

Complex Molecules. Simpler Decisions.

Accelerating mRNA and Bioconjugate Development
With Integrated MS-Based Workflows

Ying Qing Yu, Ph.D.

Director Application Science, Biologics

Guillaume Béchade, Ph.D.

Senior Principal, Biologics Marketing

Future-proofing today for the biologics of tomorrow.

Waters™



Pipelines expand and accelerate

10–15% YoY growth



Most complex drugs ever made

Genetic material + Delivery vector
Antibody scaffold + Conjugated payload



Timelines are compressing

Fast-track regulatory acceleration
QC-ready methods demanded sooner



Measurement must keep pace

New, less accessible CQAs
Regulators require absolute accuracy

Three Analytical Pillars



Secure Product Quality

Direct, dependable methods measure
every critical quality attribute:
Nothing left to chance.



Bridge R&D and Compliance

An unbroken analytical thread
connecting early development to
compliant QC.



Drive Operational Efficiency

Streamlining and future proofing
critical new applications
with end-to-end workflows

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Xevo
CDMS



Xevo
MRT P10



Cyclic
IMS P20



Deconvolution,
Now built into
Empower CDS



waters_connect

Walk-up access
to HRMS on
waters_connect



mRNA
Product Quality Attributes
Characterization



Bioconjugates
(AOCs, ADCs)
Characterization

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CDMS



Xevo
MRT P10



Cyclic
IMS P20

Xevo CDMS | Precise measurement of large and highly heterogeneous molecules previously out of reach

New: nESI AutoLoader, SEC-CDMS, Qualification ready

Xevo MRT P10 | Excellent mass accuracy <500ppb improves results across a range of bio applications

New: x20 MS/MS sensitivity boost (m/z 50–1200)
100 Hz MS, 200 Hz MS/MS
SONAR Pulse DIA mode for enhanced depth of coverage

Cyclic IMS P20 | Max measurement depth for complex biologics

New: Expanded mass range >100 kDa, >10× MS/MS sensitivity,
Improved native MS spectral resolution,
Enhanced CIU workflows
DynamX 4.0 software release for HDX

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Xevo
CDMS



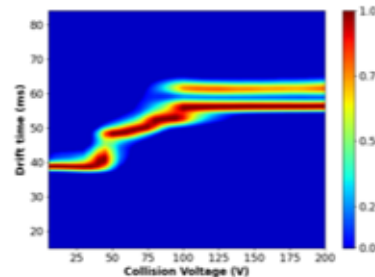
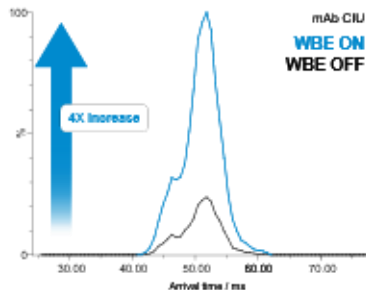
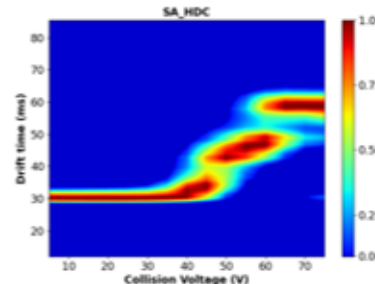
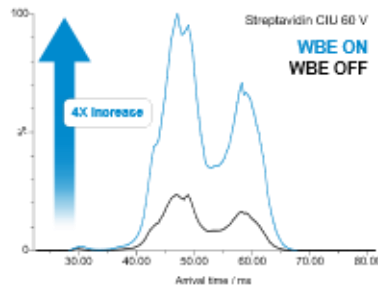
Xevo
MRT P10



Cyclic
IMS P20

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CDMS



Xevo
MRT P10

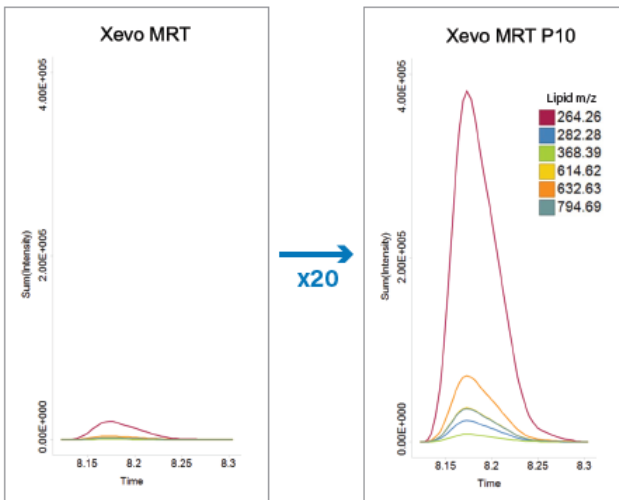


Cyclic
IMS P20

Xevo MRT P10 | Excellent mass accuracy <500ppb improves results across a range of bio applications

New: x20 MS/MS sensitivity boost (m/z 50–1200)
100 Hz MS, 200 Hz MS/MS
SONAR Pulse DIA mode for enhanced depth of coverage

a. Technology Improvements — Increased MS/MS Sensitivity



b. Competitive Positioning

Lipidomics analysis vs. another leading benchtop QTOF system

+30%
lipids detected

+40%
confidently identified

	Xevo MRT P10	Competitive Offering
Lipid IDs	1,150	880
Curated Lipids	640	460

SRM1950 NIST reference material
MS-Dial processing, same stringency

Future-proofing today for the biologics of tomorrow.

Waters™



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waters_connect



mRNA
Product Quality Attributes
Characterization



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Characterization

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Waters™

Complex biomolecule spectra become clear mass results - in-line, in real time, inside the compliant Empower CDS workflow your teams already use. SQD2 and Acquity QDa II mass detectors with ACQUITY Premier.

A clear answer, not a puzzle

Mass results your analysts can read, without specialist software or an expert review step.

No waiting for the answer

Processing happens as the run happens, so there is no gap between acquisition and answer.

Everything stays in Empower

No moving data between systems: your people stay in their compliant environment.

LC-MS your whole team can use

Routine users in Discovery, Development and QA/QC get meaningful insight themselves.

Built for

Discovery • Development • QA/QC • Oligonucleotide and genetic medicines • GLP-1 • Protein therapeutics

Takes LC-MS beyond specialist MS groups into routine, regulated analysis, with less training and support to carry.

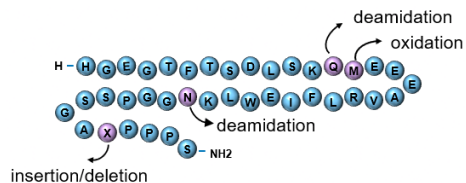
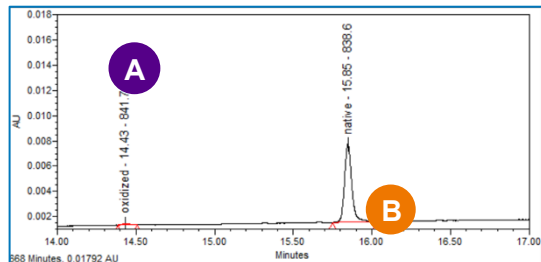


Deconvolution, now built into Empower CDS

Waters™

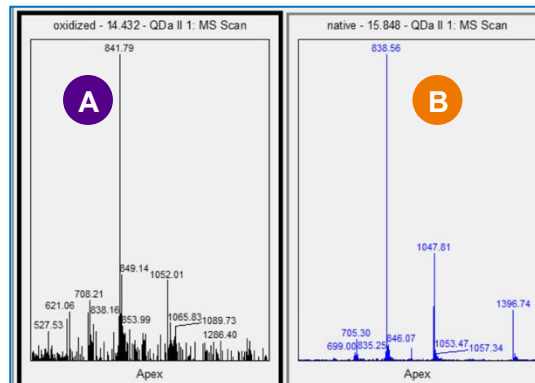
Exenatide (GLP-1 analog) using ACQUITY Premier and Qda II

1 Impurity separates by LC



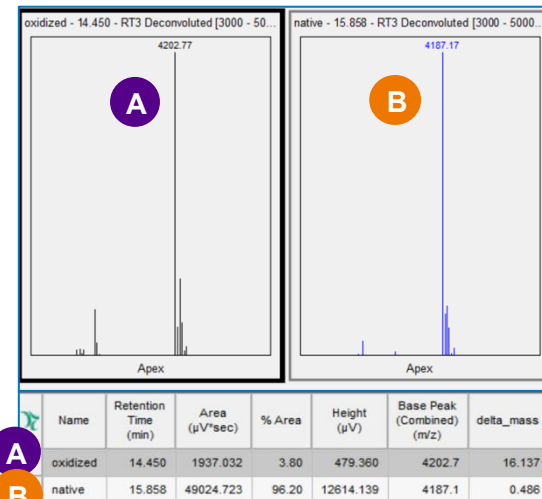
TIC chromatogram. Spectra collected across both LC peaks: A oxidised, B main product.

2 Raw m/z is hard to read



Multiply charged envelopes confirm identity, but need specialist review.

