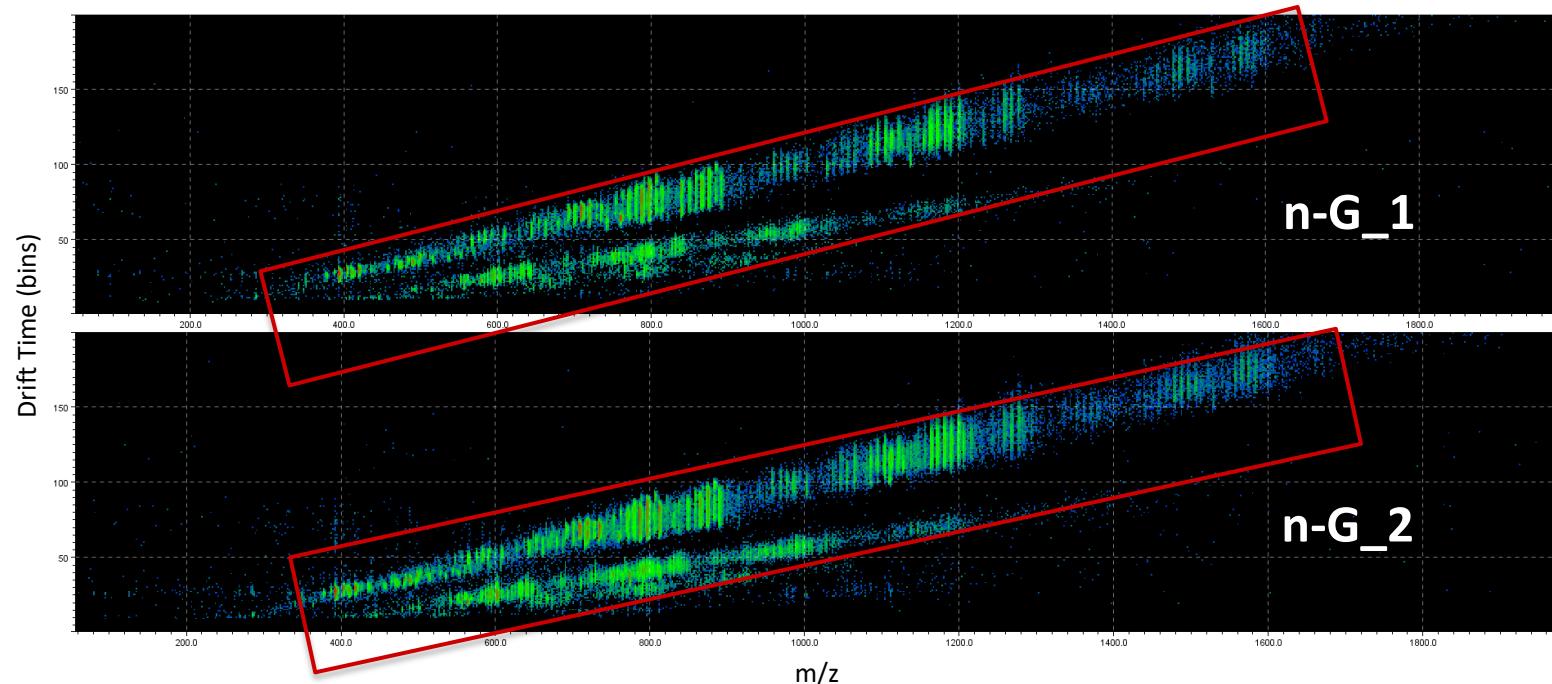
- Fragments have identical DT that aligns with the DT of precursor ions



