

Integrated Experimental and Computational Workflow Enabled by In-Source Reduction for “Truly Complete” Disulfide Mapping

He Zhu, Jin Zhang, Zhiqing Jiang, Qi Wang, Yongsheng Xiao

Analytical Science, Department of BioDev Wuxi Process Development, WuXi Biologics

CASSS Mass Spec, 2026

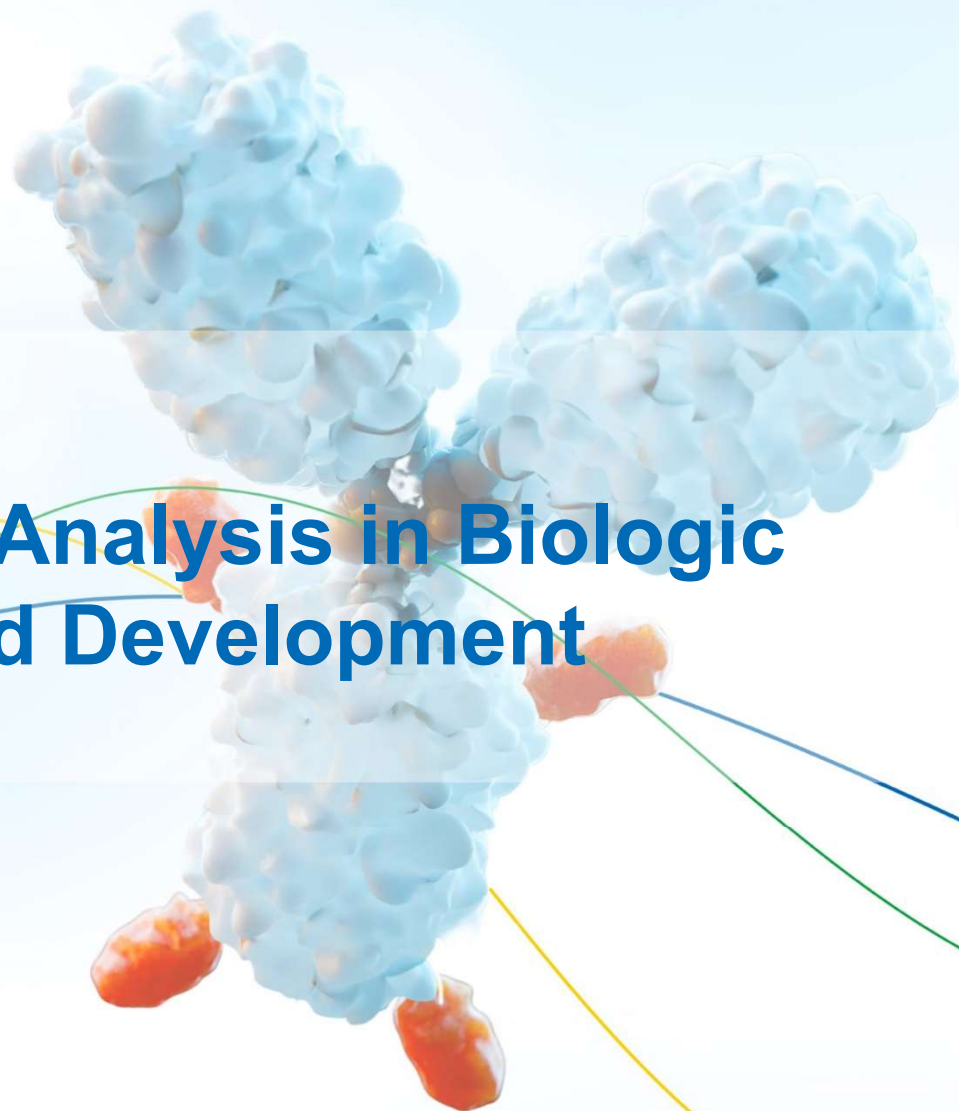


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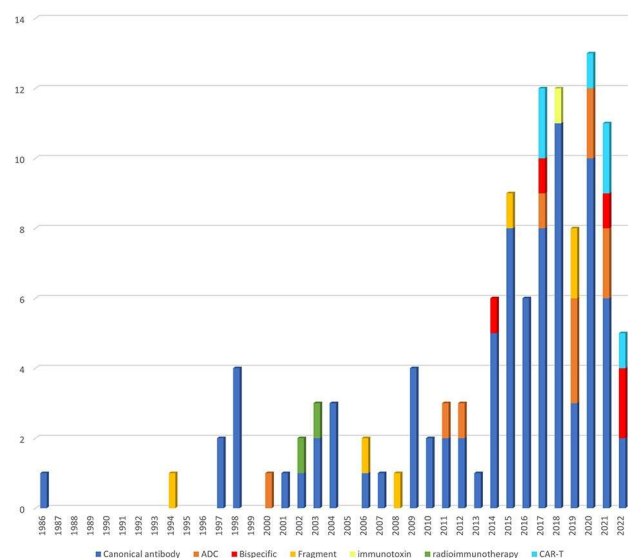
01

Disulfide Mapping Analysis in Biologic Drug Discovery and Development



Introduction

The drug market of protein therapeutics has shown a remarkable expansion in last two decades.



Monoclonal Antibody

Bispecific Antibody

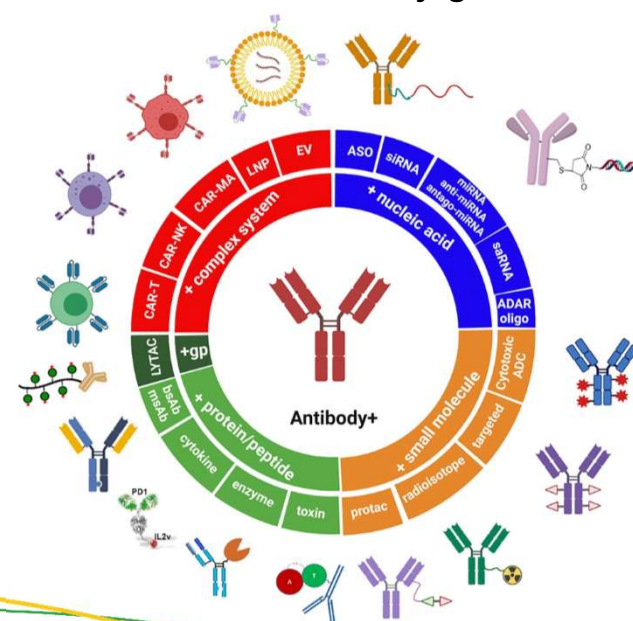
Fc-fusion Protein

Antibody Drug Conjugate

Enzyme Replacement Therapy

Antibody Fragments

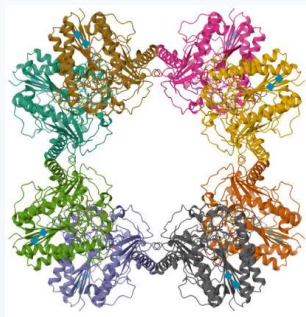
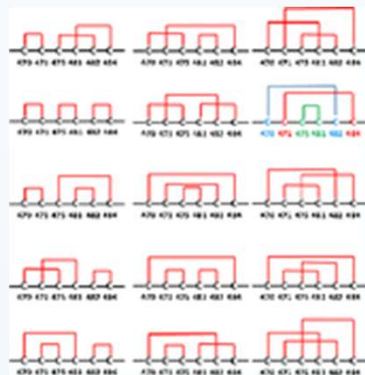
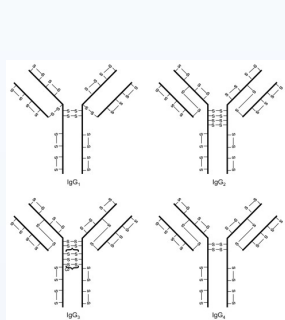
Antibody or antibody-containing therapeutics approved by the FDA as of 31 March 2022.



Antibody Ther, Volume 5, Issue 4, October 2022, Pages 280–287

Complex disulfide linkages represent a unique challenge in the discovery and development of novel biologic modalities.

Enzyme replacement therapy (ERT)



human arylsulfatase A PDB: 1AUK

J. Am. Soc. Mass Spectrom. (2013) 24:125Y133

Human IgG disulfide linkages

- Classical IgG disulfide bond structures are well defined
- Complex disulfide architectures, such as Cystine Knots, are commonly found in enzyme replacement therapy molecules

Bispecific antibody with single chain Fv (scFv)

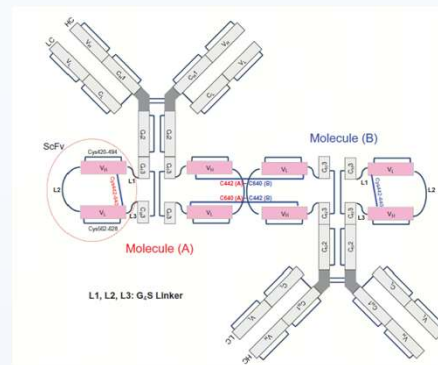
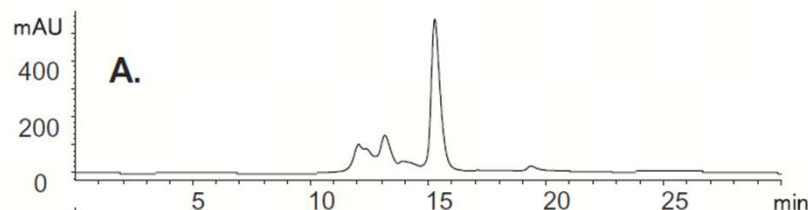


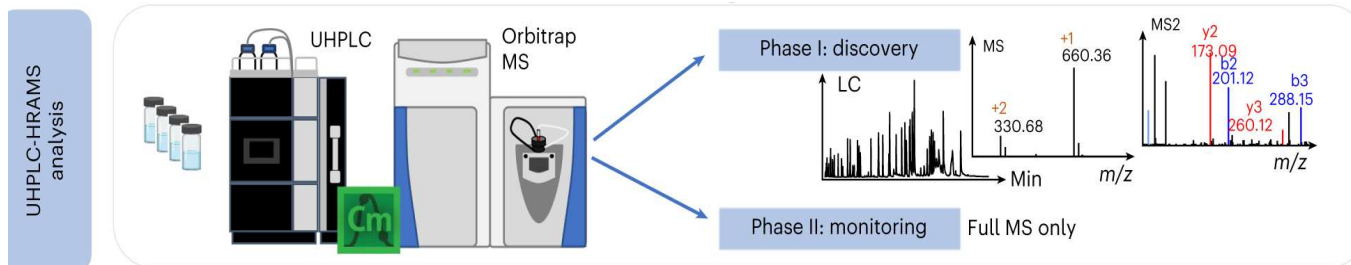
Table 1. Bioactivity of Bis-A size variants.