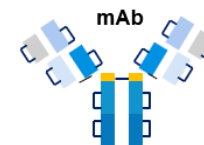
3 Deconvolution answers it



In-line deconvolution returns $z = 0$ masses: Identity of the main product and impurity ($\Delta = 15.6$ Da, oxidation) confirmed

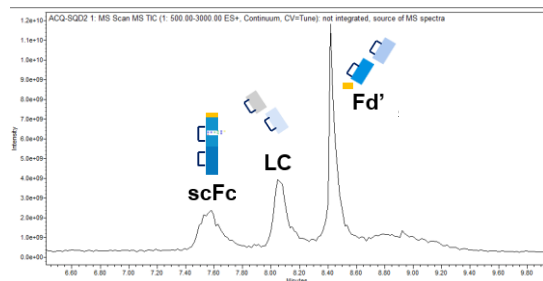
Deconvolution, now built into Empower CDS

mAb digested with IdeS, analysed using Acquity Premier and SQD 2



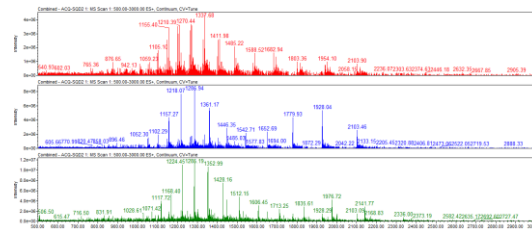
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1 Chains separated by LC



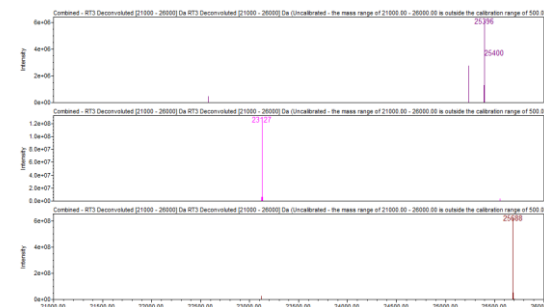
TIC chromatogram: the three mAb subunits separate chromatographically, with spectra collected across all three LC peaks.

2 Raw m/z is hard to read



Multiply charged envelopes in the m/z spectrum confirm identity, but need specialist review.

3 Deconvolution gives subunit masses



In-line deconvolution returns $z = 0$ masses for each subunit, confirming identity.

Biotherapeutic and Process Characterization and Monitoring waters_connect compliance ready ecosystem

Deployable across Discovery Development, Manufacturing and QC

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Characterization

Attribute Monitoring

Routine/QC Release

Attribute Characterization LC-MS platforms

Xevo™ MRT

Xevo™ G3 QTof MS



Users/Client PC(s)



Network Server
Managed Data Scientific Library
Compliance Tools



Attribute Analysis LC-MS systems

BioAccord™ LC-MS System



LC Optical System(s)
and Client PC



Peptide
MAM



UNIFI™



INTACT
Mass



MAP
Sequence



CONFIRM
Sequence



Bioprocess
Monitor

Ready Access | Broader access, with expert control

Waters™

Designed for discovery, development, CRO/CDMO and shared-user laboratory settings

For scientists submitting samples

-  **Guided submission**
A focused interface supports users with varying levels of MS experience.
-  **Faster access to data**
Identity and purity information can be available closer to the point of decision.
-  **Actionable output**
Automated processing generates a consistent INTACT Mass PDF report.

For LC–MS specialists and system owners

-  **Predefined methods**
Administrators determine the acquisition and processing combinations available to each submitter.
-  **Reduced routine workload**
Automated acquisition, processing and reporting reduce repeated submission tasks.
-  **More effective use of resources**
Specialists can focus on complex analyses, method development and troubleshooting.

Supported platforms

BioAccord™

Xevo™ G3 QTof

Xevo™ MRT

using the waters_connect □ INTACT Mass Application

Ready Access | A guided route from sample to result

Simplifying submission while the LC-MS specialist retains control of the methods

Waters™

1 Enter user details

Enter analysis information

Your information

Subscriber: RMA Jones

Email address: rjones@rma.com

Analysis data

Choose tray: 96

Plate: 1

Analysis data: AHS - 48 tube 0.00m, holder

Submit

Note for administrator: Any updates to the JSON file will require this app to be restarted

Choose the user.

2 Enter sample details

Enter sample information

Sample name	Sample description	Method	Sample position	Sample information	Method ID	Sample information ID	Sample information ID
01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01
01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01
01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01
01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01	01_01_01_01_01

Submit

Enter an individual sample or a sample set through a focused interface. Select from administrator-defined acquisition and processing method combinations

3 Place the samples

Follow the on-screen position guidance, then submit the analysis.

4 Review results

Access the automatically generated INTACT Mass PDF report from the designated location.

The INTACT Mass Application remains the analysis engine. Ready Access provides the simplified submission experience through its API.

Proteins & subunits

Peptides

Oligonucleotides

Small molecules

Bioconjugates

GLP-1

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waters_connect



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mRNA
Product Quality Attributes
Characterization



Bioconjugates
(AOCs, ADCs)
Characterization

Full knowledge of complex RNA structures is required

Make robust project decisions based on confident product understanding

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Comprehensive, early
RNA product
characterization

Avoids unexpected
project delays later in
development

Positions for the best
chance of regulatory
success



Legacy LCMS
methodology for RNA
analysis

Complex, manual and
requires significant
expertise

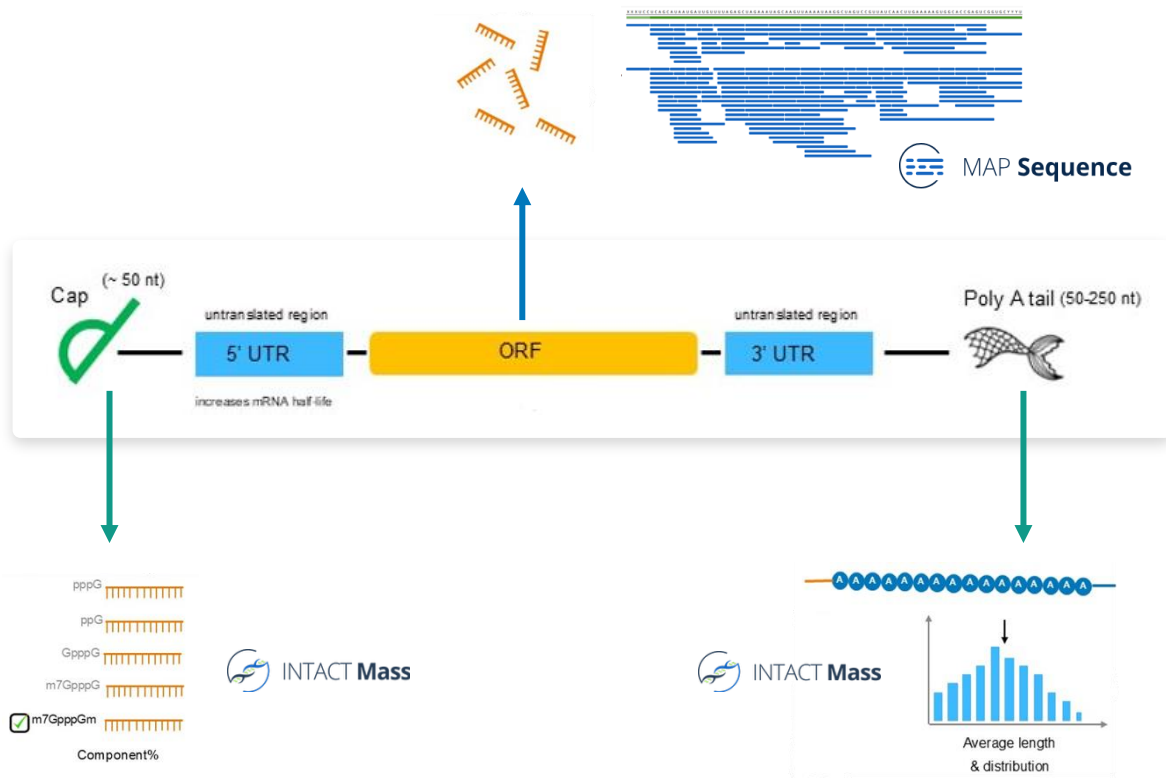
Difficult to deploy in a
regulated environment

Complex samples have historically required **time consuming** analysis, with **potential for errors**

Future-proofing mRNA Critical Quality Attributes Characterization

Automated determination for efficacy, process robustness and commercial suitability

Waters™



Confidently monitor
RNA sequence



Routine digested oligo mapping with
comprehensive sample preparation
and software workflows

Routinely track
mRNA CQAs



Automated workflows for 5' capping
efficiency and 3' Poly(A) tail
heterogeneity

Confidently monitor
RNA sequence



Digested oligo mapping: enabling routine analysis

Simple workflow tools for confident sequence assignment

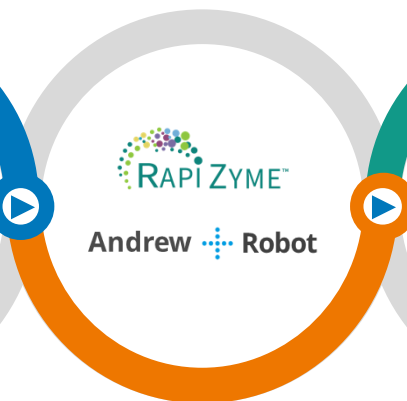
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Plan