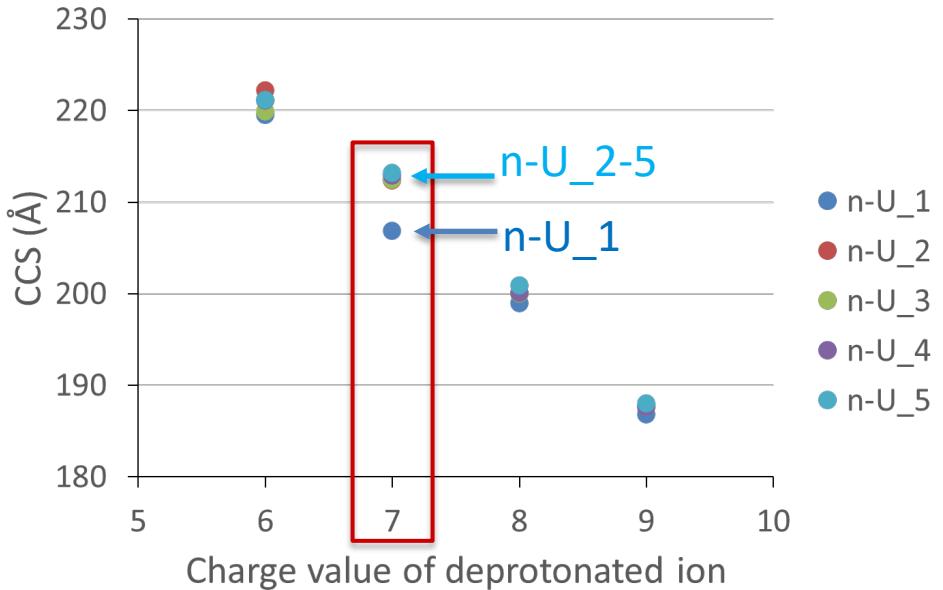
n-G Impurities (Isomers): MS/MS Before IM Separation



- Fragments undergo IM separation. Distinguishable fragments may help differentiate isomeric precursors.



n-U Impurities (Isomers): CCS



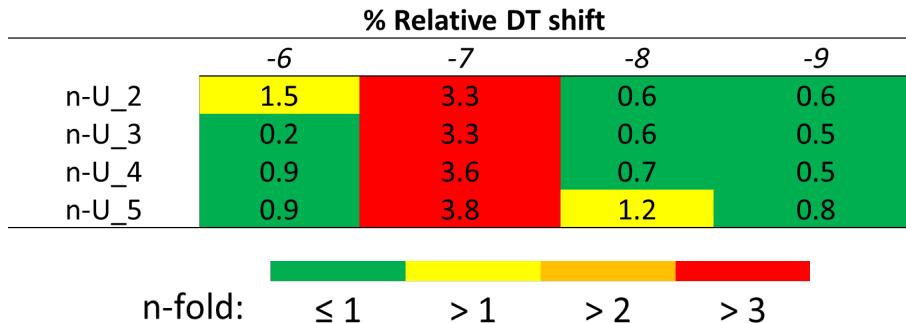
n-U_1	UCACUUUCAUAAUGCUGG
n-U_2	UCACU <u>U</u> CAUAAUGCUGG
n-U_3	UCACUUUCA <u>U</u> AAUGCUGG
n-U_4	UCACUUUCAUAA <u>U</u> GCUGG
n-U_5	UCACUUUCAUAAUGC <u>U</u> GG

n-U_1 (terminal deletion) is separated from the others.

