

Middle-down Approach Using Proton Transfer Charge Reduction Enables Unambiguous Drug-Payload Localization in Cys-linked Antibody Drug Conjugates

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September 12, 2024
CASSS: Mass Spec 2024
Rockville, MD



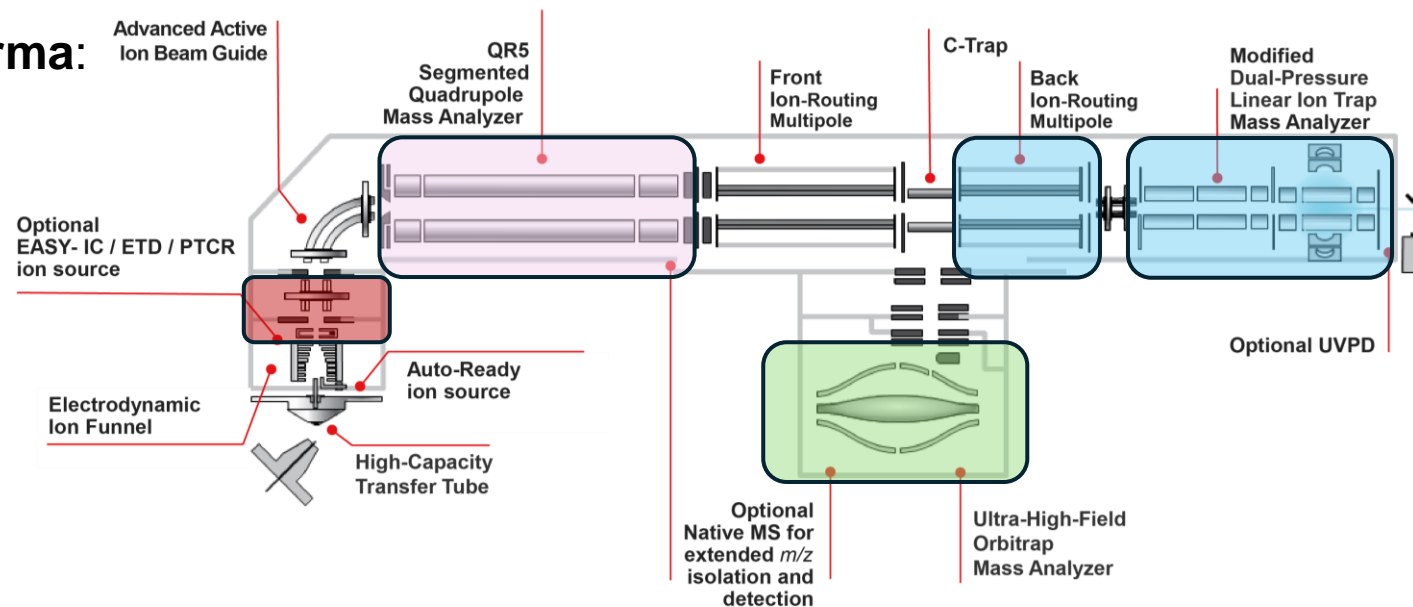
Outline

- Proton transfer charge reduction (PTCR) on Orbitrap Ascend tribrid
- Middle-down MS analysis of IgGs
- Middle-down MS analysis of antibody-drug conjugate
- Summary and future directions



Orbitrap Ascend Biopharma Edition

Relevant features of the **Orbitrap Ascend BioPharma**:



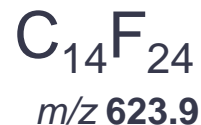
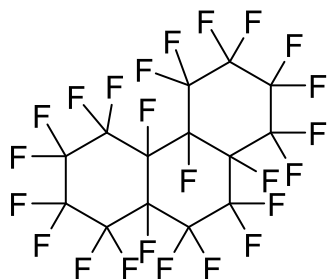
**BioPharma
Edition**



Proton Transfer Reactions in the gas-phase

- Primary Ion/Ion Reactions for Analyte Cations

Proton Transfer



A⁻ : Perfluoroperhydrophenanthrene

Commercial implementation:
Proton Transfer Charge Reduction
(PTCR)

Ion/Ion Reactions in the Gas Phase: Proton Transfer Reactions Involving Multiply-Charged Proteins

James L. Stephenson, Jr., and Scott A. McLuckey*

Contribution from the Chemical and Analytical Sciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831-6365

Received April 9, 1996

Anal. Chem. 1996, 68, 4026–4032

Ion/Ion Proton Transfer Reactions for Protein Mixture Analysis

James L. Stephenson, Jr., and Scott A. McLuckey*

Chemical and Analytical Sciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831-6365

ION/ION CHEMISTRY OF HIGH-MASS MULTIPLY CHARGED IONS

Scott A. McLuckey, James L. Stephenson, Jr.

Chemical and Analytical Sciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831-6365