Fraction	Fab activity (%), n = 2	scFv activity (%), n = 2	Dual target bioassay (%), n = 2
Fraction 1	112 (0.3)	94 (5.1)	98 (12.0)
Fraction 2	92 (2.1)	61 (0.3)	62 (4.8)
Fraction 3	NR *	68 (1.7)	78 (0.1)



- Disulfide scrambling due to the engineer Cys in scFv cause significant aggregate formation and a loss of biological activity

Disulfide characterization, employing multi-attribute method (MAM), becomes increasingly important across a wide range of CMC activities

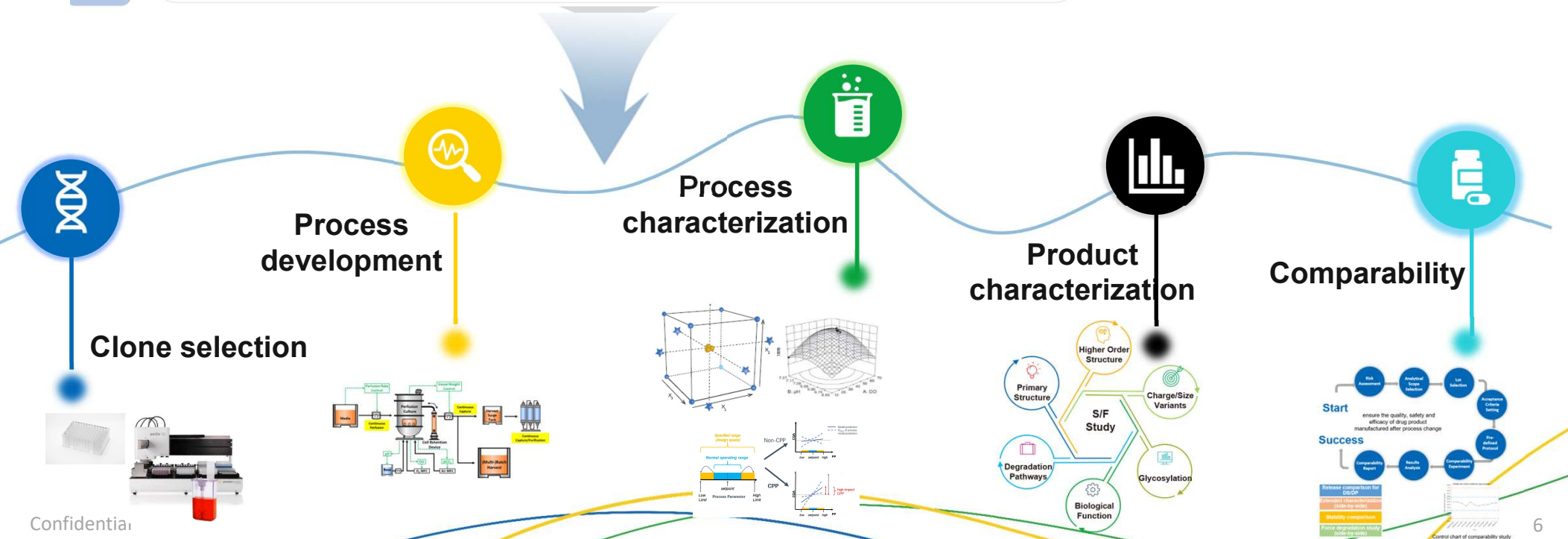


Comprehensive multi-attribute method workflow for biopharmaceutical characterization and current good manufacturing practices testing

Silvia Millán-Martín, Craig Jakes, Sara Carillo, Richard Rogers, Da Ren & Jonathan Bones

Nature Protocols 18, 1056–1089 (2023) | [Cite this article](#)

Nat Protoc 18, 1056–1089 (2023).



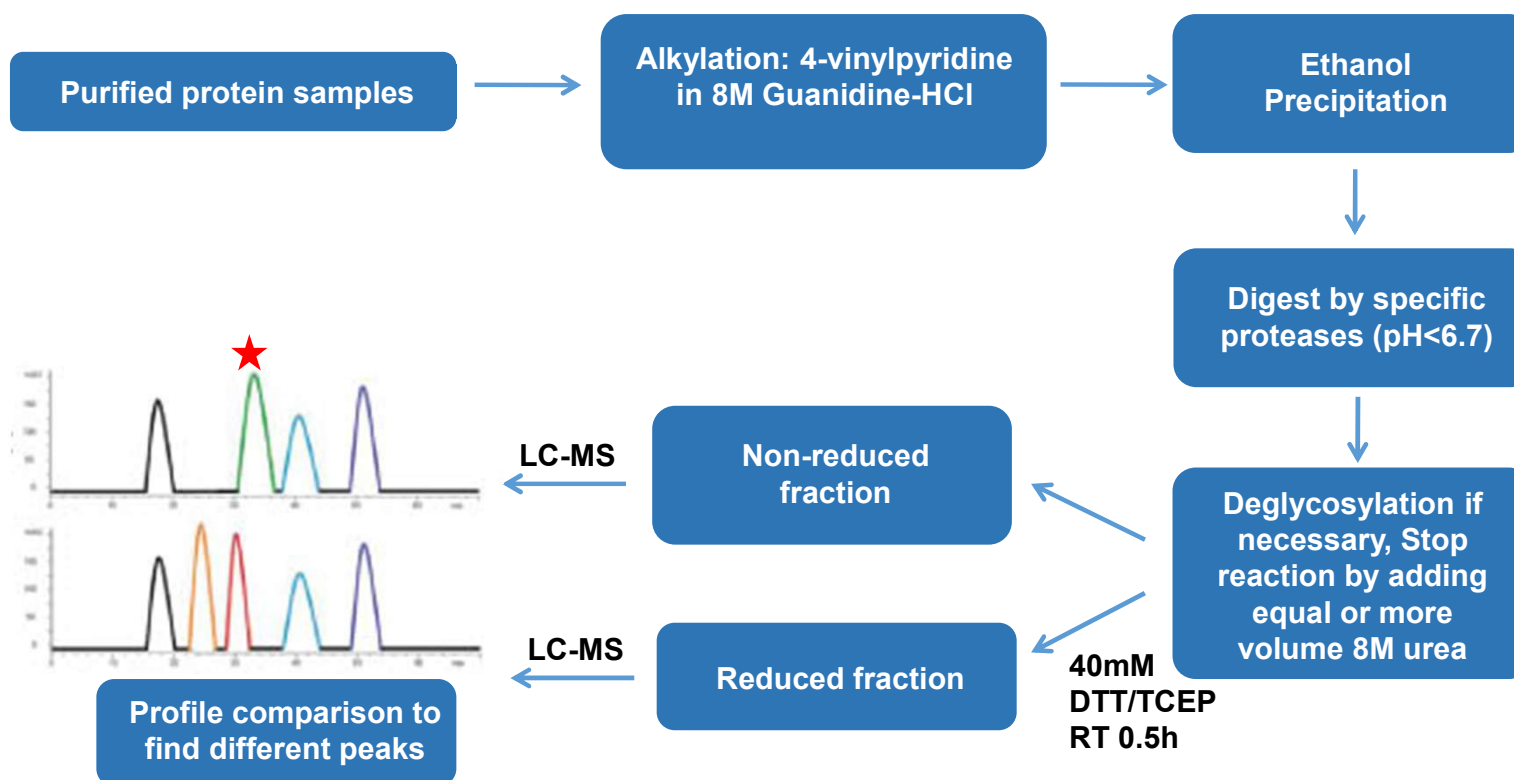
The background features a light blue gradient with faint, stylized protein ribbon structures in various colors (teal, pink, yellow). Overlaid on these are several thin, curved lines in blue, green, and yellow, creating a sense of movement and flow.

Current Disulfide Mapping Workflow: Challenges and Solutions

02

Traditional disulfide mapping analysis workflow to detect unknown disulfide linkage and disulfide scrambling

Profile comparison method: Those peaks found in the non-reduced sample, but absent in the reduced one, are considered to be disulfide-linked peptides

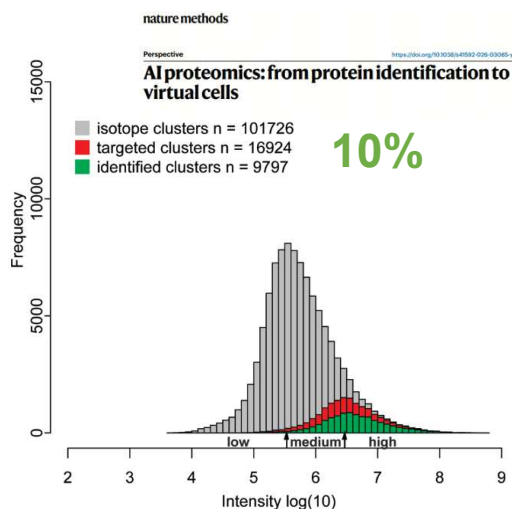


Wen. D, Y. Xiao et al., *Anal. Chem.*, 2017, 89 (7), pp 4021–4030

Challenge I: 'Dark matter' in LC-MS analysis and disulfide mapping

LC-MS analysis for protein characterization, including peptide mapping and disulfide mapping, face significant challenge due to up to 75% of unidentified peaks from current commercial software

"Dark matter" in bottom-up proteomics



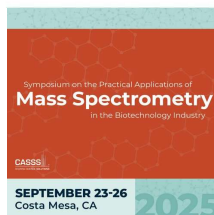
J. Proteome Res. 2011, 10, 1785–1793

- A substantial fraction of the proteome's 'dark matter' is uncharacterized proteoforms, including single amino acid variants, isoforms and PTMs