Plan your experiment
with *in-silico* digestion
prediction tools

Prepare



Digest sample with
simple and fast
protocols

Separate



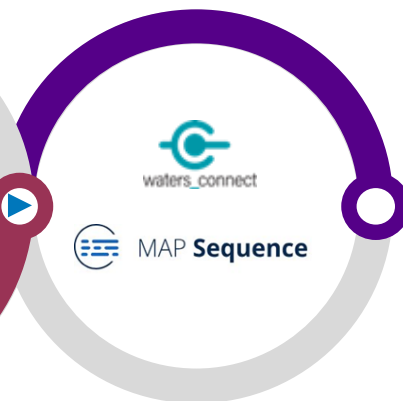
Liquid chromatography
optimised for nucleic
acids

Detect



MS/MS^E acquisition

Report



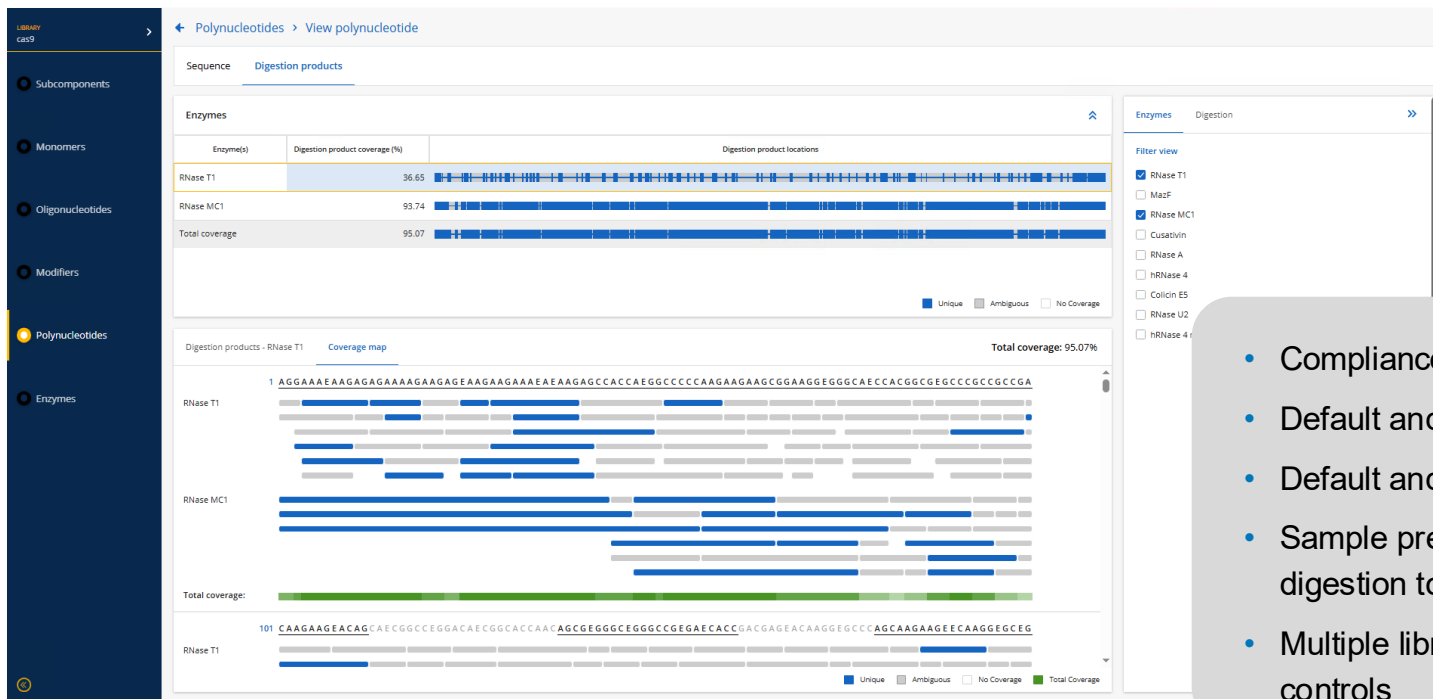
Process, review and
report with a dedicated
and streamlined
software application

Confidently monitor
RNA sequence



Plan

Waters™



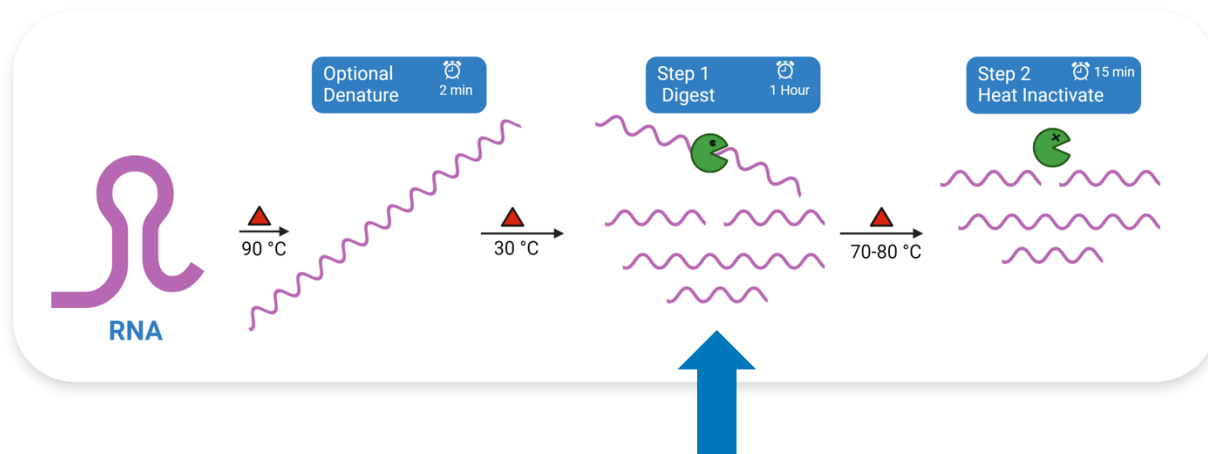
- Compliance-ready
- Default and user defined monomers
- Default and user defined enzymes
- Sample preparation planned with digestion tool
- Multiple libraries with user/role access controls

Confidently monitor
RNA sequence

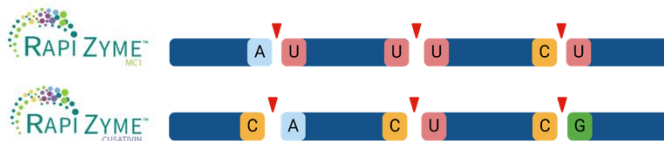


Prepare with RapiZyme RNases

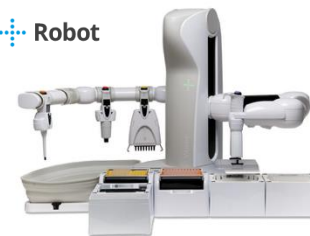
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Primary cleavage



Andrew  Robot



- Out of the box starter protocol for reproducible sample digestion with < 2-hour preparation
- Digestion protocols for Andrew+ robot available in the Protocol Library

Confidently monitor
RNA sequence

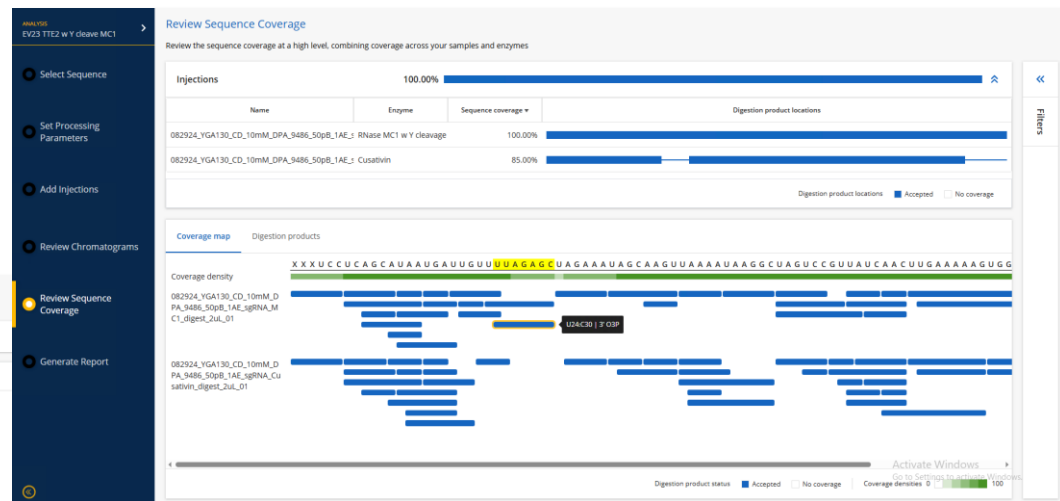
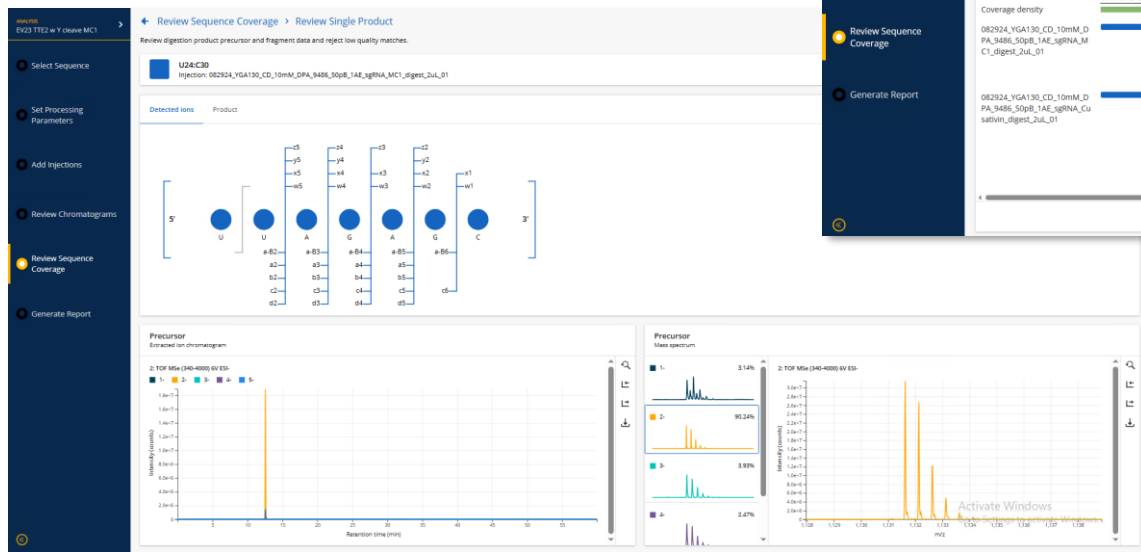