Received 1 October 1998; accepted 3 December 1998

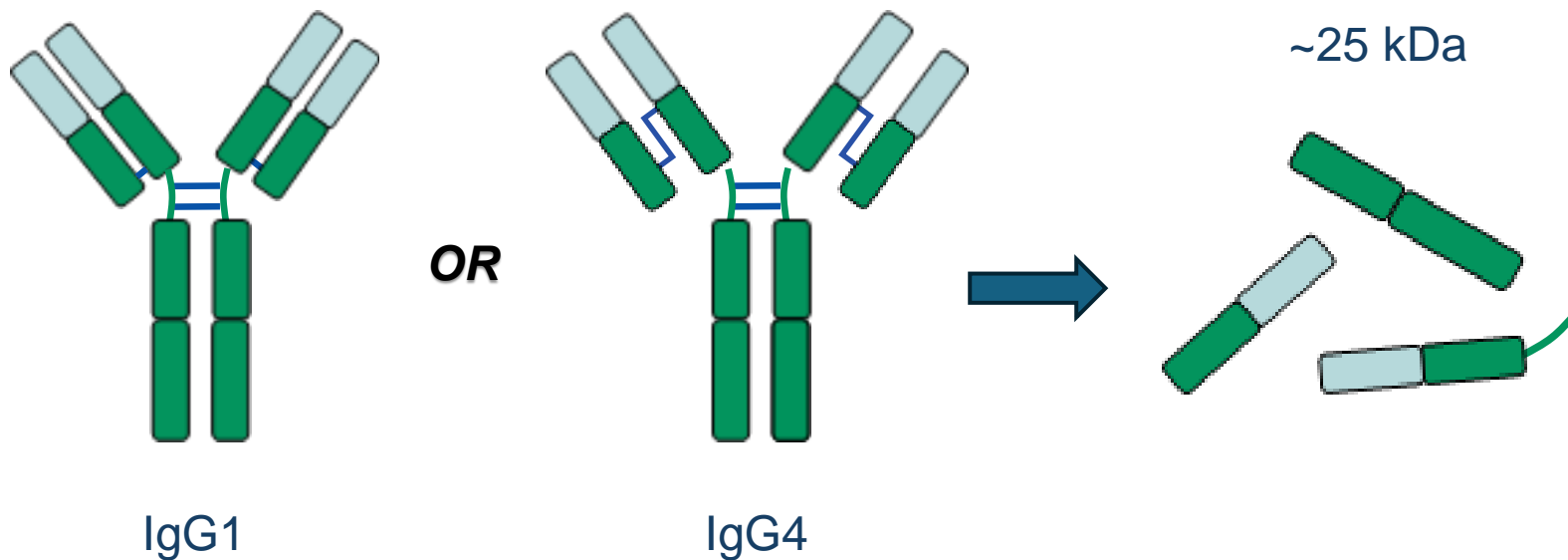
Middle-down MS analysis of IgGs



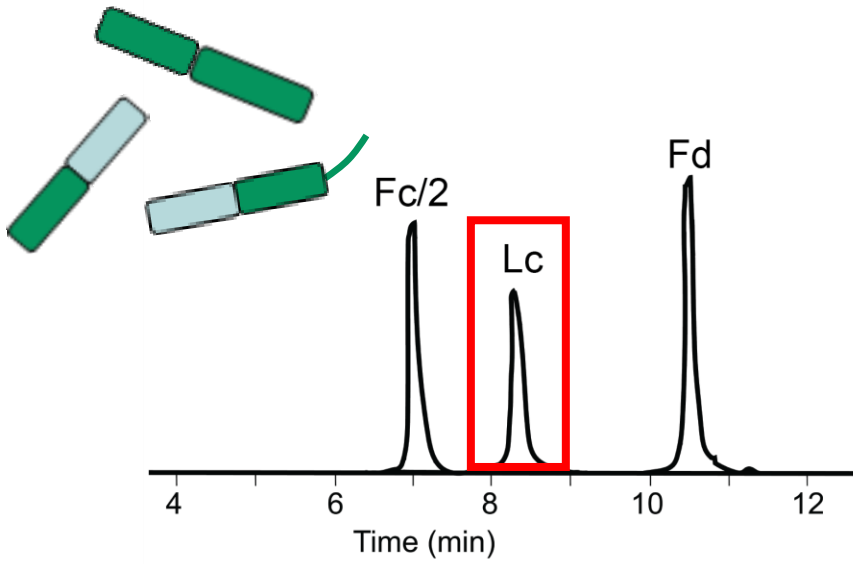
Middle-down MS for IgG characterization

Middle-down MS workflow:

- NIST (IgG1), SILu Lite (IgG1), SILu K4 (IgG4)
- IdeS digestion, reduction (TCEP) + denaturation (guanidinium HCl)
- RPLC separation + MS analysis
- Performed on an Orbitrap Eclipse Tribrid



PTCR in targeted IgG middle-down MS analysis



PTCR in targeted IgG middle-down MS analysis

PTCR improves sequencing metrics:

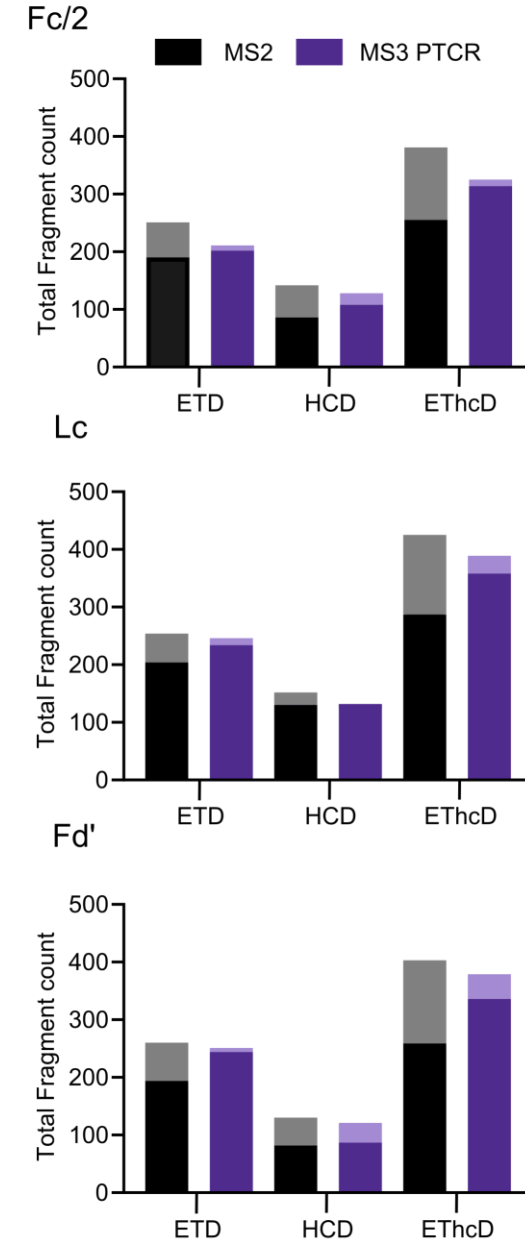
- Sequence coverage
- Number of unique fragments identified
- Number of complementary ion pairs
- Average size of matched fragments

Increased confidence in fragment assignment

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N  G|P|S|V|F|L|F|P|P|K|P|K|D|T|L|M|I|S|R|T|P|E|V|T|C| 25
26|V|V|V|D|V|S|H|E|D|P|E|V|K|F|N|W|Y|V|D|G|V|E|V|H|N| 50
51|A|K|T|K|P|R|E|E|Q|Y|N|S|T|Y|R|V|V|S|V|L|T|V|L|H|Q| 75
76|D|W|L|N|G|K|E|Y|K|C|K|V|S|N|K|A|L|P|A|P|I|E|K|T|I|100
101|S|K|A|K|G|Q|P|R|E|P|Q|V|Y|T|L|P|P|S|R|E|E|M|T|K|N|125
126|Q|V|S|L|T|C|L|V|K|G|F|Y|P|S|D|I|A|V|E|W|E|S|N|G|Q|150
151|P|E|N|N|Y|K|T|T|P|P|V|L|D|S|D|G|S|F|F|L|Y|S|K|L|T|175
176|V|D|K|S|R|W|Q|Q|G|N|V|F|S|C|S|V|M|H|E|A|L|H|N|H|Y|200
201|T|Q|K|S|L|S|L|S|P|G|C
  