"Dark matter" in top-down proteomics

Keynote II - Advanced Mass Spectrometry and Structural Biology Strategies to Characterize Therapeutic Proteins

JL Joseph Loo

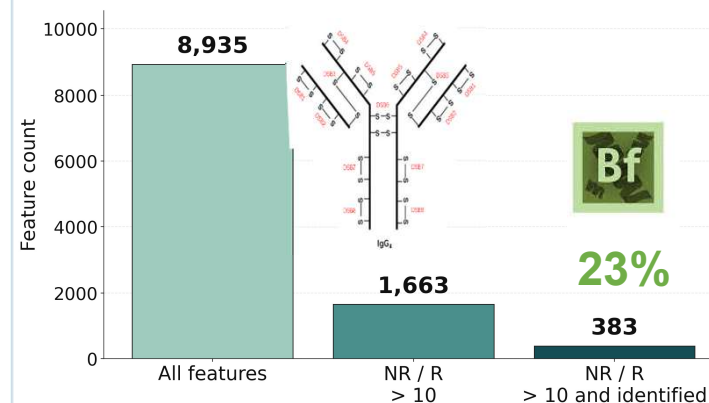


Research Article | June 08, 2021
Internal Fragments Generated from Different Top-Down Mass Spectrometry Fragmentation Methods Extend Protein Sequence Coverage
Internal Fragments Generated from Different Top-Down Mass Spectrometry Fragmentation Methods Extend Protein Sequence Coverage
Muhammad A. Zehnder, Brandon Wei, Carter Lantz, Hui Ting Wu, Tyler R. Lambeth, Juliette K. Diederich, Rachel R. Oppenheimer, Leo Ryan R. Julian, Joseph A. Loo *
* Author & Article Information
J. Am. Soc. Mass Spectrom. (2021) 32 (7): 1752–1758.
<https://doi.org/10.1021/jasms.1c00112> Article History

- Top-down mass spectra: "Up to 75% of peaks are unassigned. Why do we tolerate this?"

"Dark matter" in disulfide mapping

Nivolumab (IgG4)-disulfide by Trypsin



Characterization of trisulfide modification in antibodies

Sheng Gu, Dingyi Wen *, Paul H. Weinreb, Yaping Sun, Lihe Zhang, Susan F. Foley, Rashmi Kshirsagar, David Evans, Sha Mi, Werner Meier, R. Blake Pepinsky

Biogni Inc, Cambridge, MA 02142, USA

■ ■ ■ Challenge I: 'Dark matter' in LC-MS analysis and disulfide mapping

A risk-based approach is needed to establish an intensity threshold: Peaks above this threshold require unambiguous identification.

DSB1: P1 ATLS**C**R
P2 FSGSGSGTDFTLTISSLEPEDFAVY**C**QQSSNWPR

DSB2: P3 SGTASV**V**CLNNFYPR
P4 VYA**C**EVTHQGLSSPVT**K**

DSB3: P5 G**E****C**
P6 GPSVFPLAP**C**SR

DSB4: P7 LD**C**K
P8 AEDTAVY**C**ATNDDYWGQGLTVSSAST**K**

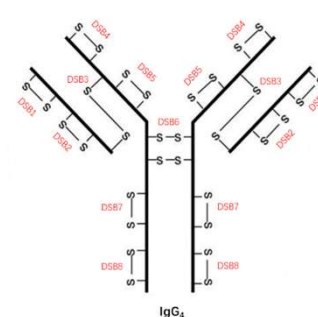
DSB5: P9 STSESTAALG**C**LVK
P10 TYT**C**NVDHKPSNT**K**

DSB6: P11 YGPP**C**PP**C**PAPEFLGGPSVFLFPPK**P**K
P12 YGPP**C**PP**C**PAPEFLGGPSVFLFPPK**P**K

DSB7: P13 TPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNA**K**
P14 C**K**

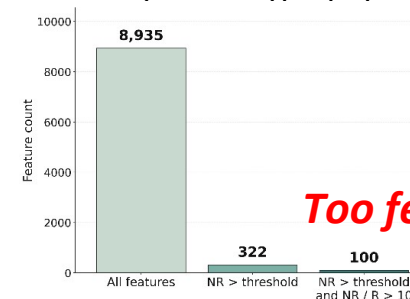
DSB8: P15 NQVSLTCLV**K**
P16 WQEGNVFSCSVMHEALHNHYTQ**K**

Disulfide-containing
species from a NR
tryptic digestion of
Nivolumab (IgG4)



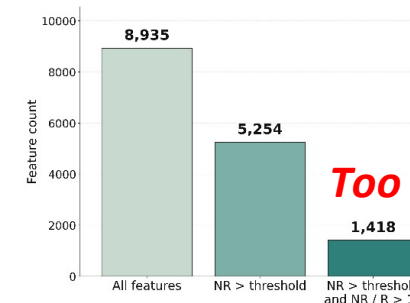
Option 1a

- Highest intensity of wildtype peptide *0.5%



Option 1b

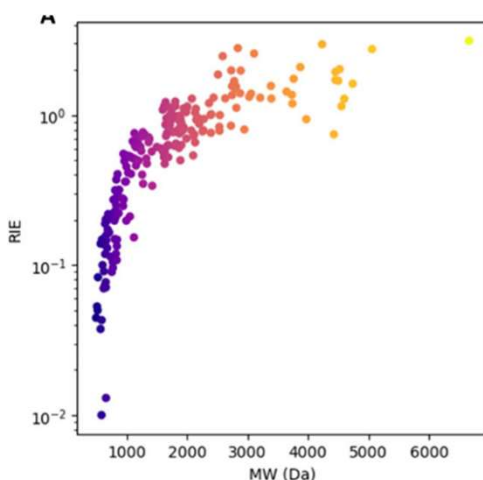
- lowest intensity of wildtype peptide *0.5%



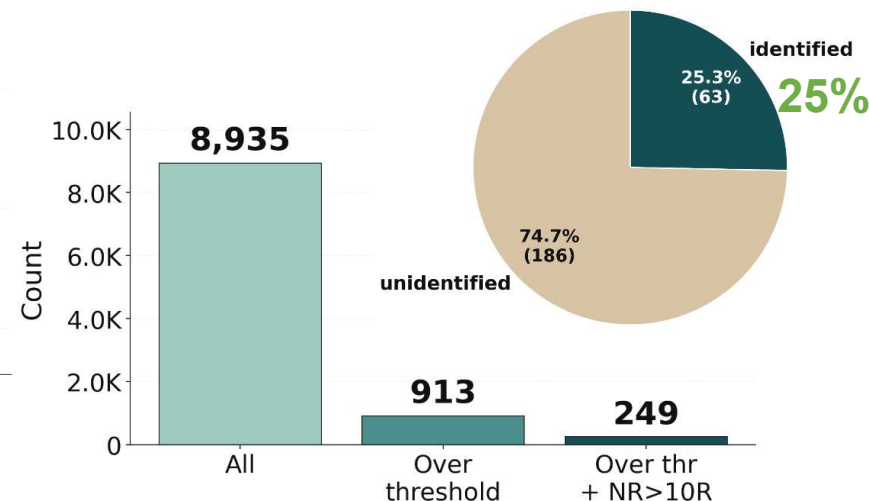
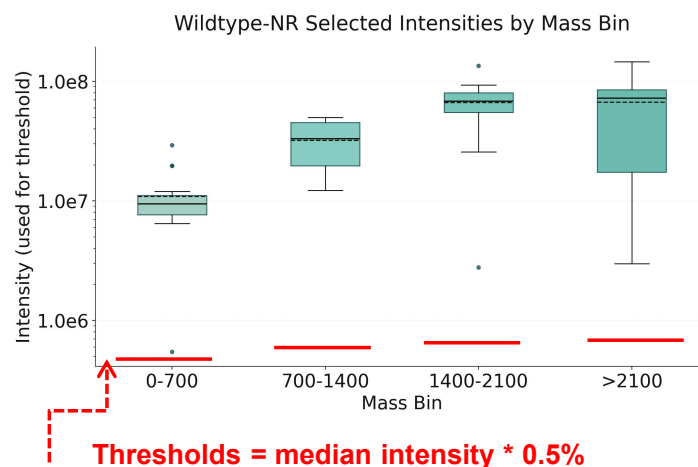
Challenge I: 'Dark matter' in LC-MS analysis and disulfide mapping

Option 2: Mass range dependent intensity threshold

- Divide wildtype peptide into four groups:
Based on molecular mass (Da). (e.g. <700Da, 700-1400Da, 1400-2100Da, >2100Da)
- Define threshold:
For each mass range, calculate the median intensity of wildtype peptide in this range, and the threshold of this range is $0.5\% \times \text{med}$.



J. Am. Soc. Mass Spectrom. 2 October 2024; 35 (10): 2297–2307



Molecular weight is the strongest predictor of a peptide's ionization efficiency

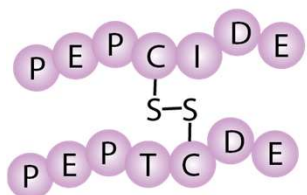
Challenge II: The difficulty for identifying disulfide-linked peptides is mainly due to the diversity of disulfide linkages



Challenge : Difficult to identify peptide sequence of each component in disulfide cluster

Type 1 (Simplest)

Intra-peptide or peptide with single Cys residue on each peptide



“1+1”
mode

Biophys Rep 2018, 4(2):68-81
<https://doi.org/10.1007/s41048-018-0050-6>

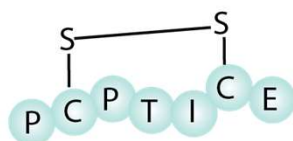
PROTOCOL

Biophysics Reports



Mapping disulfide bonds from sub-micrograms of purified proteins or micrograms of complex protein mixtures

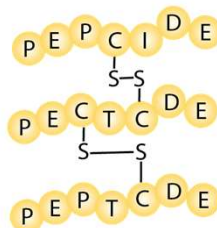
Shan Lin¹, Yong Cao², Sheng-Bao Fan^{2,3}, Zhen-Lin Chen^{2,3}, Run-Qian Fang^{2,3}, Si-Min He^{2,3,4}, Meng-Qiu Dong^{2,3}



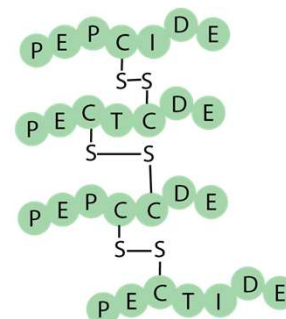
“2” mode

Type 2

One or more peptide has two Cys residues



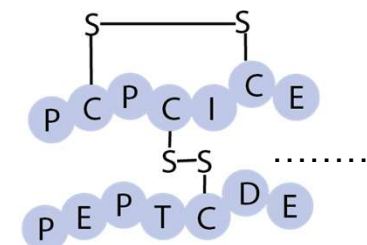
“1+2+1”
mode



Multi-“1+2+2+1” mode

Type 3

One or more peptide has three or more Cys residues



“1+3”
mode

Can only identify cluster of two peptides

Challenge II: The identification of disulfide-linked peptides is challenging mainly due to the complexity of disulfide connectivity.