Report

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MAP Sequence



- Interactive chromatogram
- Dynamic coverage map
- Drill-down to raw data
- Data-rich reporting with e-sign

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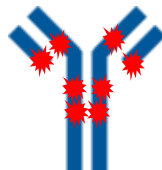
A Comprehensive LC-MS Characterization Toolbox for Antibody-Oligonucleotide Conjugates

Ying Qing Yu, PhD

Waters Corporation

Bioconjugates in the Market

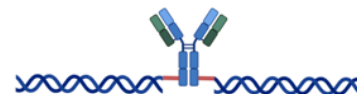
First FDA-approved ADC:
Mylotarg™ (gemtuzumab
ozogamicin) in 2000.



*ADC = Antibody
Drug Conjugate*

14+ Approved ADCs on the
market (as of 2026)

>100 ADC candidates currently in
clinical trials



*AOC = Antibody
Oligonucleotide Conjugate*

AOCs are gaining momentum,
with 10-20 programs in clinical
stage

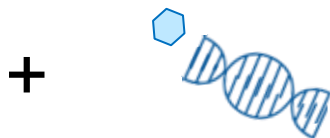
“Antibody...”



mAb

MW ~140 kDa

...Oligonucleotide...



Linker-siRNA

MW ~15 kDa

=

...Conjugate”



“AOC1”

MW ~160 kDa



“AOC2”

MW ~175 kDa

- Linker Chemistry
- Antibody-side attachment approaches
- Spacer types

- siRNA
- ASO
- SSO
- PMO
- Aptamer
- DNA and more

Case Study:

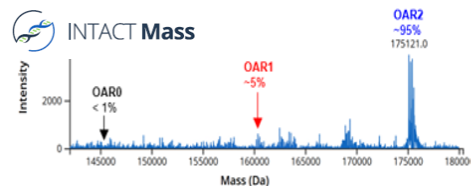


site-specific cysteine + C6
spacer + MCC linker

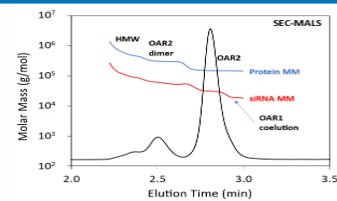
What we have done so far

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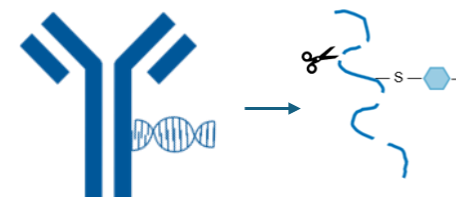
Oligo-Antibody Ratio



siRNA Confirmation



Conjugation Site ID



OAR by LC-MS: [720009048EN](#)

■ OAR & HMW by MALS: [WP8010](#)

■ siRNA: [720009066EN](#)

■ Conjugation Sites: [720009079EN](#)

plus

None Denaturing HILIC – MS for *Peptide-Oligo-Conjugates (POC)*

OAR and Oligo Distribution

BioAccord™
SYSTEM




waters_connect

 **INTACT Mass**



BioResolve™
COLUMNS



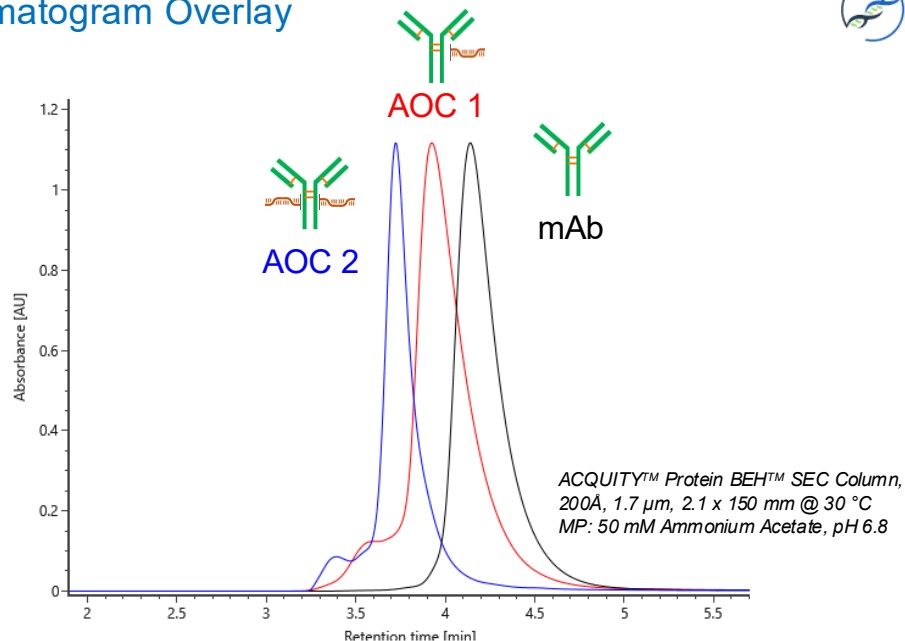
OAR and AOC Integrity: SEC-MS

OAR analysis and quantification

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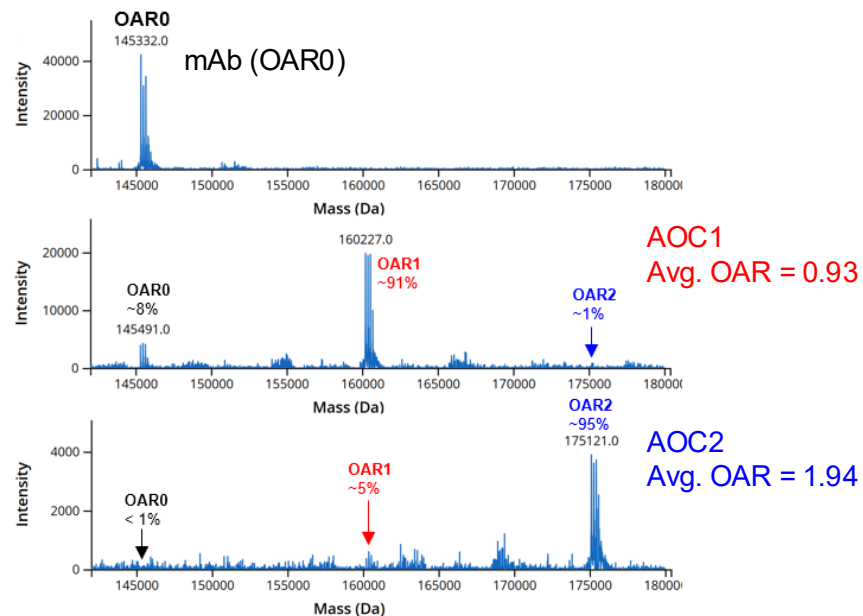
App Note [720009048EN](#)

Chromatogram Overlay



INTACT Mass

Deconvoluted Masses



Confidently obtain average OAR and oligo distribution by MS for discovery, conjugation, & formulation development

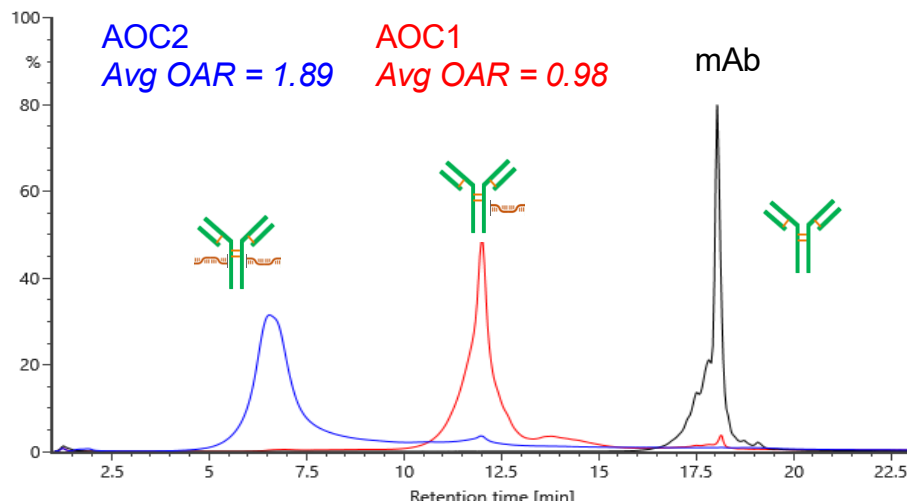
OAR and AOC Integrity: SCX-MS

Orthogonal non-denaturing method for High-Resolution analysis

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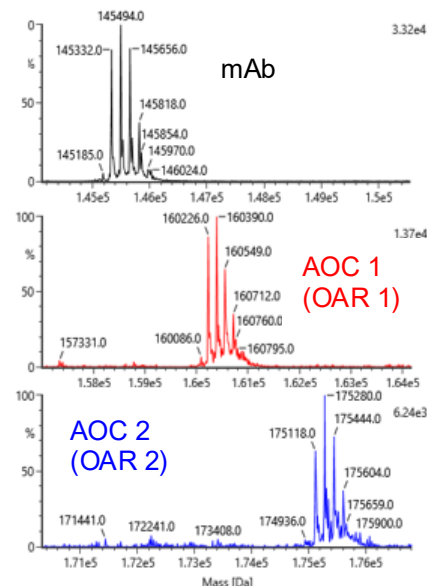
App Note [720009048EN](#)