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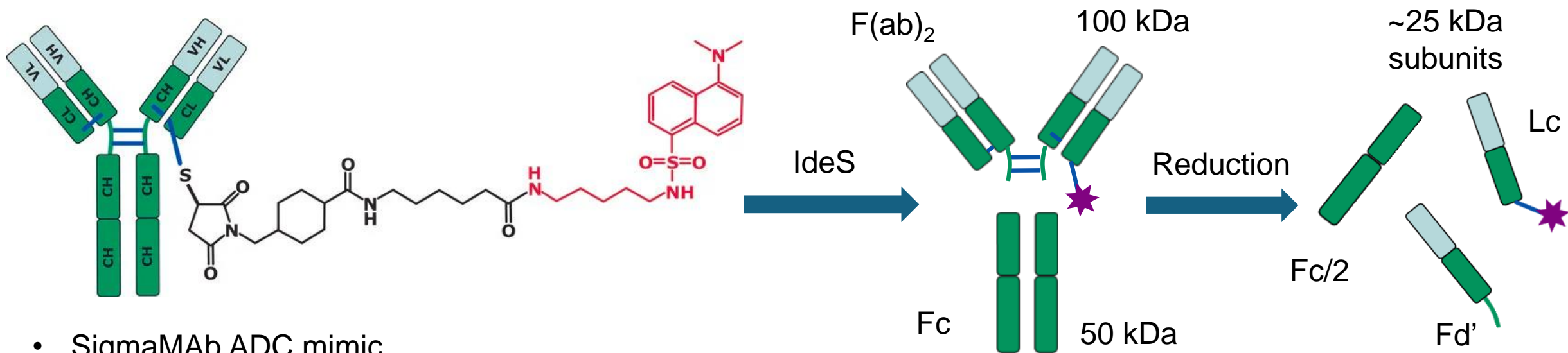
Combined Fc/2 – 95.7% sequence coverage!



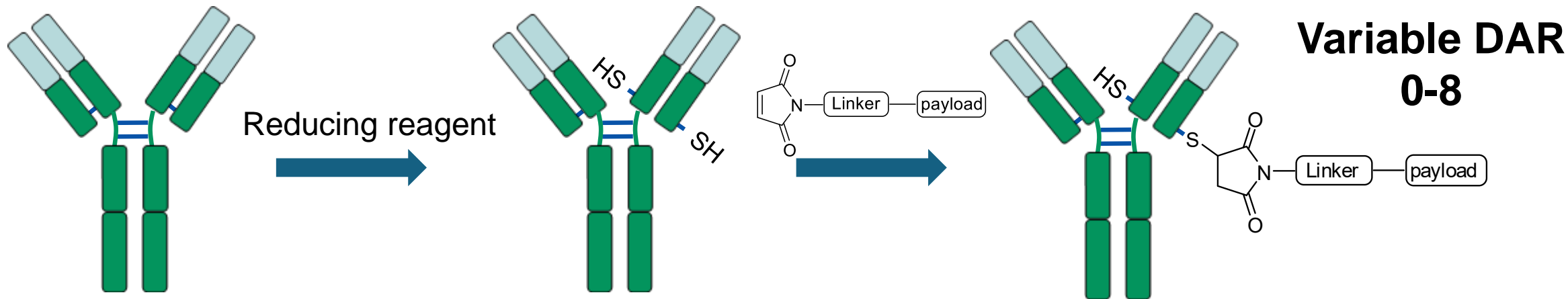
Middle-down MS analysis ADC subunits



Middle-down MS Workflow

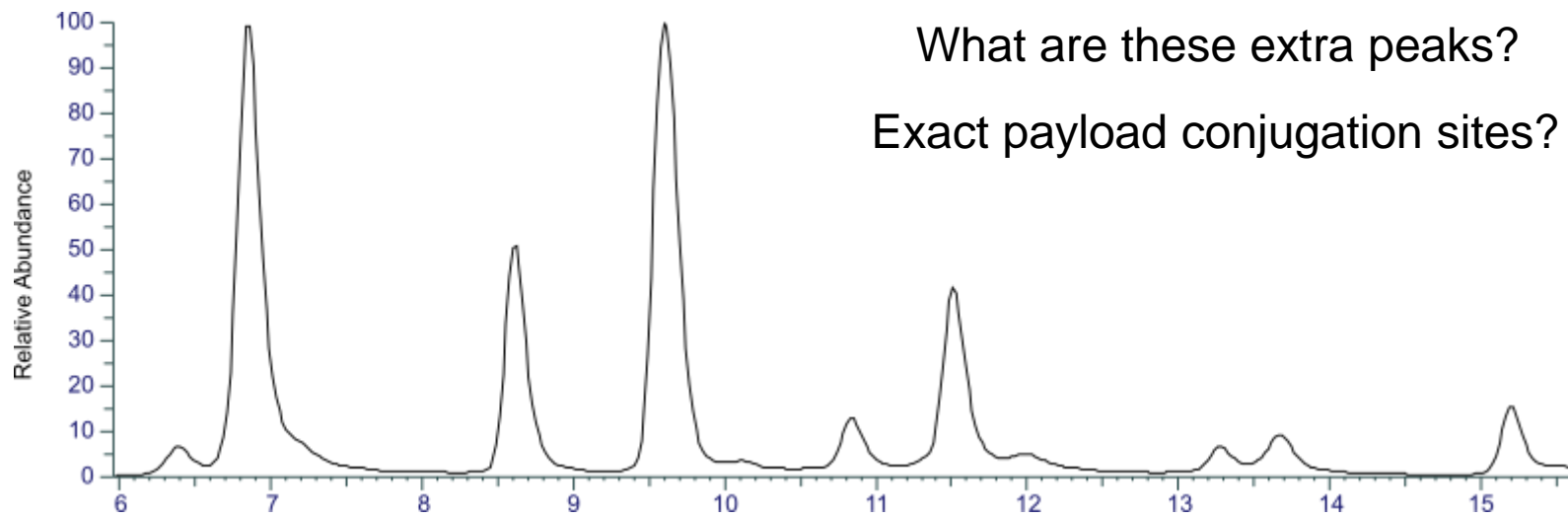
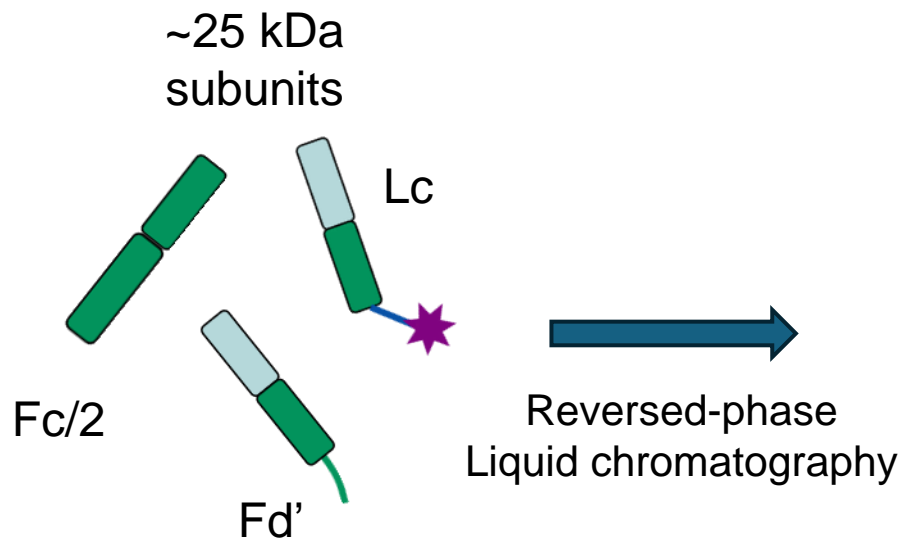