Challenge : Difficult to determine disulfide connectivity

$C_8GVRPGGSFLFMGWSR == DGAC_5RPC_6S == FGEAWLGC_9APR$

“1+2+1”
mode

- ETD-CID/HCD MS3 strategy to determine disulfide linkage: ETD to generate partial reduced products with single disulfide bond

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Determination of the Disulfide Structure of Murine Meteorin, a Neurotrophic Factor, by LC-MS and Electron Transfer Dissociation-High-Energy Collisional Dissociation Analysis of Proteolytic Fragments

Dingyi Wen¹, Yongsheng Xiao, Malgorzata M. Vecchi, Bang Jian Gong, Jana Dolnikova, and R. Blake Pepinsky

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Publication Date: February 28, 2017
https://doi.org/10.1021/acs.analchem.6b04600
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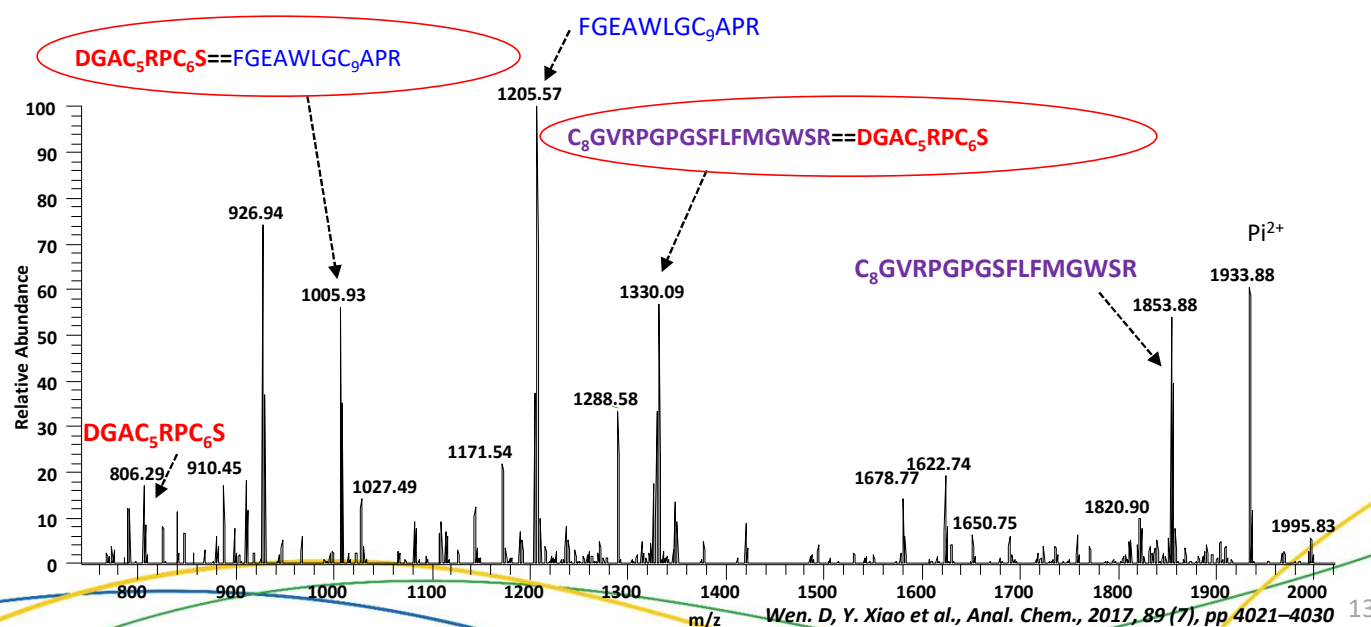
Mendeley (17)

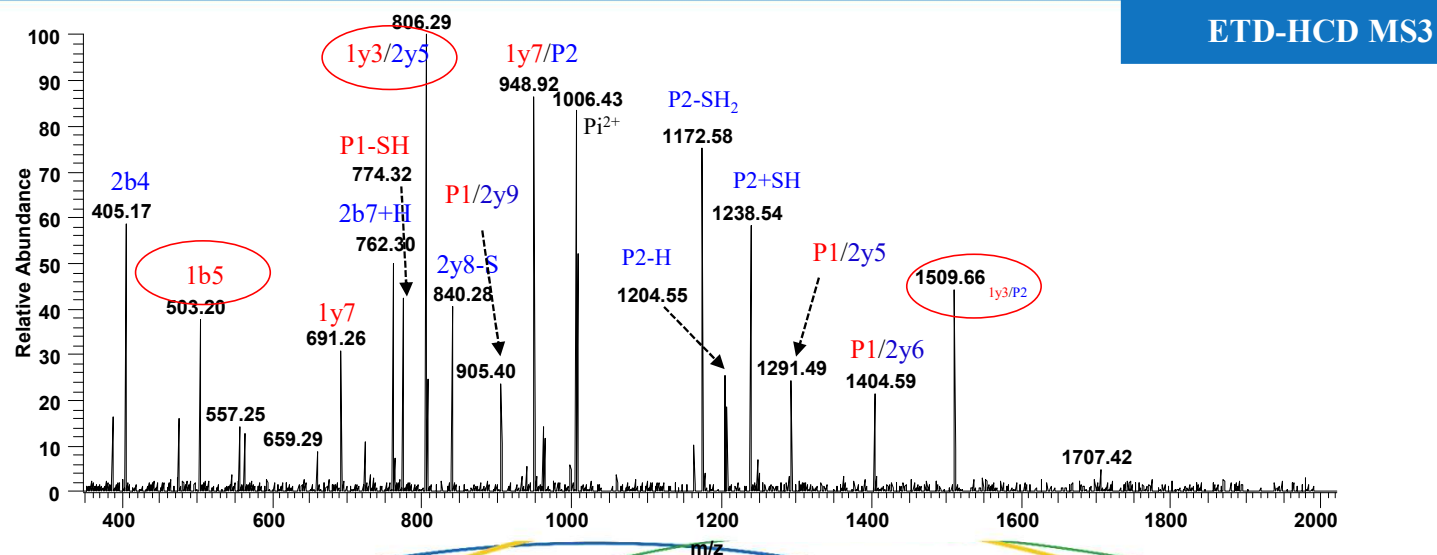
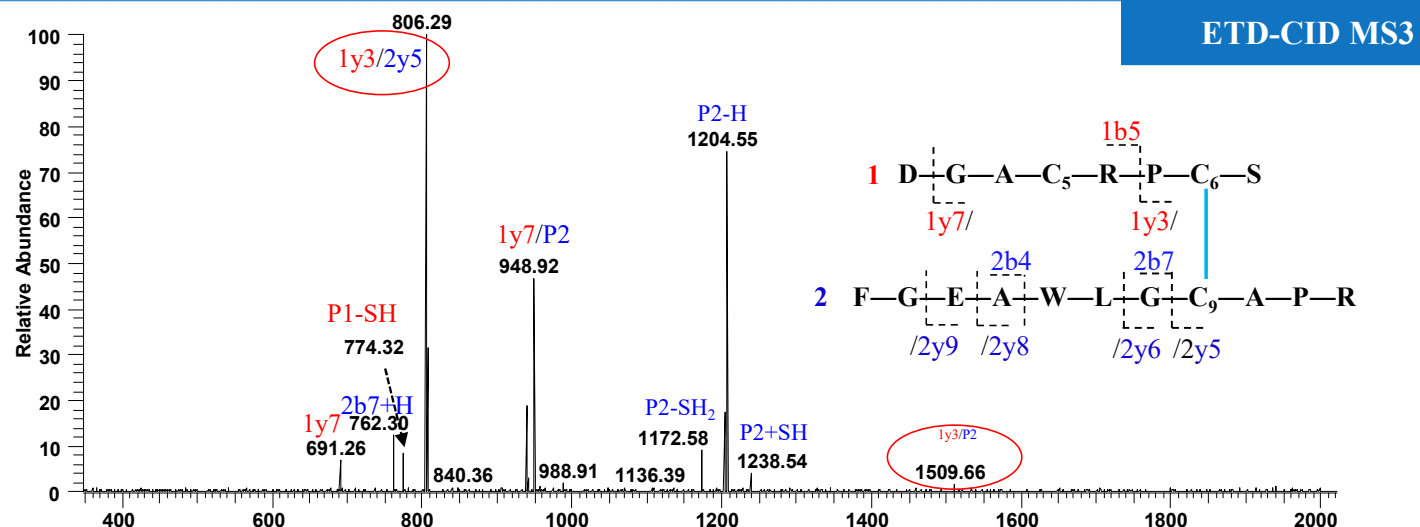
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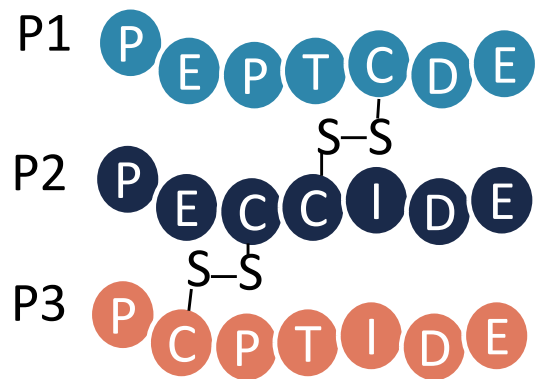
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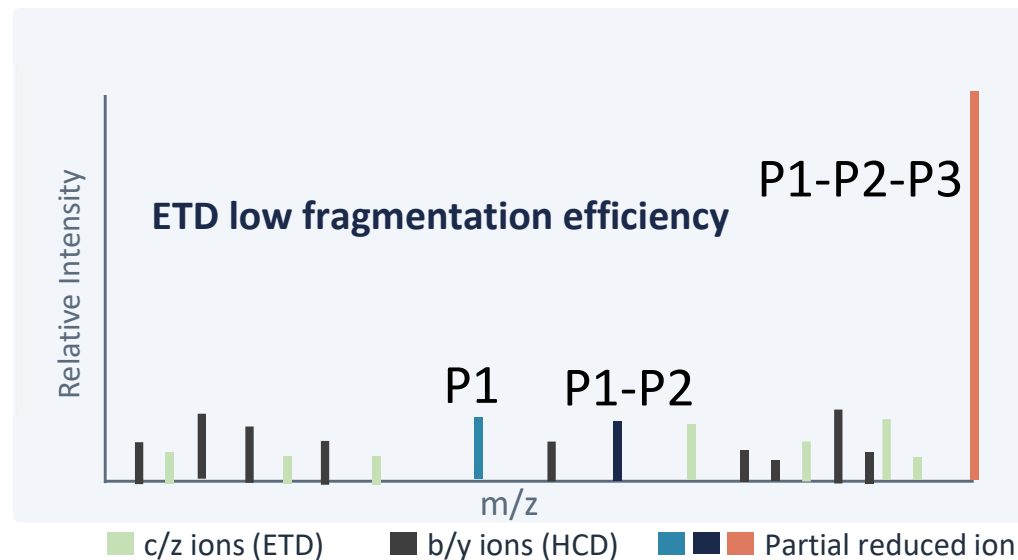