n-U Impurities (Isomers): Relative DT Shift



Reference:	RSD (%) of DT			
	-6	-7	-8	-9
n-U_1	1.1	1.0	1.1	1.1

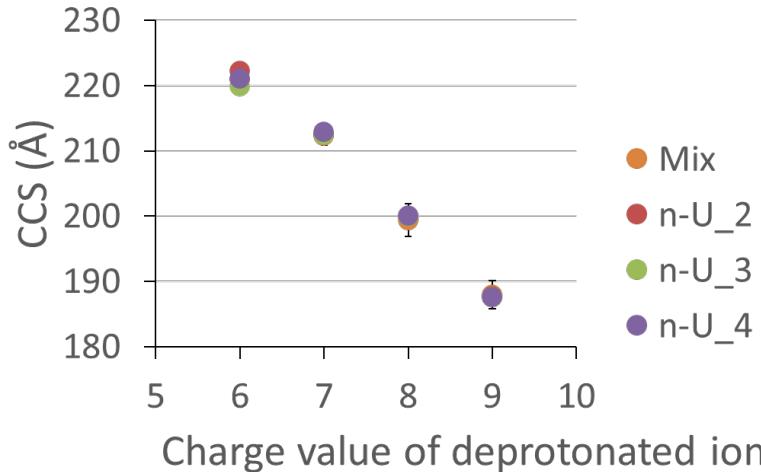


$$n = \% \text{ Relative DT shift} / \text{RSD (\%)} \text{ of DT of reference}$$

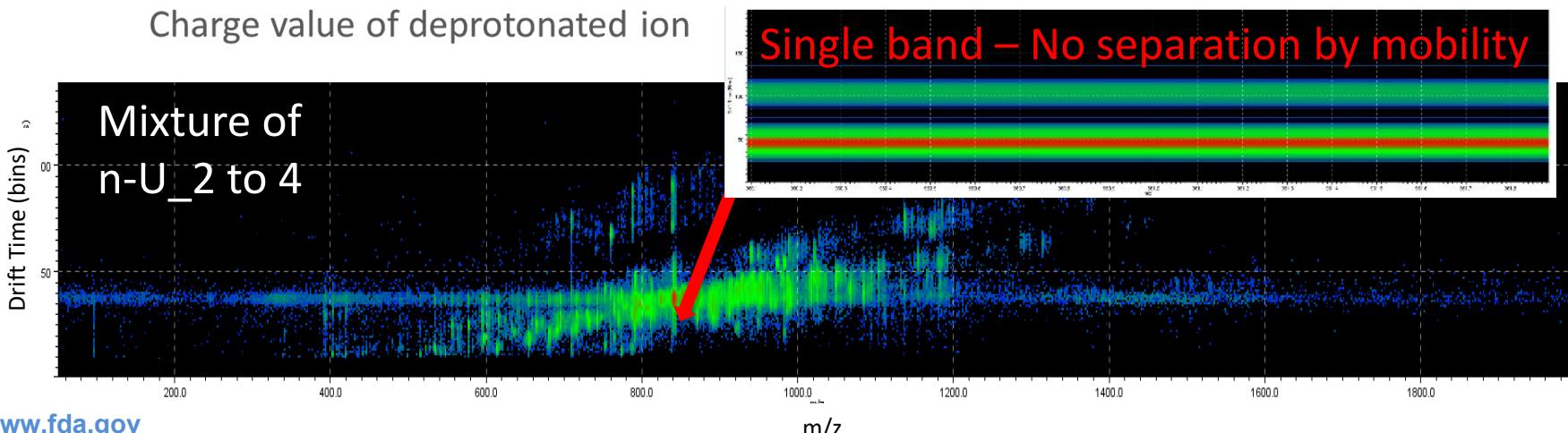
**n > 1 or above indicates a detected difference in mobility between a tested compound vs reference.*

% Relative DT shift of the n-U_2 to 5 isomers exceeds the RSD (%) of n-U_1 by over 3-fold for $[M - 7H]^{7-}$, i.e., red coded for $n > 3$