- SigmaMAb ADC mimic
- Cys-conjugation to dansyl-cadaverine-SMCC

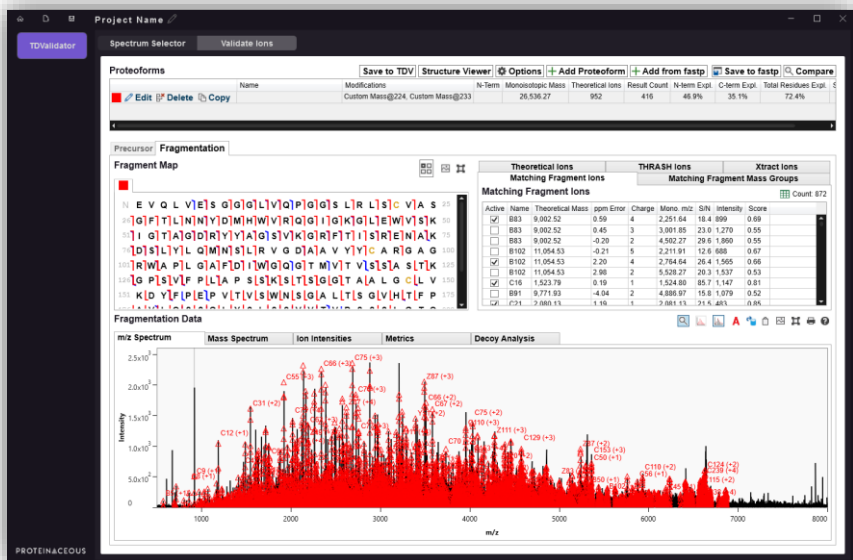




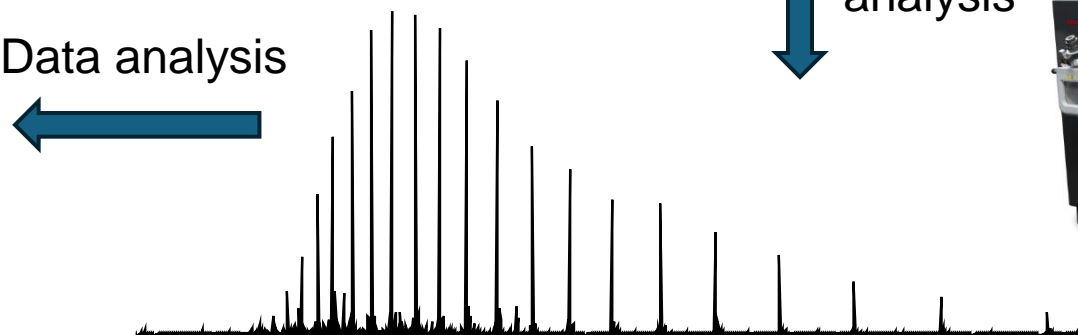
Middle-down MS Workflow



Manual data validation using TDValidator



Data analysis

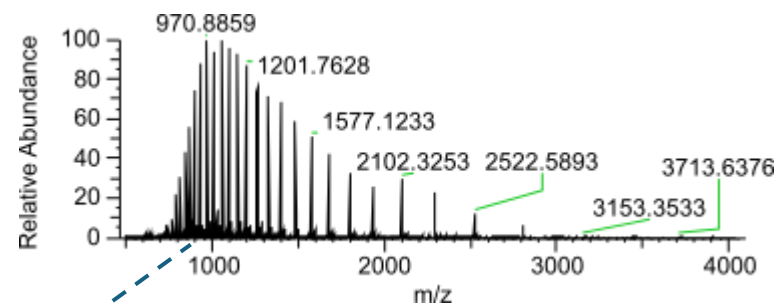
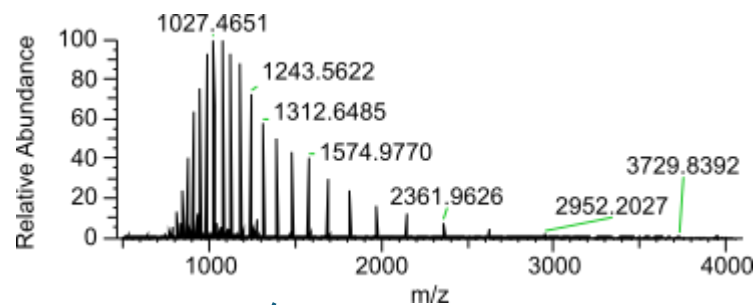
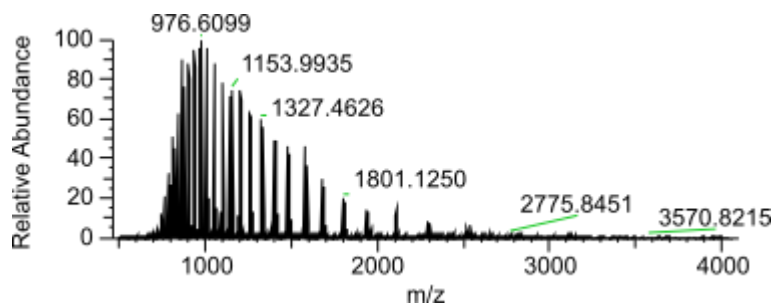