■ ■ ■ Limitation of ETD-CID/HCD MS3 methods



EThcD

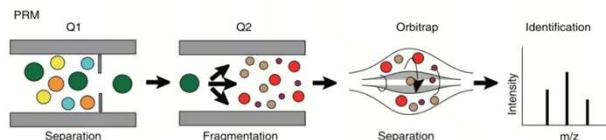


Key Technical Bottlenecks

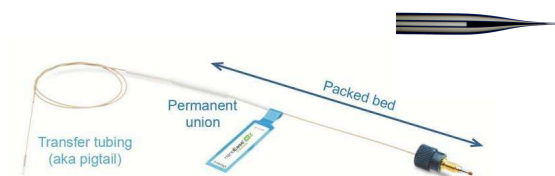
Instrument with ETD and MS3 capability



Method optimization for individual peptide target prevents automated data-dependent acquisition (DDA)



NanoLC is typically used to increase sensitivity



Disulfide mapping analysis based on In-Source Reduction (ISR)

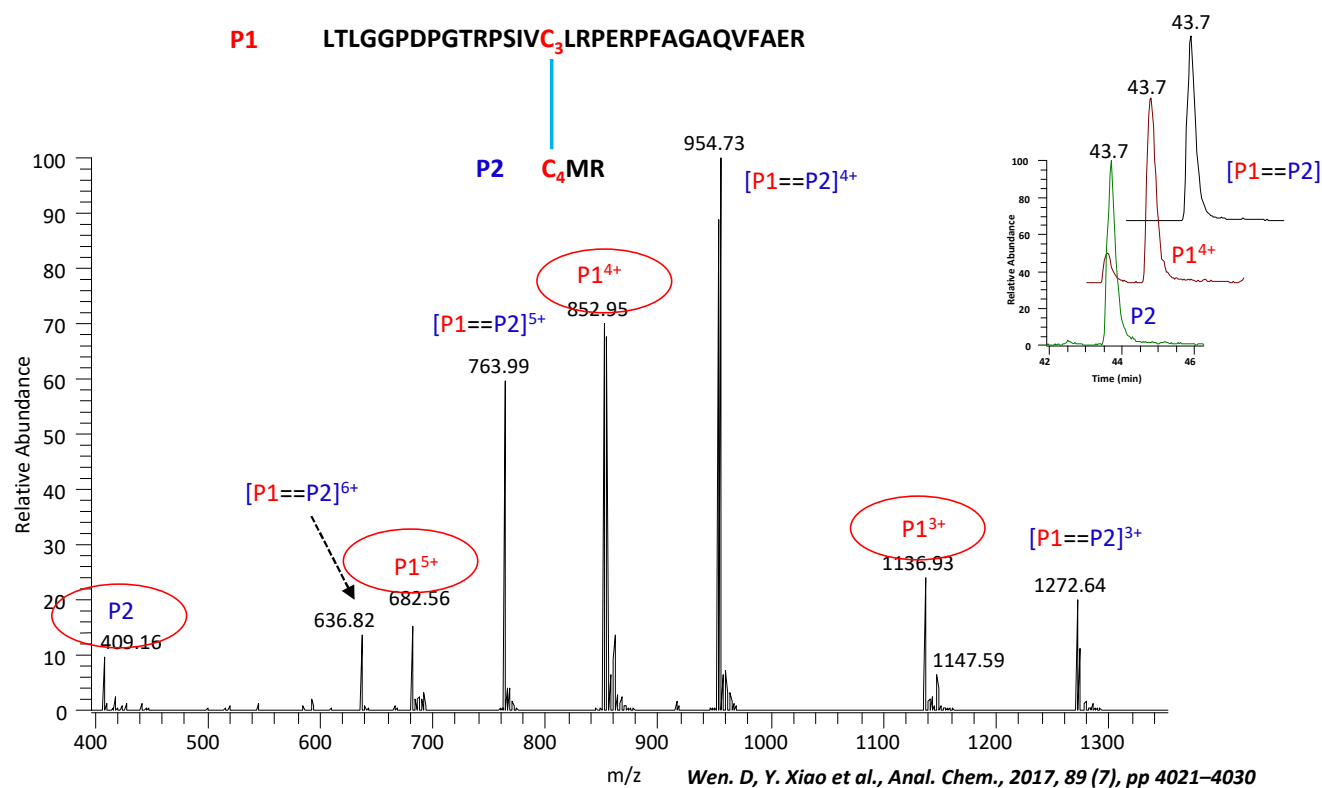
In-Source Reduction (ISR) strategy to determine disulfide composition: The original non reduced disulfide-linked peptide and its composing reduced peptides will have exact same RT

Complete Mapping of Complex Disulfide Patterns with Closely-Spaced Cysteines by In-Source Reduction and Data-Dependent Mass Spectrometry

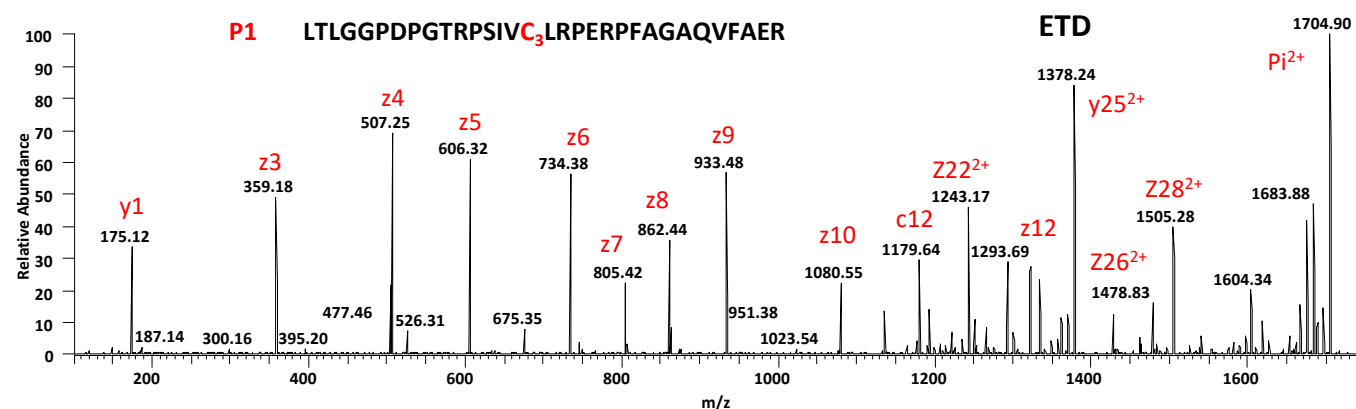
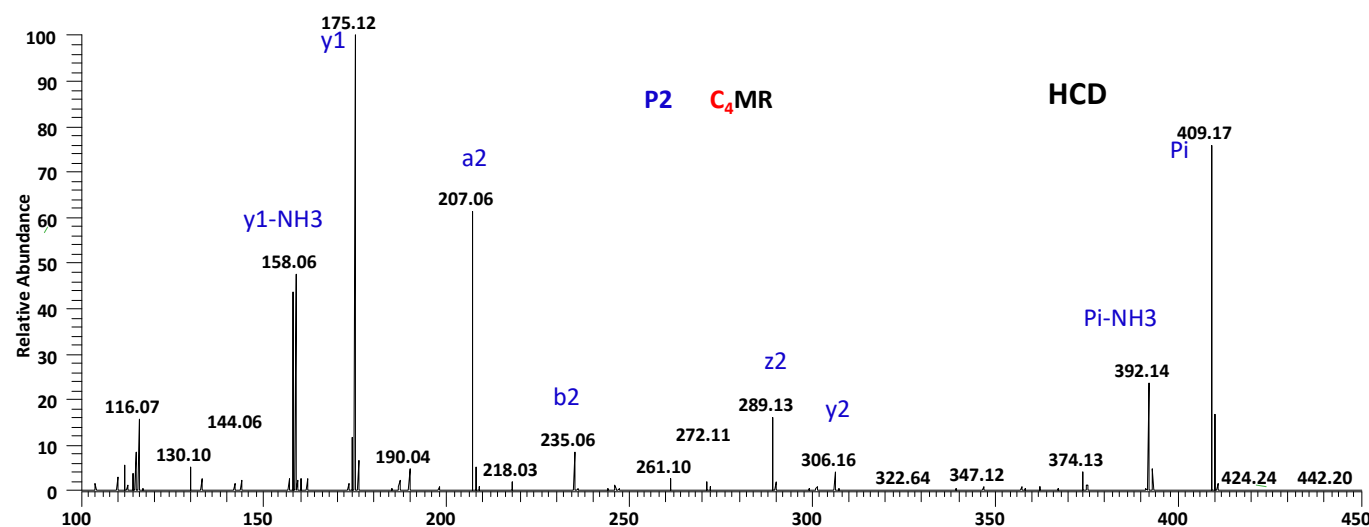
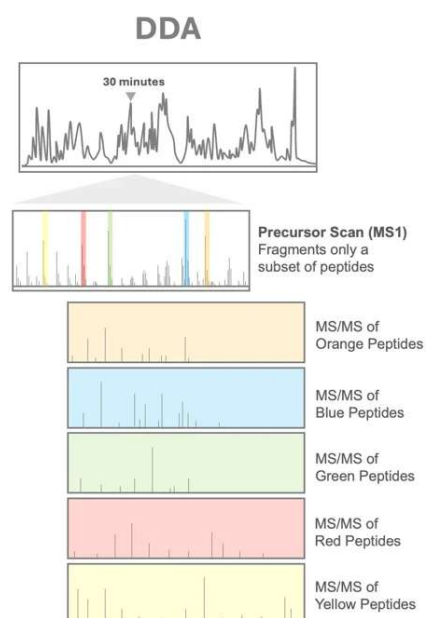
Christian N. Cramer,^{†,‡} Christian D. Kelstrup,[‡] Jesper V. Olsen,[‡] Kim F. Haselmann,[†] and Peter Kresten Nielsen^{*,†}