Chromatogram Overlay



BioResolve™ SCX mAb Column, 3 μ m, 2.1 x 100 mm @ 30 °C
MPA: IonHance™ CX-MS Conc. A (50 mM Amm. Acet, pH 5.0)
MPB: IonHance CX-MS Conc. B (160 mM Amm. Acet, pH 8.5)

Deconvoluted Masses



OAR values can be calculated via either integrated UV area or extracted ion chromatograms (XIC)
Method chromatographically separates OAR species, preferred for later stages of development and QA/QC

OAR Results: Method Comparisons

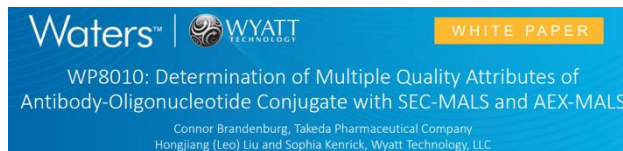
LC-MS OAR & Drug Distribution

AOC 1	SEC-MS	SCX-UV-MS
OAR0	~8%	~5%
OAR1	~92%	~92%
OAR2	~1%	~3%
Average OAR Value	0.93	0.98

AOC 2	SEC-MS	SCX-UV-MS
OAR0	< 1%	< 1%
OAR1	~5%	~11%
OAR2	~95%	~89%
Average OAR Value	1.94	1.89

OAR Methods: LC-MS & MALS

Sample	SEC-MS	SCX-UV MS-based	SCX-MS XIC-based	SEC-MALS	AEX-MALS
1	0.93	0.98	0.97	1.02	1.03
2	1.94	1.89	1.97	1.99	2.07



- Consistent drug distribution results between LC-MS methods
- Average OAR values obtained from both SEC-MS, SCX-MS, SEC-MALS, & AEX-MALS are comparable

Conjugation *Site* Analysis via Nucleoside Digestion



The Challenge: Conjugation Site Determination

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	Peptides	Oligonucleotides
Characteristics	Usually Less Polar & More Hydrophobic, Often Carry Positive Charge	Highly Polar, Negatively Charged
Typical LC conditions	RP (acidic pH)	IPRP or HILIC (neutral / slightly basic pH)
Typical MS and MSMS Mode	+	-
Obstacles	<u>LC Challenges:</u> • Oligo-peptide species likely not recovered in acidic RP conditions <u>MS Challenges:</u> • Oligo-peptide species is likely more negatively charged → May have ionization challenges or differences in (+) mode • Fragmentation could occur on oligo, peptide, or both	

Sample Pre-Treatment: The Novel Workaround

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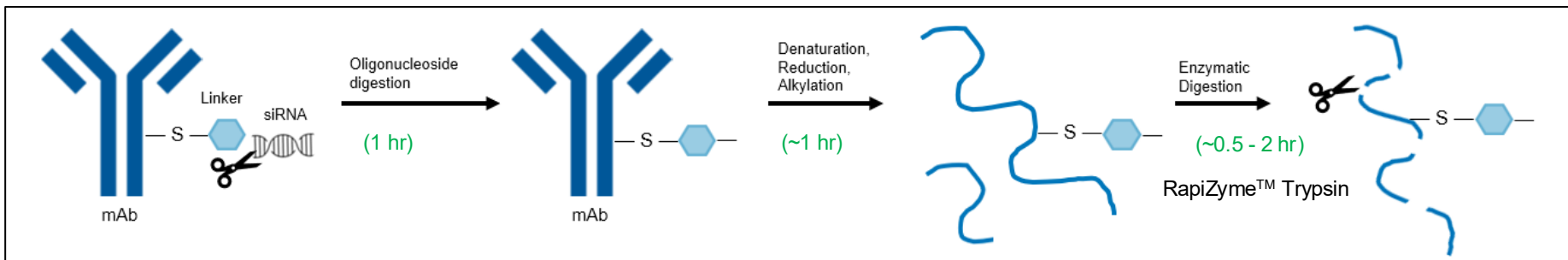
Xevo G3 QToF Mass
Spectrometer (MS^E &
DDA analyses)



waters_connect™
Informatics Platform

■ Development of a generic AOC peptide mapping protocol

- Sample pre-treatment with oligonucleoside digestion mix (NEB)
- Resulting digested product behaves just like an antibody with small modification
 - Standard peptide mapping sample preparation & LC-MS Analysis (RPLC-MS in acidic condition & ESI Positive MS & MSMS)

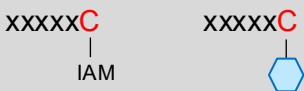


Peptides of Interest:

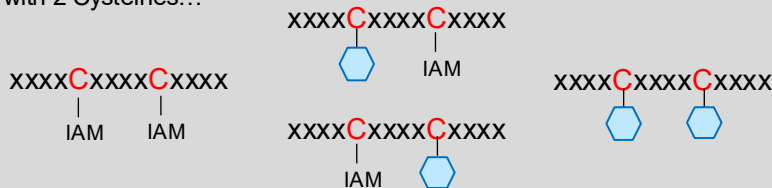
⬡ = MCC-C6

IAM = iodoacetamide
(carbamidomethylated Cys)

Peptide with 1 Cysteine...



Peptide with 2 Cysteines...

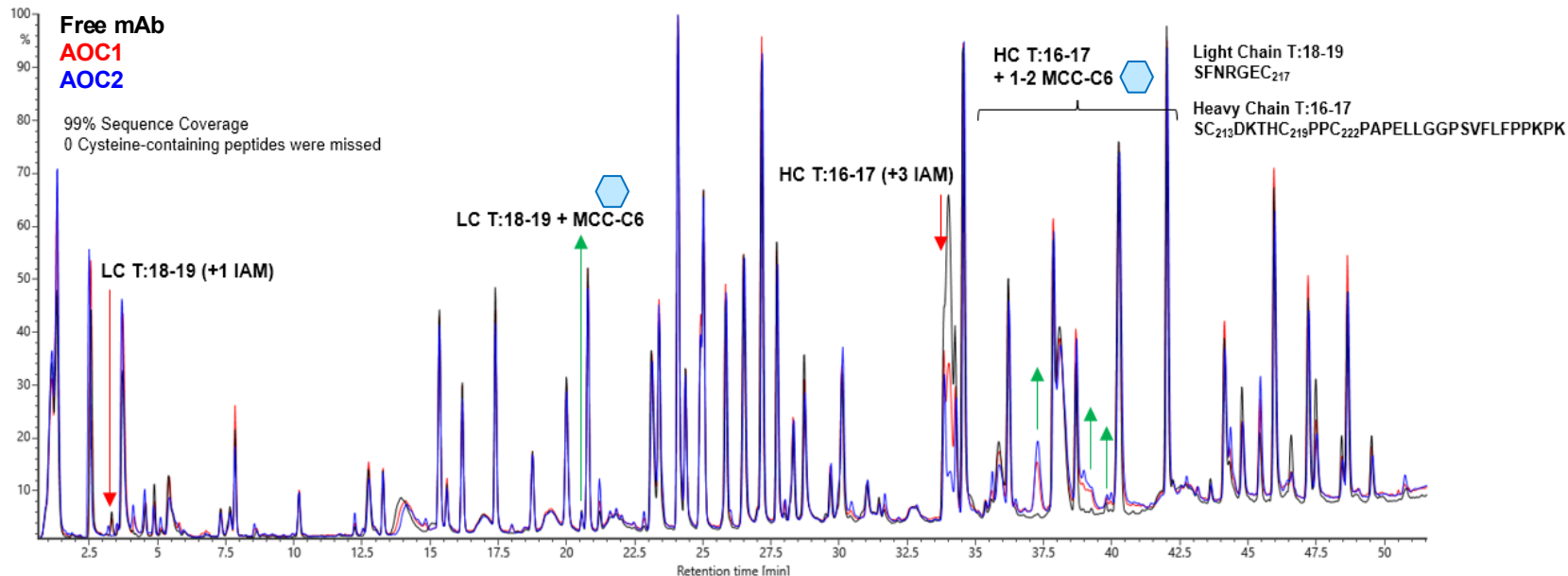


Conjugation site: RPLC-MS (Xevo G3 QToF Mass Spectrometer)

Waters™

Peptide mapping with AOC pre-digestion enables site localization

4 cysteine sites were conjugated



ACQUITY Premier CSH™ C18 Column, 130Å, 1.7 µm, 2.1 x 100 mm @ 60 °C

MPA: 0.1% Formic Acid in water

MPB: 0.1% Formic Acid in ACN

App Note [720009079EN](#)