Mass spectrometry analysis



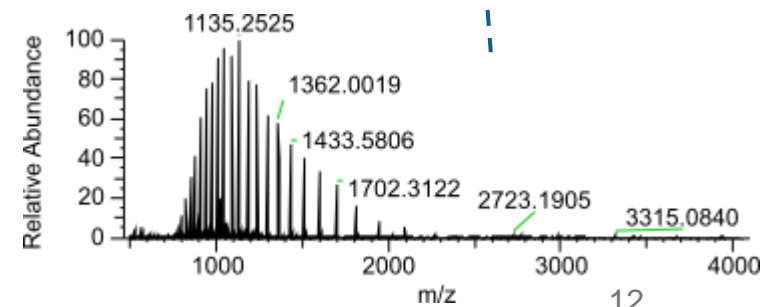
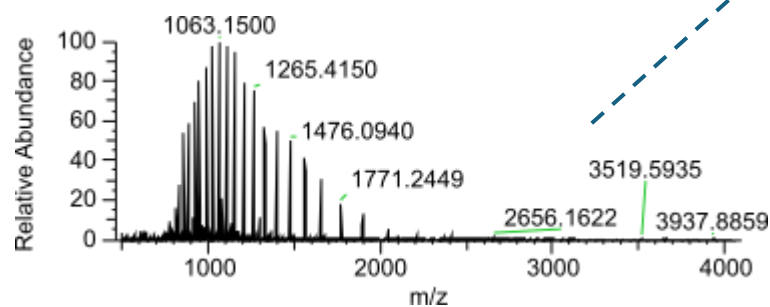
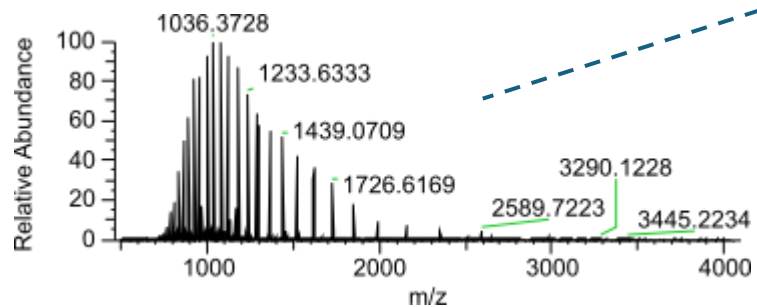
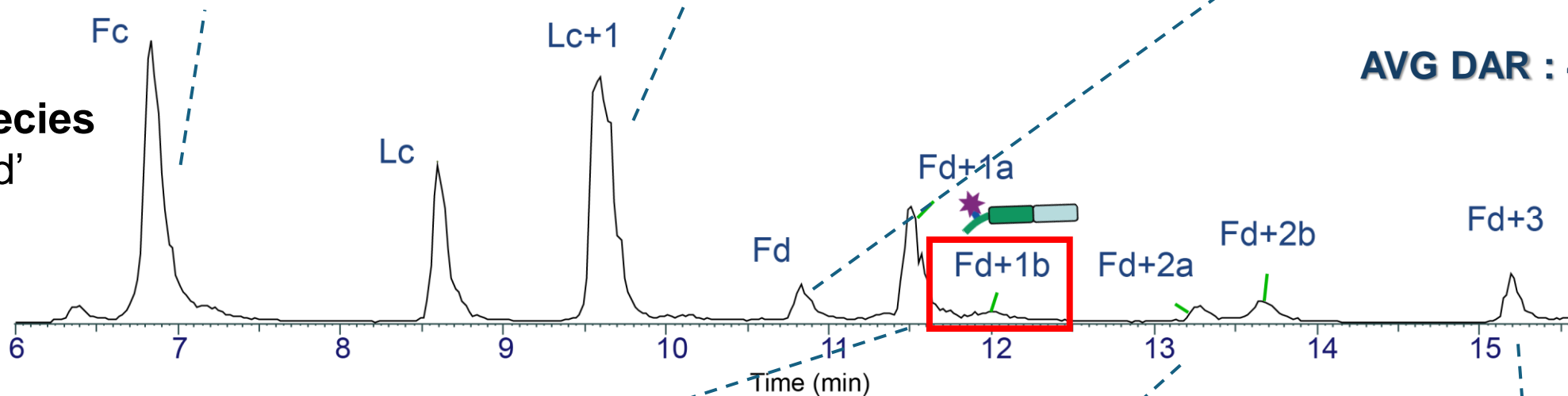