[†]Protein Engineering, Global Research, Novo Nordisk A/S, Novo Nordisk Park, 2760 Måløv, Denmark

[‡]Proteomics Program, The Novo Nordisk Foundation Center for Protein Research, Faculty of Health and Medical Sciences, University of Copenhagen, 2200 Copenhagen, Denmark



Disulfide mapping analysis based on In-Source Reduction (ISR)



Fully compatible with data-dependent acquisition (DDA) with CID/HCD/ETD

Wen, D, Y. Xiao et al., Anal. Chem., 2017, 89 (7), pp 4021–4030

Disulfide mapping analysis based on In-Source Reduction (ISR)

In-Source Reduction (ISR) strategy to determine disulfide linkage without ETD: ISR to generate partial reduced products with single disulfide bond

Complete Mapping of Complex Disulfide Patterns with Closely-Spaced Cysteines by In-Source Reduction and Data-Dependent Mass Spectrometry

Christian N. Cramer,^{1,2} Christian D. Kelstrup,² Jesper V. Olsen,² Kim F. Haselmann,² and Peter Kresten Nielsen^{2*}

¹Protein Engineering, Global Research, Novo Nordisk A/S, Novo Nordisk Park, 2760 Måløv, Denmark

²Proteomics Program, The Novo Nordisk Foundation Center for Protein Research, Faculty of Health and Medical Sciences, University of Copenhagen, 2200 Copenhagen, Denmark

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Determination of the Disulfide Structure of Murine Meteorin, a Neurotrophic Factor, by LC-MS and Electron Transfer Dissociation-High-Energy Collisional Dissociation Analysis of Proteolytic Fragments

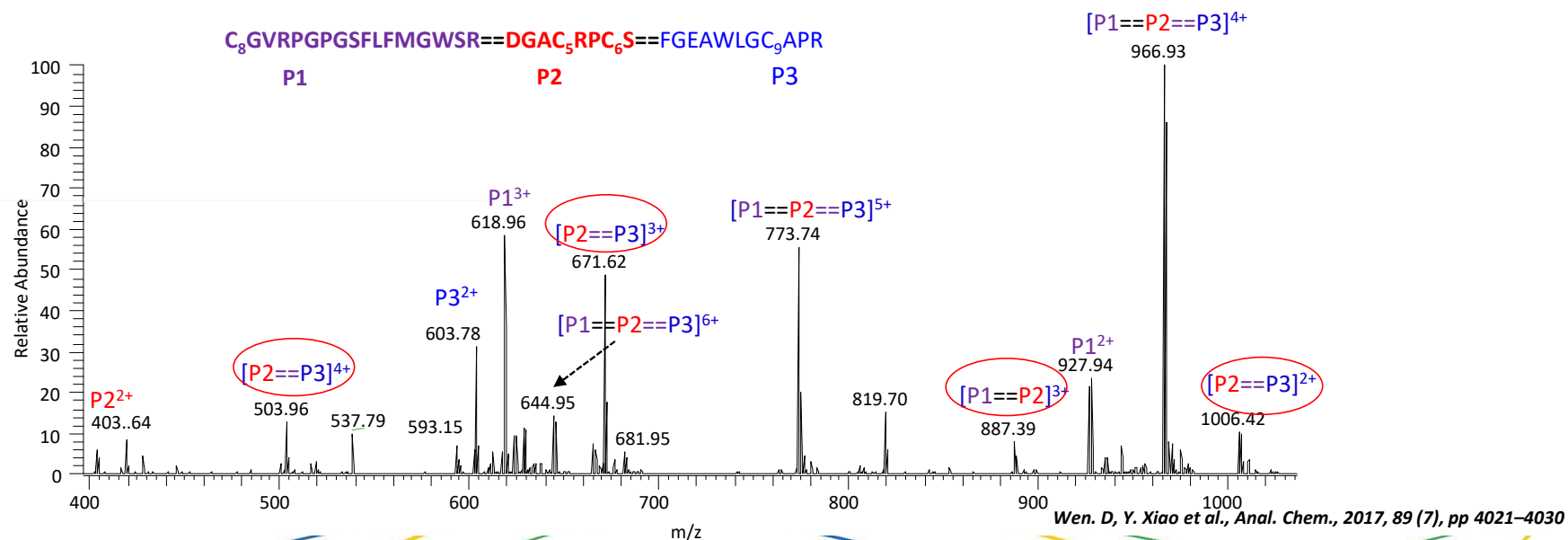
Dingyi Wen¹, Yongsheng Xiao, Malgorzata M. Vecchi, Bang Jian Gong, Jana Dolnikova, and R. Blake Pepinsky

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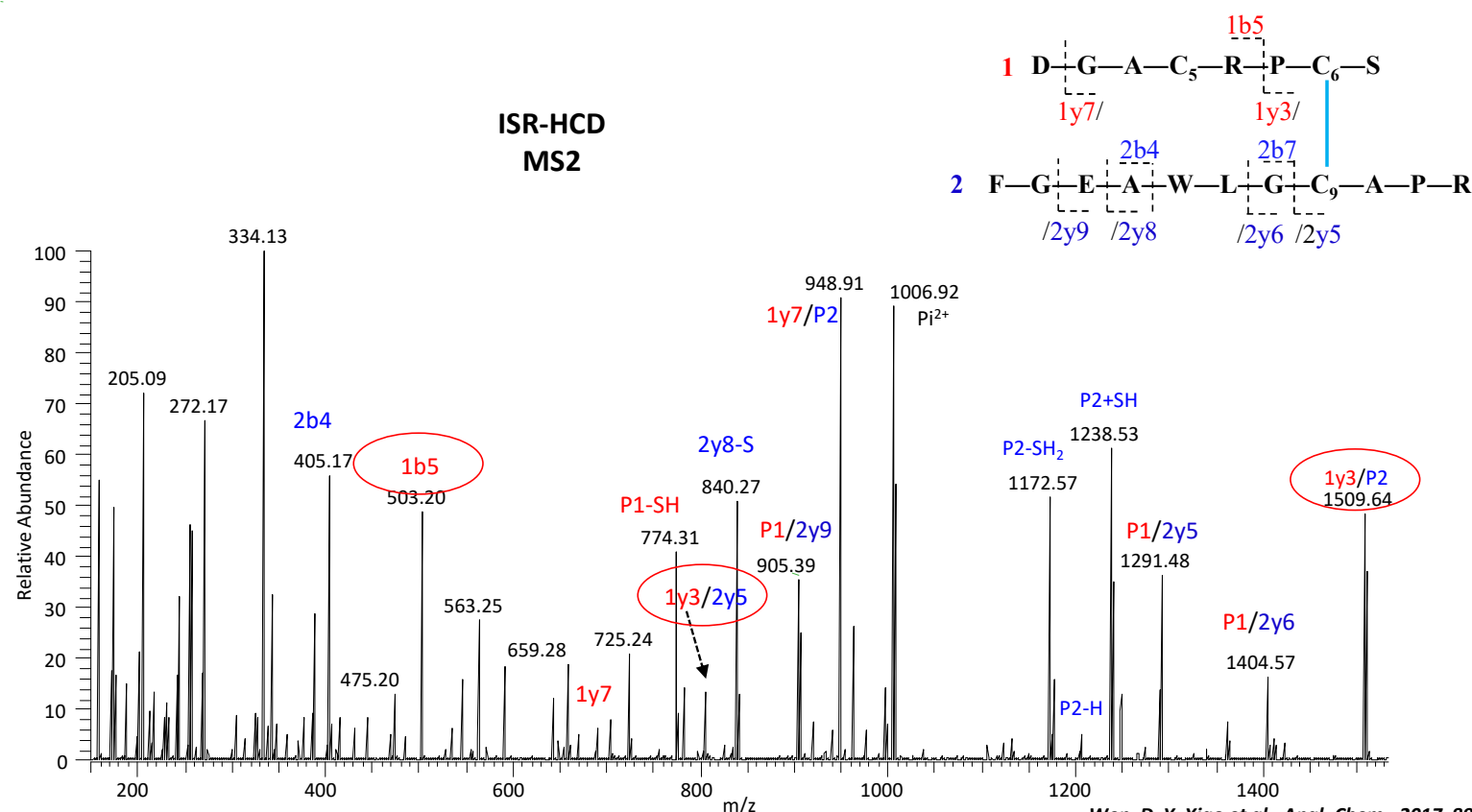
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Disulfide mapping analysis based on In-Source Reduction (ISR)

In-Source Reduction (ISR) strategy to determine disulfide linkage without ETD: ISR to generate partial reduced products with single disulfide bond