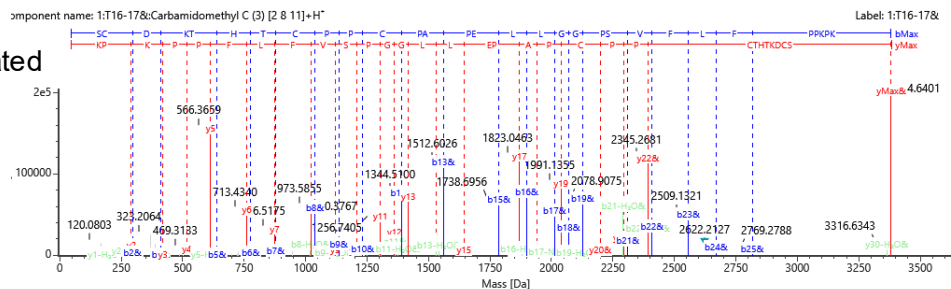
Conjugation site: RPLC-MS (Xevo G3 QToF Mass Spectrometer)

Waters™

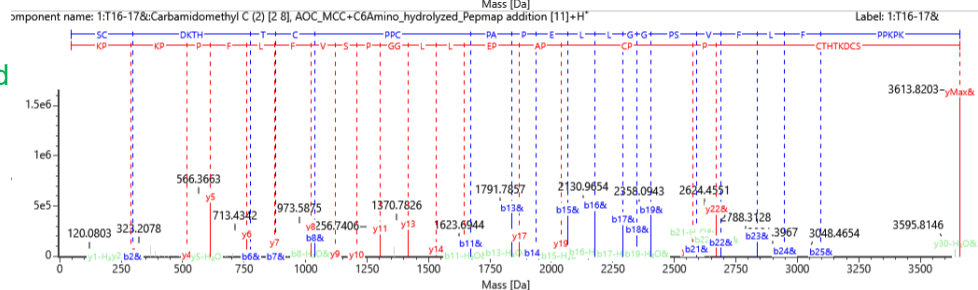
Peptide mapping with AOC pre-digestion enables site localization

App Note [720009079EN](#)

Unconjugated

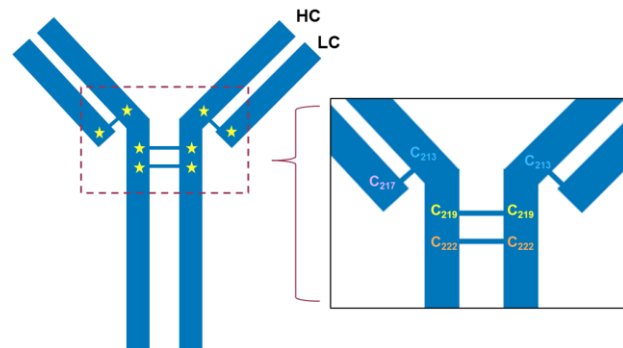


Conjugated



Fragment series beginning at b11 confirms conjugation site location C222

HC T16-17: SC₂₁₃DKTHTC₂₁₉PPKC₂₂₂PAPELLGGPSVFLFPPKPK



10-33% site occupancy detected per site

	AOC1	AOC2
LC: C ₂₁₇	14.3%	32.8%
HC: C ₂₁₃	16.3%	31.2%
HC: C ₂₁₉	15.7%	28.8%
HC: C ₂₂₂	9.9%	18.4%

Enzymatic removal of the oligo enables CID fragmentation and analysis with well-established software tools for confident conjugation site ID & quantitation

Native MS for Peptide-Oligo Conjugates (POC)

→ Synthesized POC mimicking the AOC tryptic peptide HC T16-17 with sense strand

BioAccord[™]
SYSTEM

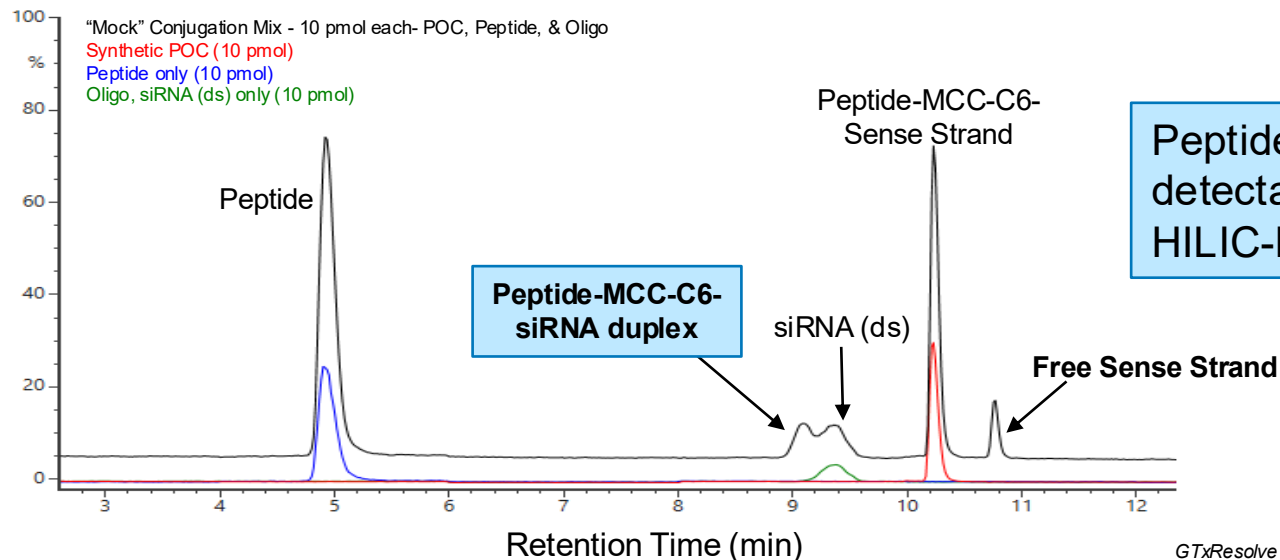



waters_connect



Non-Denaturing HILIC-MS Confirms Presence of Peptide-siRNA Duplex

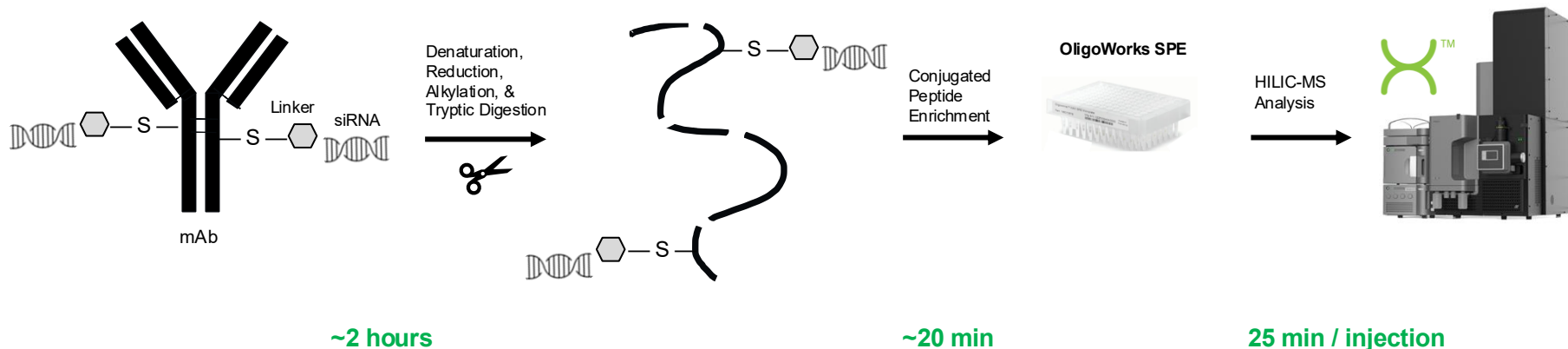
- Molar equivalent amounts of *unconjugated peptide*, *peptide-MCC-C6-Sense Strand*, & *unconjugated siRNA duplex* were mixed in solution to create *peptide-siRNA duplex species*
- *Duplex siRNA* species is separated from single stranded POC by HILIC & confirmed by mass

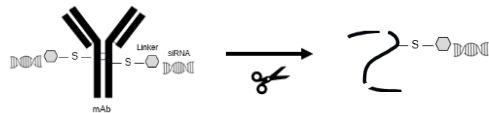


Peptide siRNA Duplex is only detectable via non-denaturing HILIC-MS method

Can We Apply the HILIC-MS Method for POC to AOC Digests?

- A successful method for non-denaturing HILIC-MS method was developed for synthetic POC species (including all components--peptide, oligo, conjugate) in a single analysis.
- *Could we apply the same methodology to proteolytically digested AOCs to identify and characterize the sites of conjugation?*
- ... YES... but we need some help from OligoWorks™ SPE Enrichment!