Middle-down MS: Payload localization



AVG DAR : 4.18

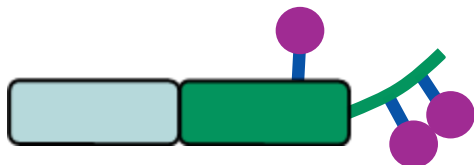
Isobaric species present at Fd' subunit



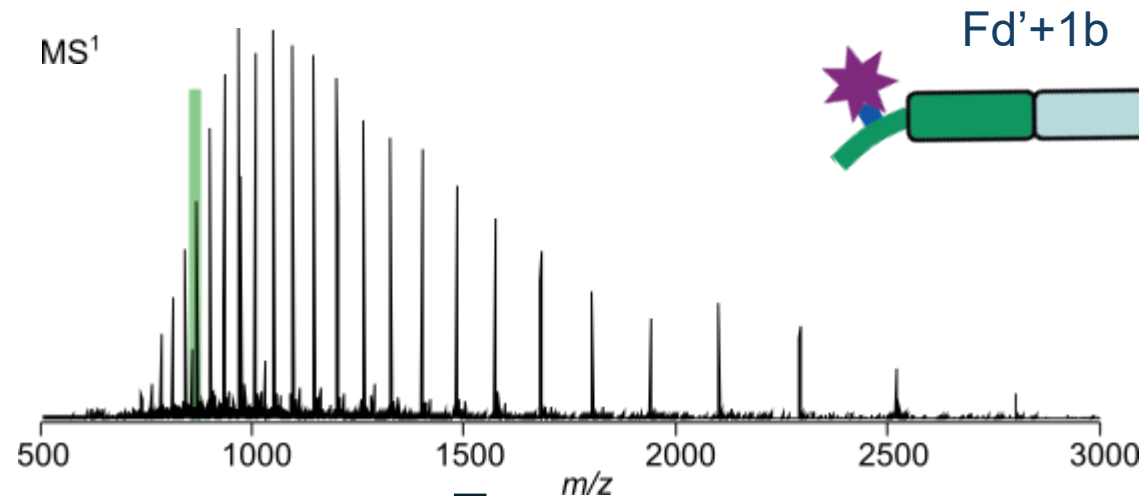


Middle-down MS: Payload localization

C D K T H T **C** P P **C**
 224 230 233



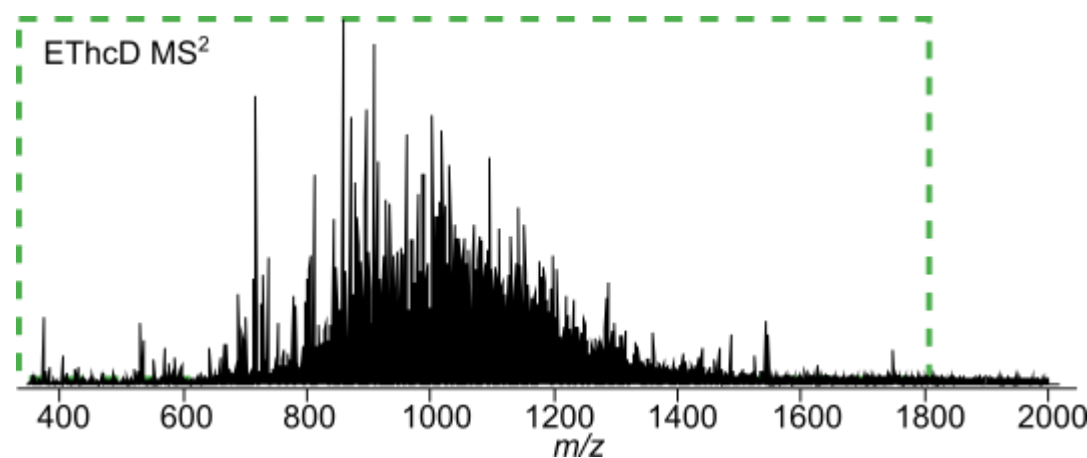
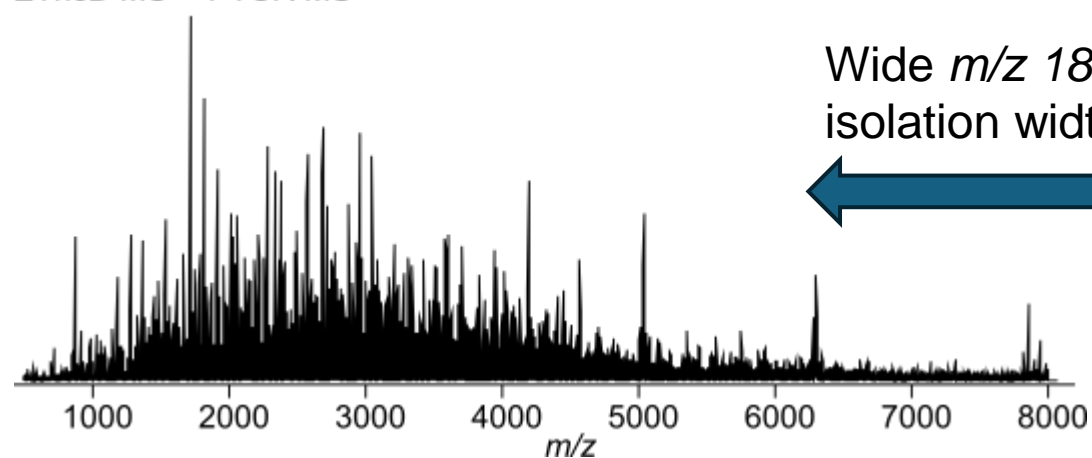
- 3 possible sites conjugation sites for Fd' subunit!
- Why is PTCR necessary?



Single precursor m/z 5
isolation width

ETHcD MS² - PTCR MS³

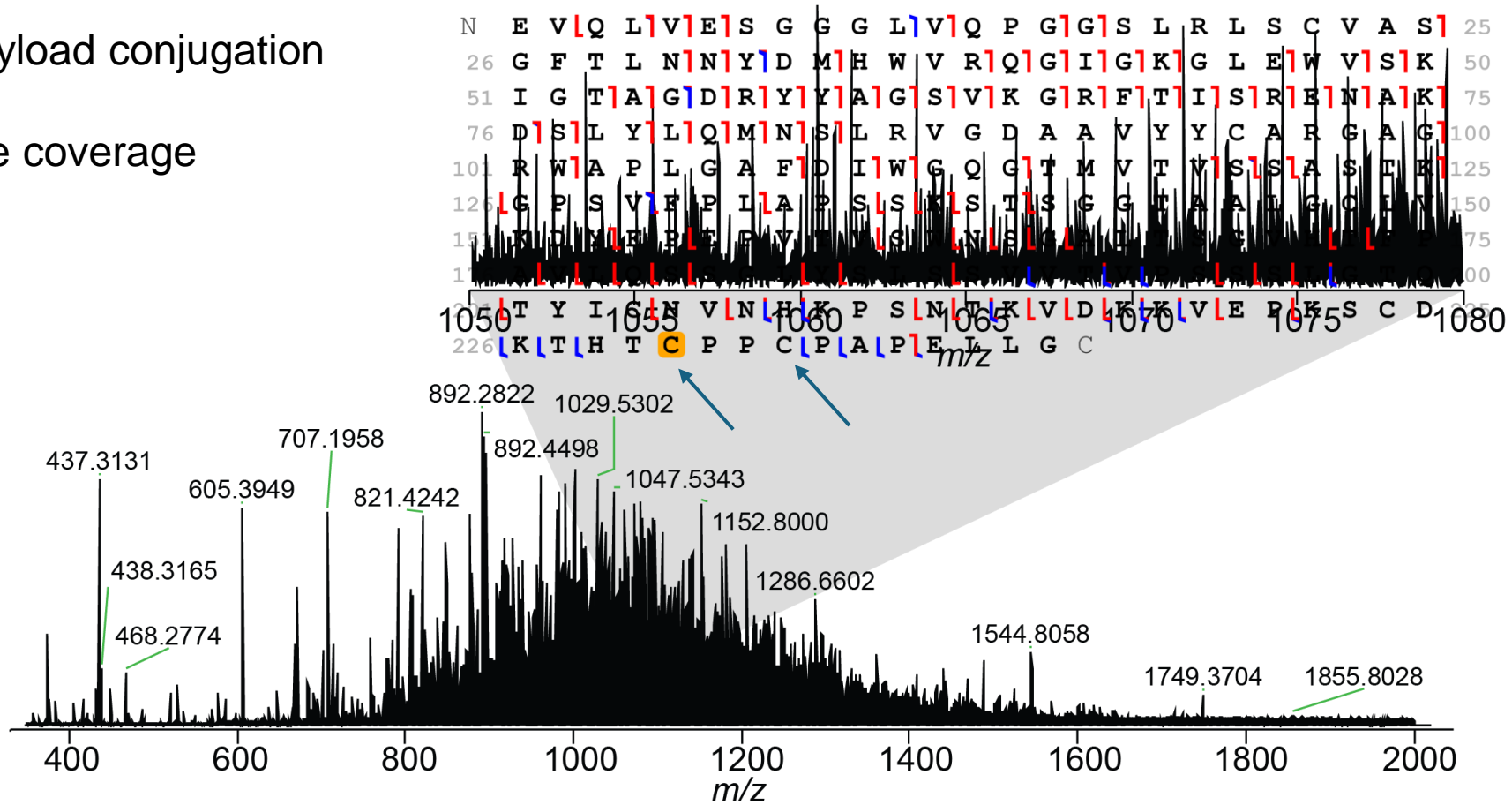
Wide m/z 1800
isolation width



CU Middle-down MS² for ADC characterization: Fd+1b subunit

Traditional targeted MD MS²:

- Ambiguity in payload conjugation
- ~50% sequence coverage



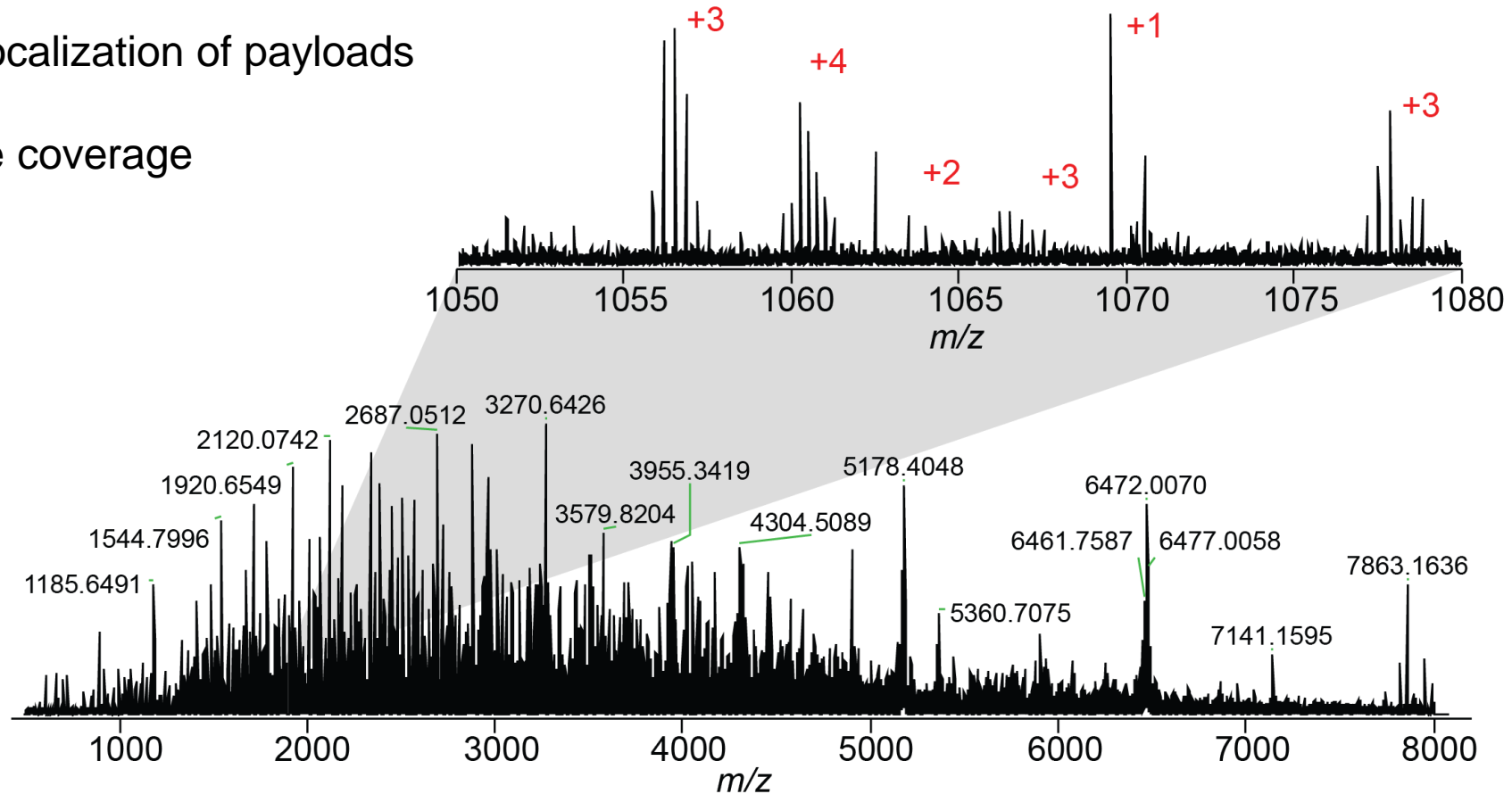
ETHcD MS²

Middle-down MS³ for ADC characterization: Fd+1b subunit

Targeted MD MS² – PTCR MS³:

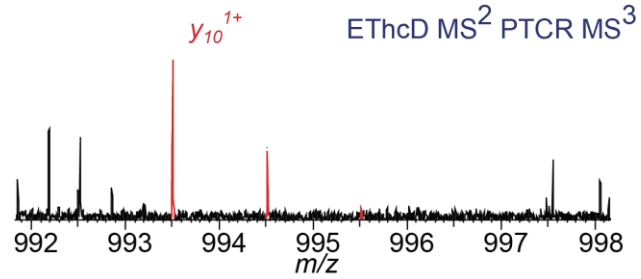
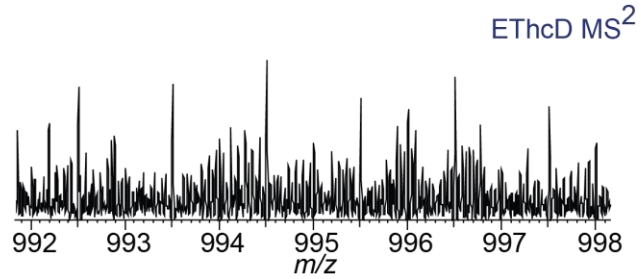
- Unambiguous localization of payloads
- >70% sequence coverage

Lowly charged product ions



ETHcD MS² – PTCR MS³

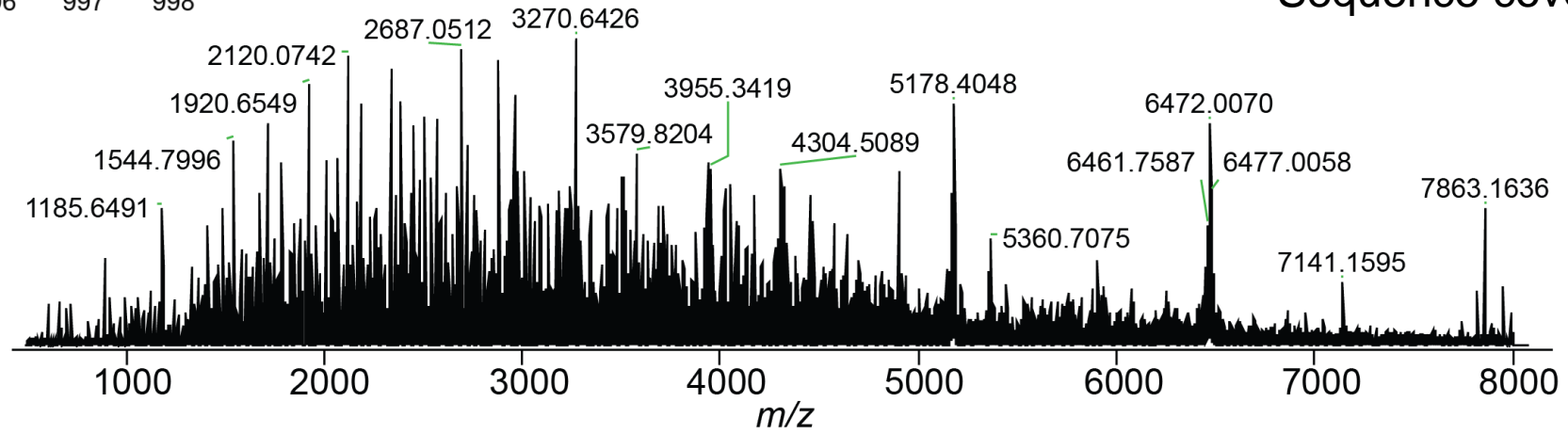
Middle-down MS³ for ADC characterization: Fd+1b subunit