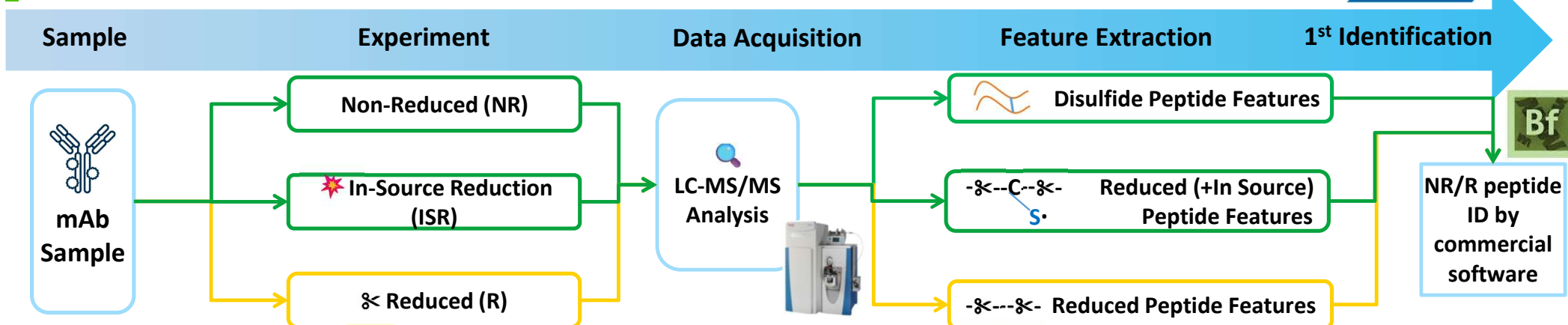


03 Integrated Experimental & Computational Workflow



Integrated Experimental & Computational Workflow

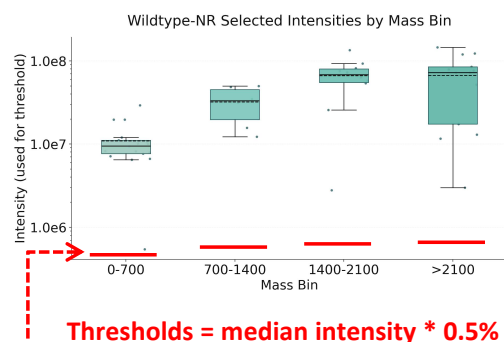
WuXi Biologics
Global Solution Provider



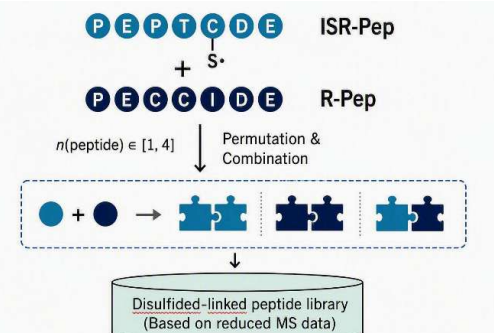
2nd Preprocess

Data Analysis Process

1. Calculate mass-dependent intensity thresholds for 'dark matter' filtering



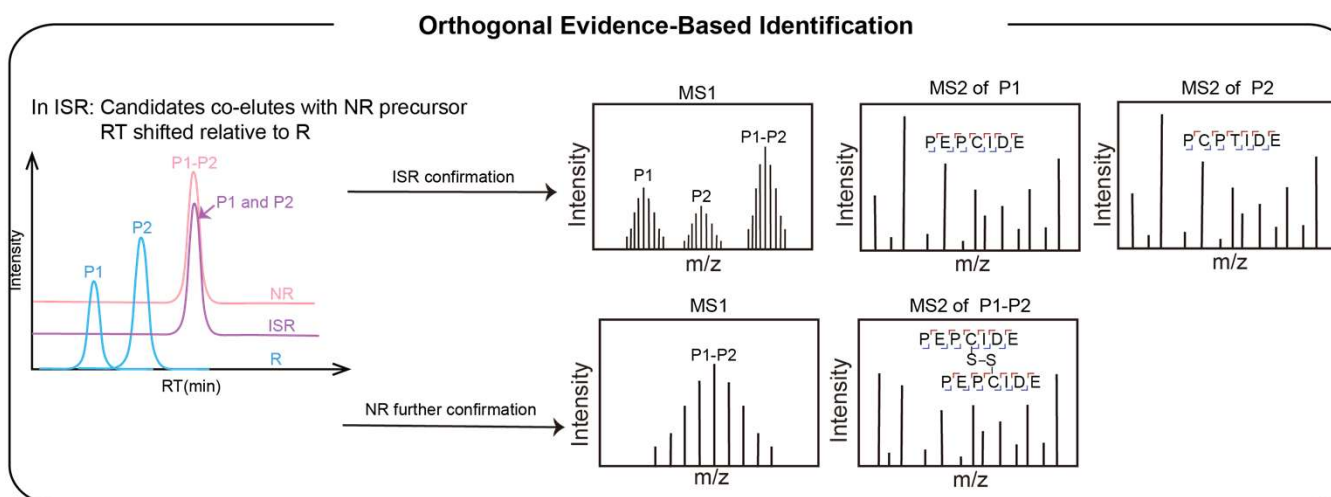
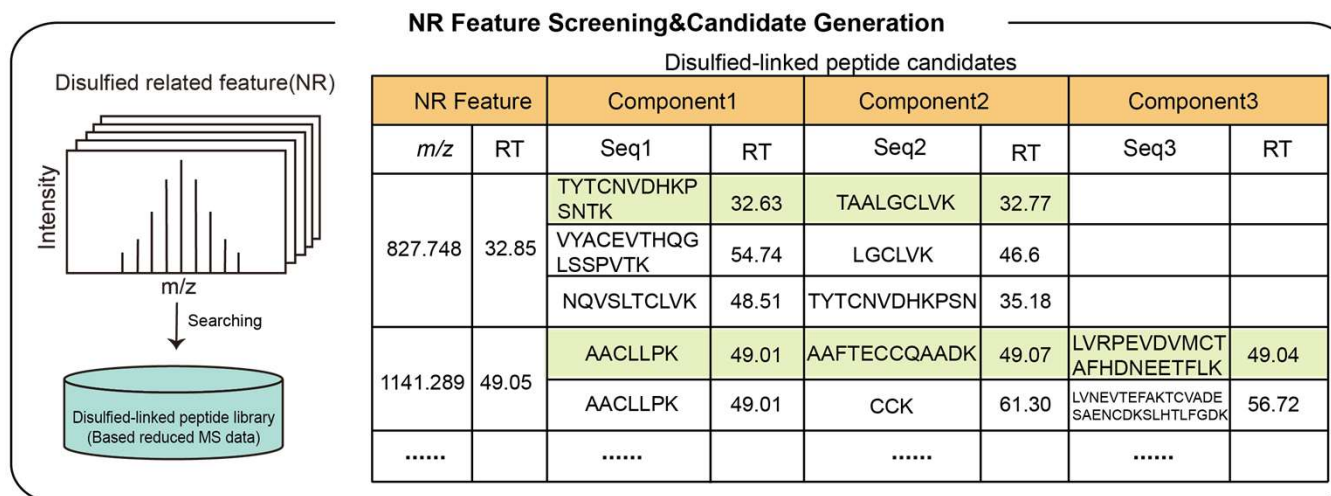
2. Identification of R/ISR Peptides & Generation of *in silico* disulfide-cluster sequence database with accurate mass by considering all possible combinations



Identification of disulfide peptides and connectivity

3rd Identification

Data Analysis Process



4th Manual
Check

User Defined Peptides

Selected: MP206_0754.xlsx

Level	No.	Identification	Positions	Peptide Sequence	Modification	Site
Component	1044	1:A193-K200 = 843.47026(nonunique)	193-200	ALPSSIEK		
Component	1054	1:A193-K200 = 843.47026(nonunique)	193-200	ALPSSIEK		
Component	1061	1:A193-K200 = 843.47026(nonunique)	193-200	ALPSSIEK	Ca2+	
Component	1068	1:A193-K200 = 843.47026(nonunique)	193-200	ALPSSIEK	His	
Component	2092	1:A1-K22 = 2547.07256(nonunique)	1-22	AMRSCPEEQMDPLLGTCOSK		
Component	2093	1:A1-K22 = 2547.07256(nonunique)	1-22	AMRSCPEEQMDPLLGTCOSK		
Component	1820	1:A1-K22/1:Q70-K78 = 3647.47006(2ss)	1-22 70-78	AMRSCPEEQMDPLLGTCOSK/QAYFENK	2ss	1:-C5,-C18,-C21/1:-C71,-C75
Component	1821	1:A1-K22/1:Q70-K78 = 3647.47006(2ss)	1-22 70-78	AMRSCPEEQMDPLLGTCOSK/QAYFENK	2ss	1:-C5,-C18,-C21/1:-C71,-C75
Component	1846	1:A1-K22/1:Q70-K78 = 3647.47006(2ss)	1-22 70-78	AMRSCPEEQMDPLLGTCOSK/QAYFENK	2ss	1:-C5,-C18,-C21/1:-C71,-C75/1:C25
Component	1847	1:A1-K22/1:Q70-K78 = 3647.47006(2ss)	1-22 70-78	AMRSCPEEQMDPLLGTCOSK/QAYFENK	3ss	1:-C5,-C18,-C21/1:-C71,-C75/1:C25
Component	1848	1:A1-K22/1:Q70-K78 = 3647.47006(2ss)	1-22 70-78	AMRSCPEEQMDPLLGTCOSK/QAYFENK	3ss	1:-C5,-C18,-C21/1:-C71,-C75/1:C25
Component	1822	1:A1-K22/1:152-K18/1:1723-K18 = 3647.47006(2ss)	1-22 32-38	AMRSCPEEQMDPLLGTCOSK/TCAMCR/T	3ss	1:-C5,-C18,-C21/1:-C33,-C37/1:C25

Read disulfide linked peptide directly from search results or from manual input

User Defined Peptides

Selected: MP206_0754.xlsx

Generate Peptides Display Peptides 2 Calc Possible DSS 4 Clear Peptides Clear All Connected Lines: P1_25-P2_75 P2_71-P1_5