■ Peptide Mapping

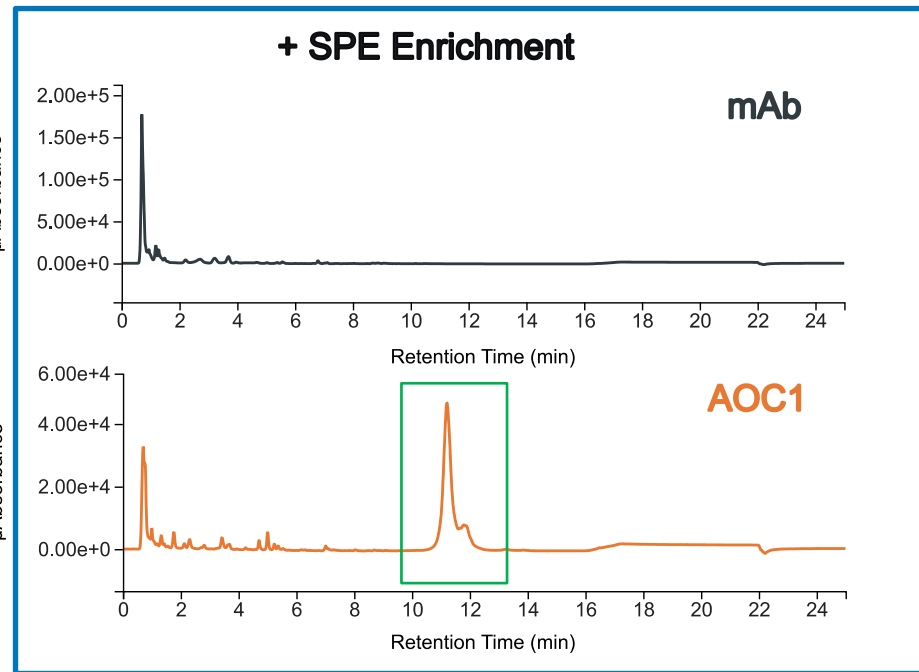
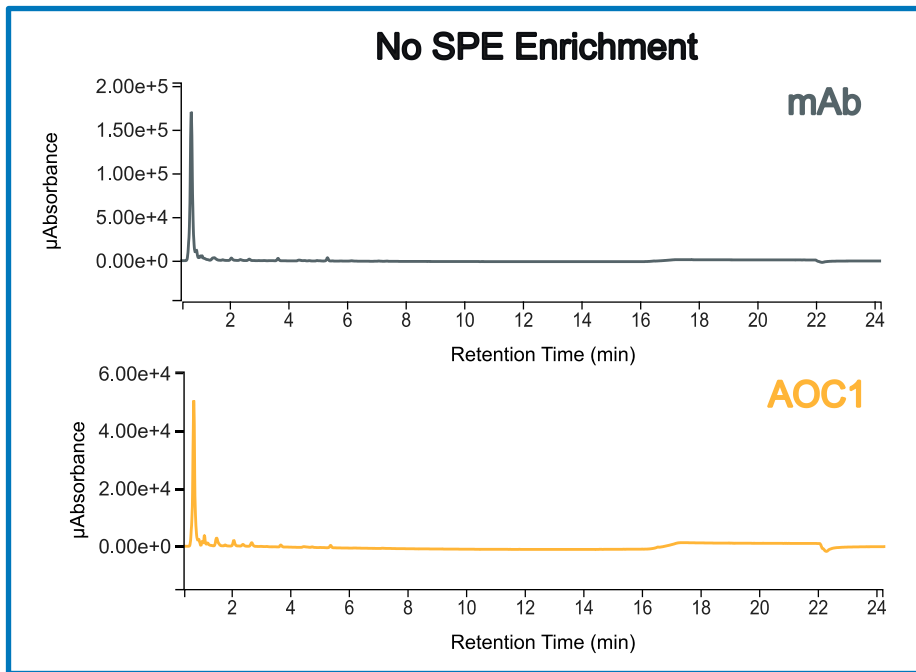
- Denaturation/Reduction: 4M Guanidine HCl, 10mM DTT (dithiothreitol) for 30 min at 50 °C
- Alkylation: 20 mM IAM (iodoacetamide) for 20 min at room temperature, followed by quenching with additional DTT.
- Dilution & Tryptic Digestion: Dilute sample 5x with 50 mM ammonium acetate, pH 6.8 and add 1:10 (w/w) RapiZyme Trypsin. Incubation for 1 hour at 37 °C.
- Split digested sample 1:1→
 - A) LC-MS analysis
 - B) Continue to SPE enrichment

■ OligoWorks SPE

1. Condition plate: 200 µL 50 mM Ammonium Acetate pH 5.5
2. Load sample (AOC digest diluted 1:1 with Wash Buffer 1 (50 mM Ammonium Acetate, pH 5.5)
3. Wash 1: 1 x 200 µL 50 mM Ammonium Acetate pH 5.5
4. Wash 2: 1 x 200 µL 30% Methanol
5. Elution: 2 x 25 µL SPE Elution buffer (100 mM TEA in 50% Methanol, 0.3% ammonium hydroxide, pH 3)
6. Dilute 1:1 with Acetonitrile to bring starting concentration of organic solvent to ~75% for HILIC-MS

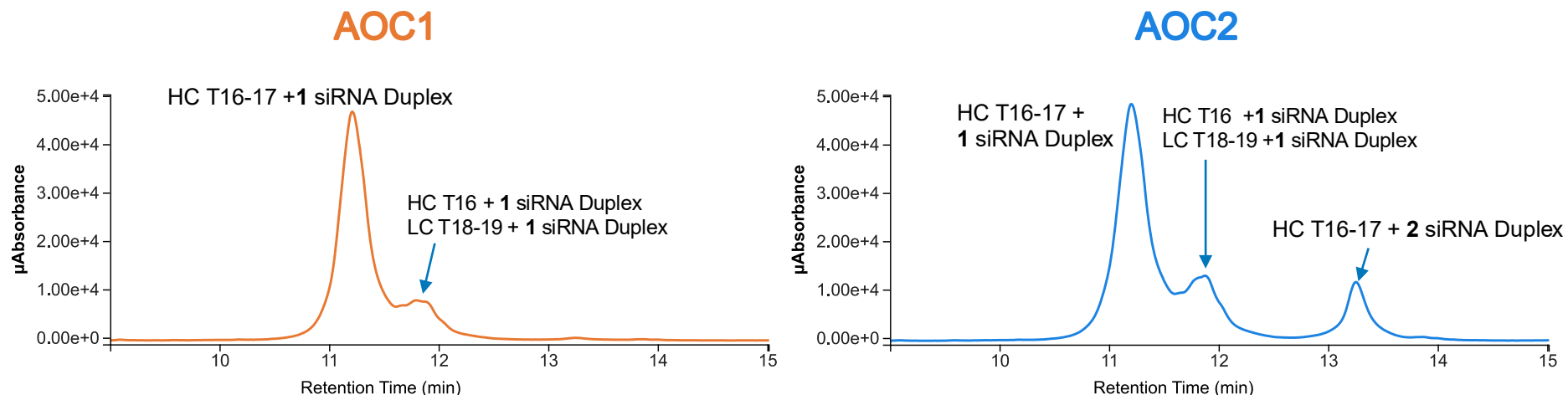
HILIC-MS Analysis of AOC Tryptic Digests $\pm$ SPE Enrichment

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OligoWorks SPE enrichment enables the detection of oligonucleotide-conjugated peptides by HILIC-MS. Species detected include hinge region peptides conjugated to 1 siRNA duplex (HC T16-17, HC T16, & LC T18-19), the same peptides identified by previous nucleoside digestion workflow.

Non-Denaturing HILIC-MS of AOC1 & AOC2 Enriched Digests

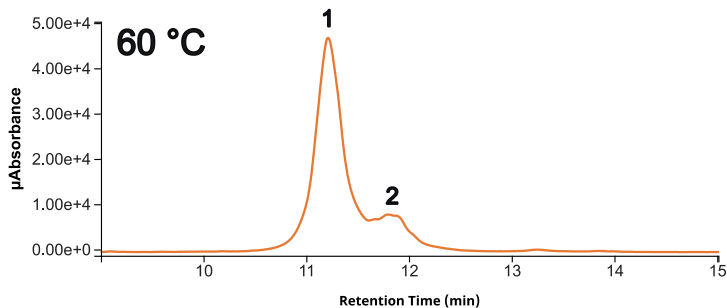


Non-denaturing HILIC-MS analysis of SPE-enriched digestions of AOC1* & AOC2** reveal the same hinge region peptides conjugated to 1 siRNA duplex (Peaks 1 & 2). AOC2 contains an additional species (Peak 3), corresponding to HC T16-17 peptide with 2 siRNA duplexes conjugated!