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N  E V Q L V E S G G G L V Q P G G S L R L S C V A S 25
26  G F T L N N Y D M H W V R Q G I G K G L E W V S K 50
51  I G T A G D R Y Y A G S V K G R F T I S R E N A K 75
76  D S L Y L Q M N S L R V G D A A V Y Y C A R G A G 100
101 R W A P L G A F D I W G Q G T M V T V S S A S T K 125
126 L G P S V F P L A P S S K S T S G G T A A L G C L V 150
151 L K D Y F P E P V T V S W N S G A L T S G V H T F P 175
176 L A V L L Q S S G L L Y S L S S V V T V P S S S L G T Q 200
201 T Y I C N V N H K P S N T K V D K K V E P K S C D 225
226 K L L H T C P P C P A P E L L G C
    
```

Sequence coverage: 70.7%



EThcD MS² – PTCR MS³

PTCR kinetics proportional to z²



Multiple ion activations for enhanced sequencing

ETD

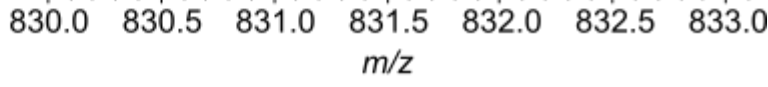
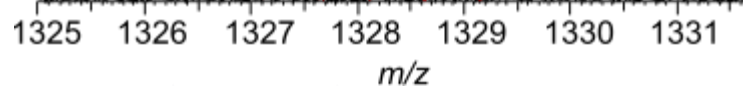
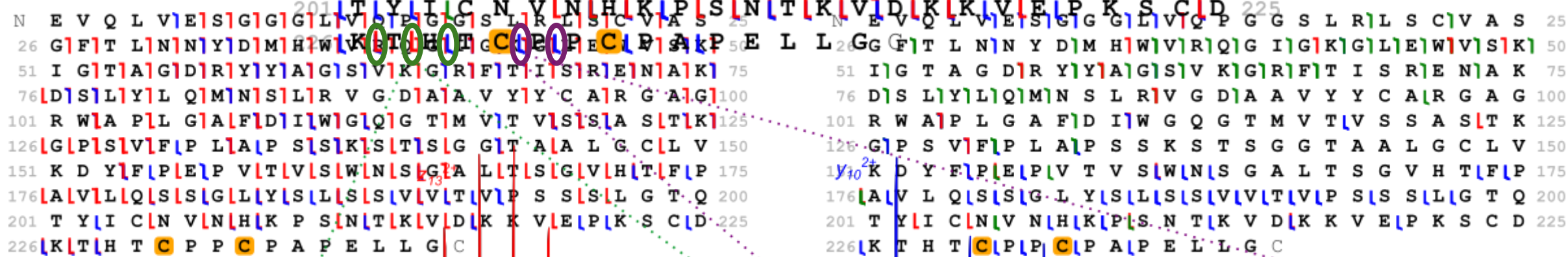
~85% sequence coverage!

HCD



ETHcD

UVPD



ETHcD MS² – PTCR MS³

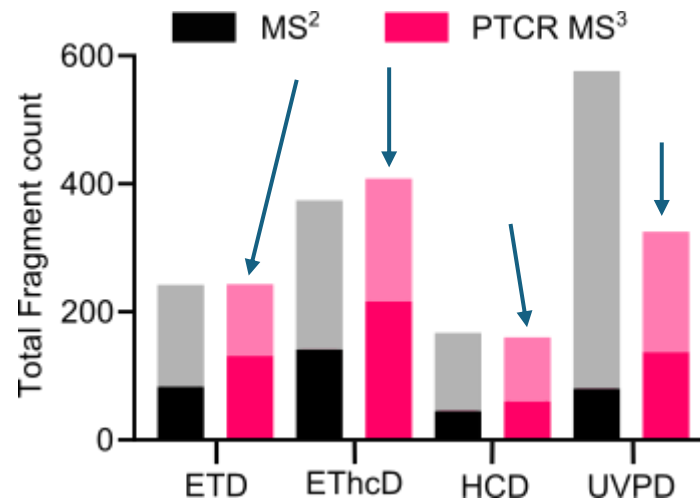
UVPD MS² – PTCR MS³



Summary: PTCR enables unambiguous localization

- Enhanced ADC characterization
 - Improved sequence coverage
 - Unambiguous payload localization

Subunit	Experiment	Fd + 1a		Fd + 1b		Fd + 2a		Fd + 2b	
		Sequence Coverage (%)	Localization	Sequence Coverage (%)	Localization	Sequence Coverage (%)	Localization	Sequence Coverage (%)	Localization
MS ²	HCD	23.9	C224 or C230	25.9	Ambiguous	25.9	Ambiguous	28	C230+C233
	ETD	40.6	C224	41.4	C230 or C233	41.4	C224+C230 or C224+C233	43.9	C230+C233
	UVPD	30.5	C224 or C230	29.3	C230 or C233	27.6	C224+C230 or C224+C233	30.1	C230+C233
	EThcD	50.6	C224	52.7	C230 or C233	53.6	C224+C230	55.6	C230+C233
PTCR - MS ³	HCD	27.6	Ambiguous	28	Ambiguous	30.5	Ambiguous	31.4	C230+C233
	ETD	60.3	C224	57.3	C230 or C233	56.9	C224+C230 or C224+C233	61.9	C230+C233
	UVPD	43.1	C224 or C230	45.2	C230 or C233	40.6	C224+C230 or C224+C233	41.1	C230+C233
	EThcD	71.1	C224	70.7	C230	72	C224+C233	71.1	C230+C233
	Combined	87.9		79.5		86.6		85.4	





Acknowledgments

Fornelli Group

Luca Fornelli

Jake Kline

Cynthia Nagy

Amy Carfagno

Amal Eltobshi

Alyssa Williams



Collaborators

ThermoFisher
SCIENTIFIC

PROTEIN|||CEOUS

Funding Agency



National Institutes
of Health



Thank you!