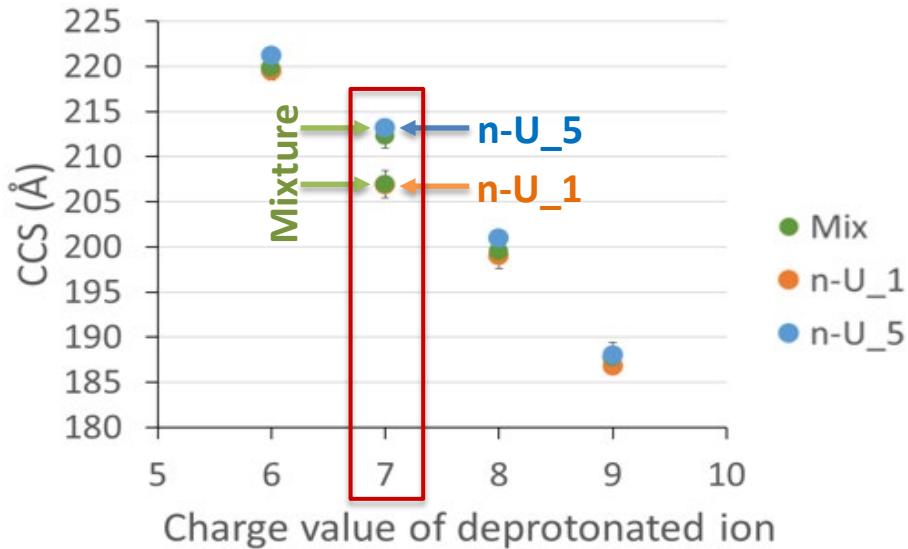
Mixture of n-U Impurities (n-U_2 to 4): CCS



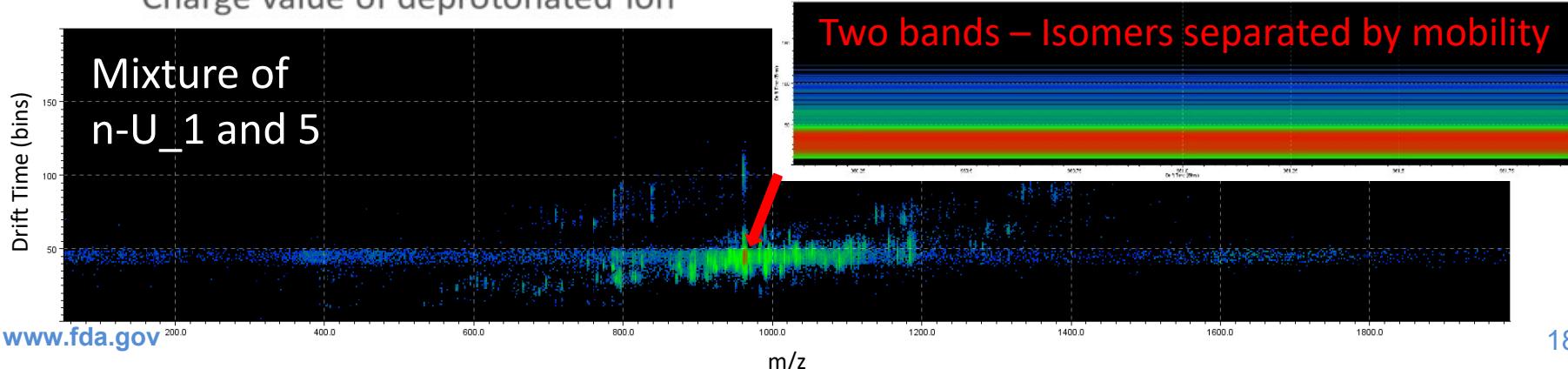
No difference in CCS
regardless of charge state.