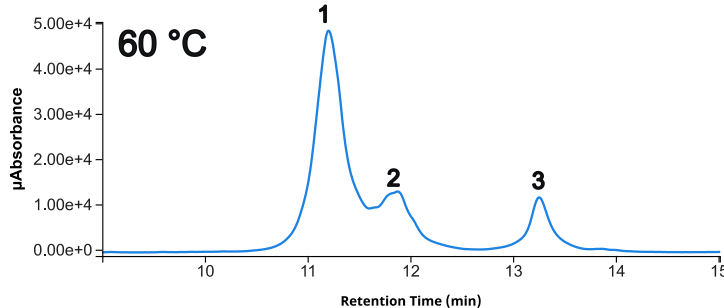
*AOC1 = average of 1 siRNA per mAb **AOC2 = average of 2 siRNA per mAb

Non-Denaturing & Denaturing HILIC-MS of AOC Digests

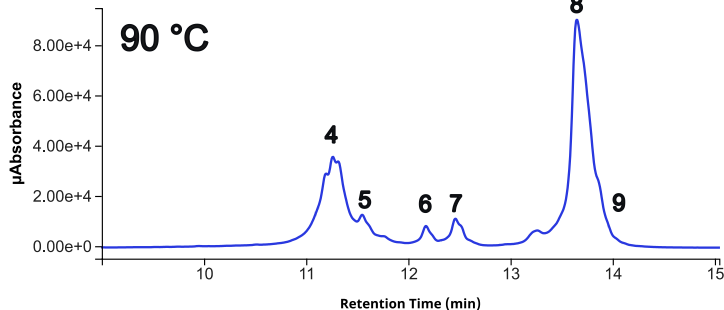
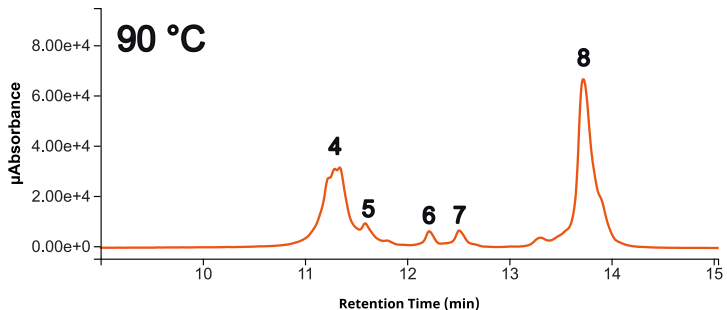
AOC1



AOC2



1. HC T16-17 + 1 siRNA duplex
2. HC T16 + 1 siRNA duplex & LC T18-19 + 1 siRNA duplex
3. HC T16-17 + 2 siRNA duplexes

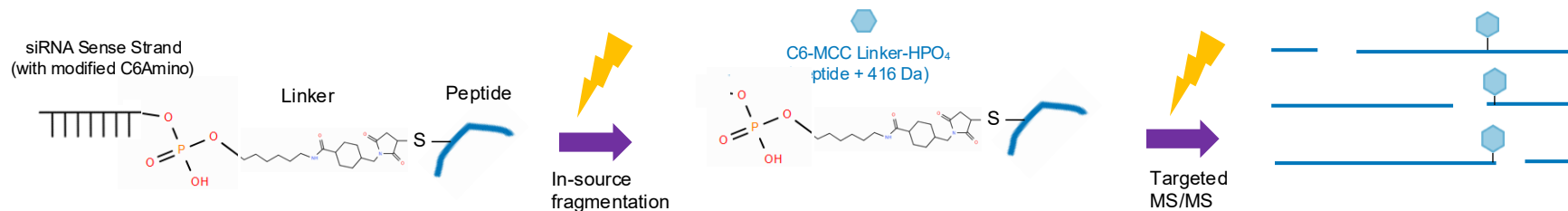


4. HC T16-17 + 1 Sense Strand
5. HC T16-17 + 1 Sense Strand +18 Da
6. LC T18-19 + 1 Sense Strand
7. HC T16 + 1 Sense Strand
8. Free Antisense Strand
9. HC T16-17 + 2 Sense Strand (AOC 2 only)

Denaturing HILIC-MS confirms the same hinge region peptides conjugated to the siRNA sense strand. Denaturing HILIC-MS is used for further investigation of the conjugation sites.

MS Approach for Oligo-Peptide Confirmation & Site Information

HILIC-MS (ESI-Positive mode)



1 Intact peptide-oligo ID

(First LC-MS run with lower source cone voltage (e.g. 40V)) to identify the peptide-oligonucleotide species.

2 Generate Precursor Ion

Use in-source fragmentation (via elevated source cone voltage (e.g. 160-165V)) to generate a predictable Peptide-MCC-C6-HPO₄ species (among other fragments)

3 Targeted MSMS

Use quadrupole to isolate Peptide-MCC-C6-HPO₄ precursor ion, & perform MS/MS on this species with collision energy ramp → generates peptide backbone fragment ions for ID (& use UNIFI to match fragments)

- Bioconjugates such as ADCs, AOCs, & POCs are a unique class of biotherapeutics gaining momentum in the industry.
- ...which come with additional CQAs to monitor (DAR/OAR, conjugation site determination..), on top of already complex biomolecule components.
- These conjugated moieties pose new analytical challenges, which require novel approaches using robust & reliable hardware and instrumentation. Many of these CQAs have been successfully addressed in these case studies!
 - *DAR/OAR by SEC or IEX coupled to MS or MALS*
 - *AOC/POC conjugation site determination by Nucleoside-assisted RPLC-MS*
 - *POC characterization via non-denaturing and denaturing HILIC-MS*
 - *OligoWorks (WAX) SPE can enrich POC, improves MS detection of the intact POC*

Acknowledgement

Sample generation while at Takeda Pharma

- Connor Brandenburg, Senior Research Associate
- Tara MacCulloch, Ph.D., Scientist

Waters

- Samantha Ippoliti, M.S., Principal Scientist
- Ying Qing Yu, Ph.D., Director
- Martin Gilar, Ph. D., Research Fellow
- Nick Pittman, Senior Marketing Manager
- Leo Liu, Ph.D., Senior Field Application Specialist
- Sophia Kenrick, Ph.D., Director
- Michelle Chen, Ph.D., Senior Director
- Brad Williams, Ph.D., Principal Sales Application Chemist



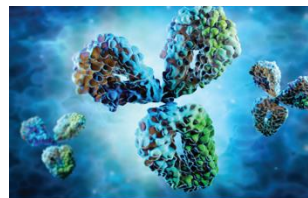
■ ADCs

- ADCs (Native SEC-MS) on Xevo MRT Mass Spectrometer ([720009175EN](#))
- ADCs on Xevo G3 QToF Mass Spectrometer ([720008214EN](#))
- ADCs on BioAccord System ([720006570EN](#))
- INTACT Mass Application- Automatic ADC DAR Feature ([720008818EN](#))

– [Bioconjugates Landing Page](#)

■ AOCs

- Part 1: Intact AOC & OAR ([720009048EN](#))
- Part 2: siRNA Characterization ([720009066EN](#))
- Part 3: Conjugation Site Localization ([720009079EN](#))
- Waters-Wyatt White Paper: SEC-MALS & AEX-MALS ([WP8010](#))



Waters™

**Characterizing
Antibody Conjugates**

Efficient tools for purity, payload, sequence
confirmation, concentration determination,
testing, and more.

Guidebook:
[720009004EN](#)

Thank you!

Reference: Common Columns for LC & LC-MS

	Small Molecules	Oligonucleotides	Peptides	Proteins
Reversed Phase (RP)	ACQUITY Premier BEH™ C18 Column, 130Å, 1.7 µm, 2.1 x (50/100/150) mm	ACQUITY Premier BEH C18 Oligonucleotide Columns, 130 & 300Å, 1.7 µm, 2.1 x (50/100/150) mm	- ACQUITY Premier CSH Peptide C18 Column, 130Å, 1.7 µm, 2.1 x (50/100/150) mm - ACQUITY Premier BEH C18 Peptide Column, 130Å, 1.7 µm, 2.1 x (50/100/150) mm *New* BioResolve™ Peptide Phenyl-Hexyl Column	- ACQUITY Premier Protein BEH C4 Column, 300Å, 1.7 µm, 2.1 x (50/100/150) mm - BioResolve mAb RP Polyphenyl Column, 450 Å, 2.7 µm, 2.1 x (50/100/150) mm - MassPREP™ Micro Desalting Column, 1000Å, 20 µm, 2.1 x 5 mm
Size Exclusion Chromatography (SEC)	N/A	GTxResolve SEC Columns, 450, 1000, 2000Å, 4.6 x 150/300 mm	ACQUITY Premier BEH SEC Column, 125Å, 1.7 µm, 2.1 x 150 mm	ACQUITY Protein BEH SEC Column, 200Å, 1.7 µm, 2.1 x 150 mm
Strong Cation Exchange (SCX)	N/A	N/A	N/A	BioResolve SCX mAb Column, 3 µm, 2.1 x (50/100/150) mm
Anion Exchange (AEX)	ACQUITY Premier BEH C18AX Column, 130Å, 1.7 µm, 2.1 x (50/100/150) mm	- Protein-Pak™ Hi Res Q, 5 µm, 4.6 x 100 mm - Gen-Pak™ FAX, 2.5 µm, 4.6 x 100 mm	N/A	Protein-Pak Hi Res Q Column, 5 µm, 4.6 x 100 mm
Hydrophilic interaction chromatography (HILIC)	- ACQUITY Premier BEH Amide Column, 130Å, 1.7 µm, 2.1 x (50/100/150) mm - ACQUITY Premier BEH Z-HILIC Column, 130Å, 1.7 µm, 2.1 x (50/100/150) mm	GTxResolve Premier BEH Amide Column, 300Å, 1.7 µm, 2.1 x (50/100/150) mm	- ACQUITY Premier Glycoprotein BEH Amide Column, 300Å, 1.7 µm, 2.1 x (50/100/150) mm - GTxResolve Premier BEH Amide Column, 300Å, 1.7 µm, 2.1 x (50/100/150) mm	- ACQUITY Premier Glycoprotein BEH Amide Column, 300Å, 1.7 µm, 2.1 x (50/100/150) mm - GTxResolve Premier BEH Amide Column, 300Å, 1.7 µm, 2.1 x (50/100/150) mm
Other		Lipid RP: GTxResolve Lipid Phenyl-Hexyl+ RP Column, 1.7 µm, 2.1 x (50/100/150) mm		