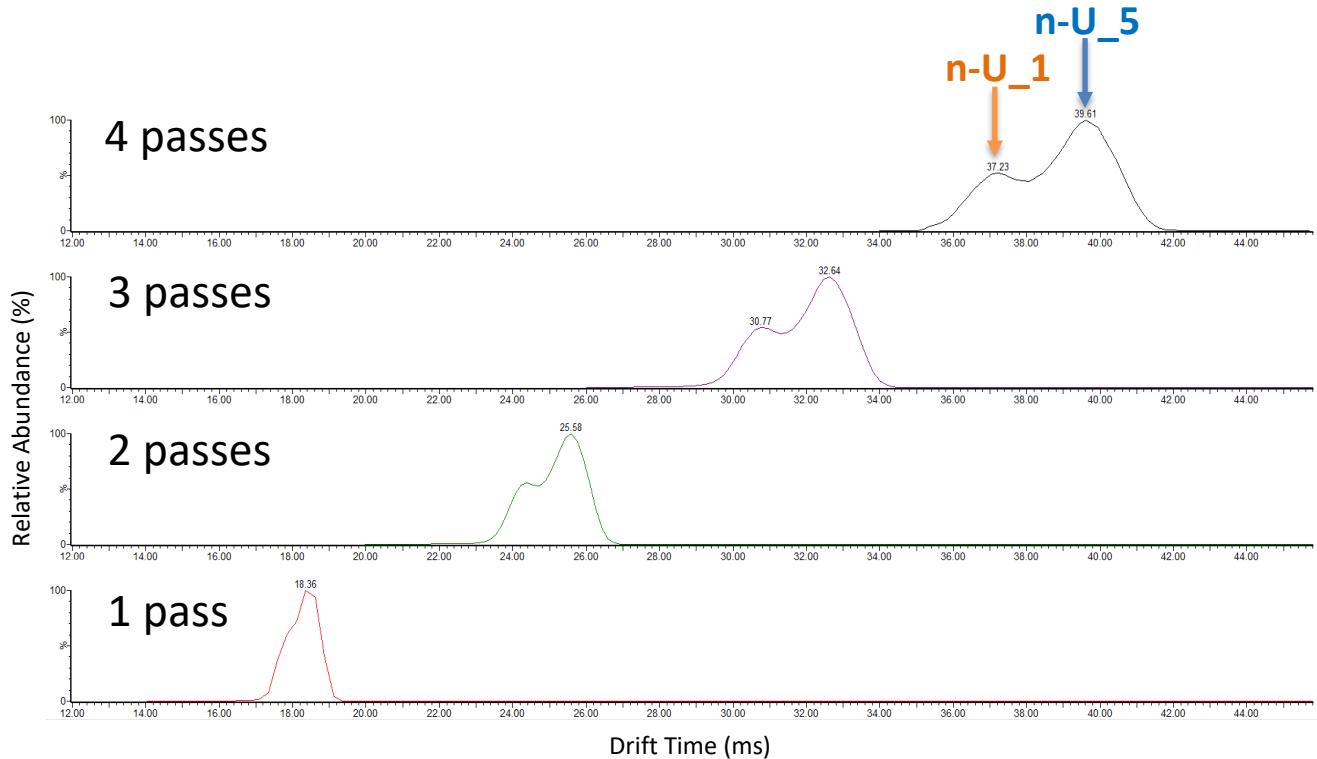
Mixture of n-U Impurities (n-U_1 and 5): CCS



CCS values for the two ion populations of the mixture overlay with those for individual isomers measured separately.



Mixture of n-U Impurities (n-U_1 and 5): cIM Multi-pass



Multi-pass enables better-resolved separation of coeluting isomers.

Summary



- IM provides an additional dimension of separation orthogonal to LC and MS.
- An inflection point is observed in the plot of CCS vs charge state of oligonucleotide molecules. CCS decreases inversely with charge state after the point.
- IM separation of isomeric or isobaric molecules may be sequence- and charge state-dependent.
- cIM multi-pass has the potential to improve the separation resolution of structurally similar molecules.

Acknowledgement



- **Office of Testing and Research (OTR)**
 - ✓ MS team of OTR St. Louis: Josh Shipman
 - ✓ Division of Complex Drug Analysis (DCDA): Cynthia Sommers, Jason Rodriguez
- **Office of Generic Drugs (OGD)**
 - ✓ ORISE fund
 - ✓ Deyi Zhang, Darby Kozak
- **FDA Critical-Path Research Grants**
 - ✓ PI – Kui Yang (OTR/OPQ)
 - ✓ Collaboration offices: OPQ, OGD, OND, NCTR
- **FDA ORISE Fellowship Program at CDER through an agreement between the U. S. Department of Energy and U.S. FDA**
 - ✓ Mentors: Kui Yang (OTR/OPQ), Deyi Zhang (ORS/OGD)