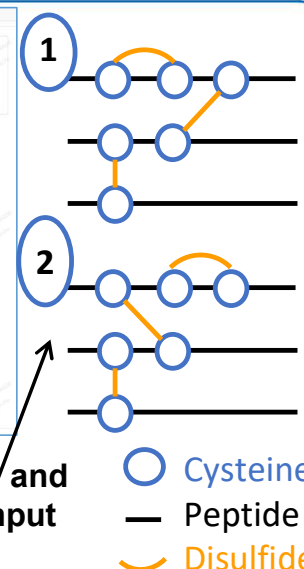
Peptide	Add Mod
AMRSCPEEQMDPLLGTCOSK	1
QAYFENK	70
TCAMCR	23

A M R S C P E E Q Y W D P L L G T C M S C K
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

Q C A Y F C E N K
70 71 72 73 74 75 76 77 78

T I C N H Q S Q R
23 24 25 26 27 28 29 30 31

Generate all the possible linkage forms and obtain the theoretical form from user input



Visualization
Tool for Data
Analysis

A S^{b2} R^{b3} M^{b4} C P A E Q Y S A D L L G S C M^{v4} T^{v3} L^{v2} C^{v1} K

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

T I^{b2} C^{b3} N^{b4} K^{b5} Q^{b6} S^{b7} L^{b8} Q^{b9} R^{b10}

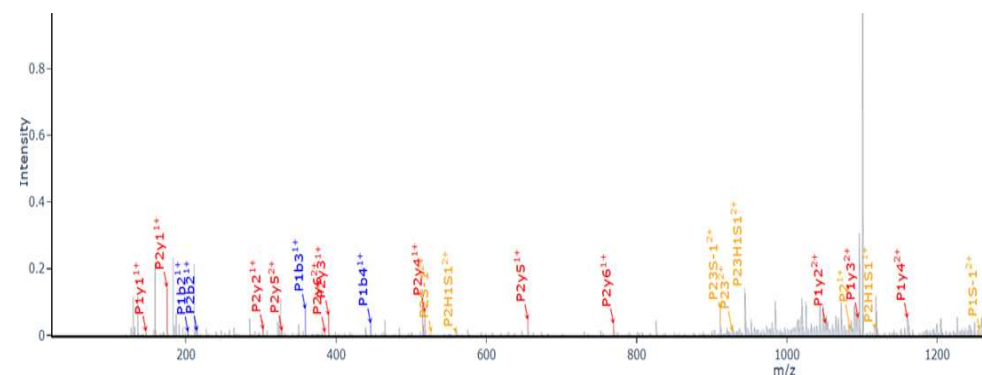
1 2 3 4 5 6 7 8 9

S C^{b2} Q^{b3} M^{b4} F^{b5} L^{b6} C^{b7} R^{b8}

1 2 3 4 5 6 7

Peptide Index	Ion Type	m/z
1	b3	315.178
1	b4	446.218
1	γ2 (+ P2 & P3)	2199.991
2	b2	215.139
...	...	...

Enable Customized Input & Show Match Details



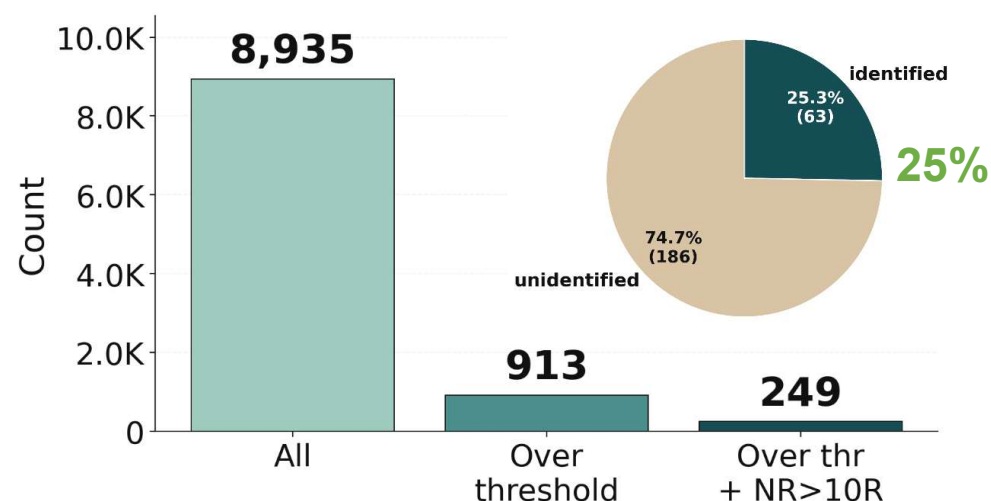
Annotate MS1/MS2 Spectra

The background features a light blue gradient with faint, stylized protein ribbon structures. On the left, there are three distinct protein folds: a light blue one at the top, a pink one in the middle, and a magenta one at the bottom. Three curved lines in yellow, green, and blue arc across the right side of the image, framing the text.

Case Studies *04*

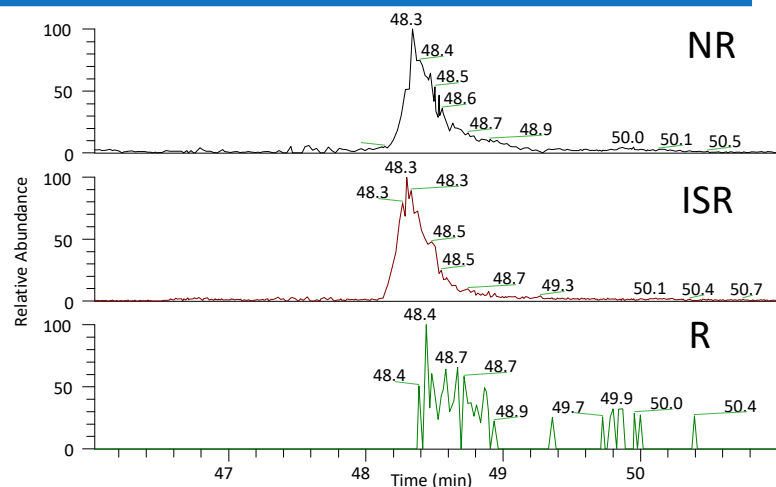
WuXi Biologics
Global Solution Provider

Although all disulfide cluster from IgG4 tryptic digest are simplest “1+1” mode, the identification rate is still low.

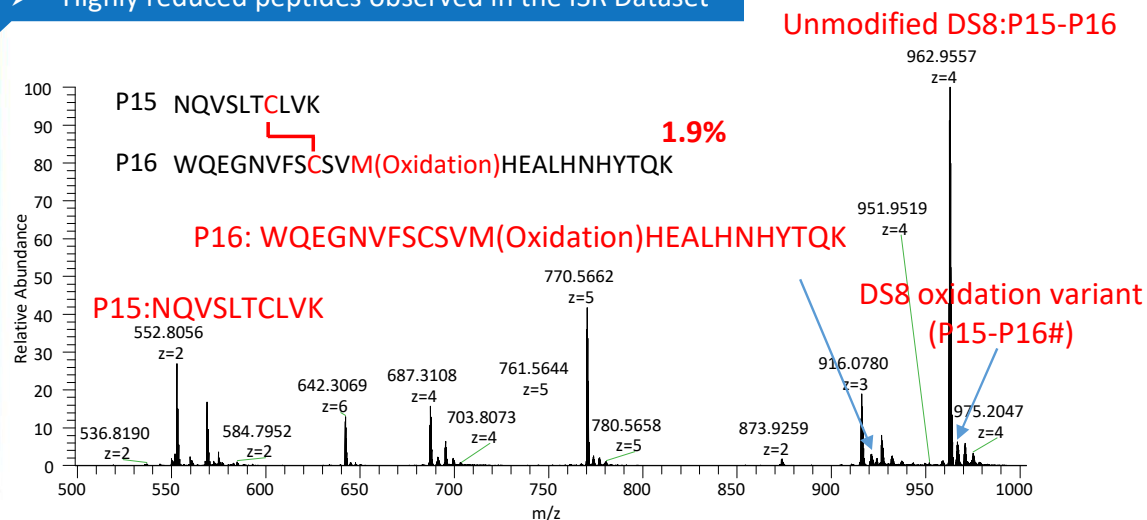


ISR-assisted identification of disulfide-linked peptides with PTM

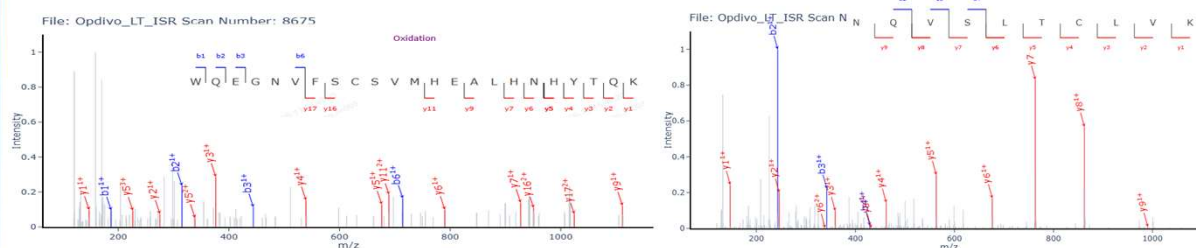
The EIC of precursor and in-source reduced peptides



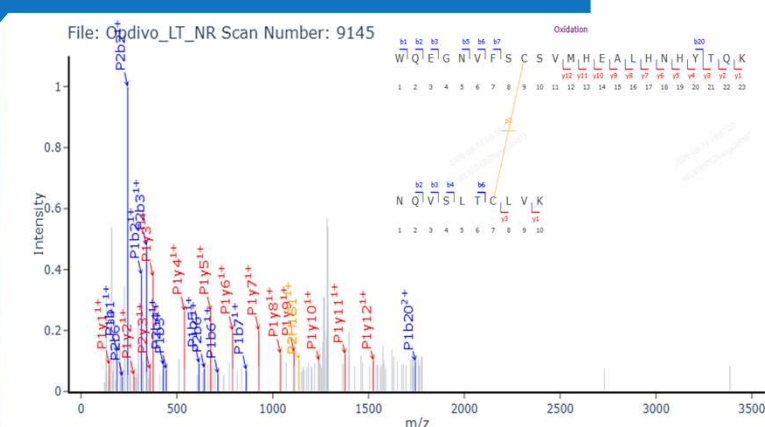
Highly reduced peptides observed in the ISR Dataset



MS2 of P15# and P16# in ISR dataset

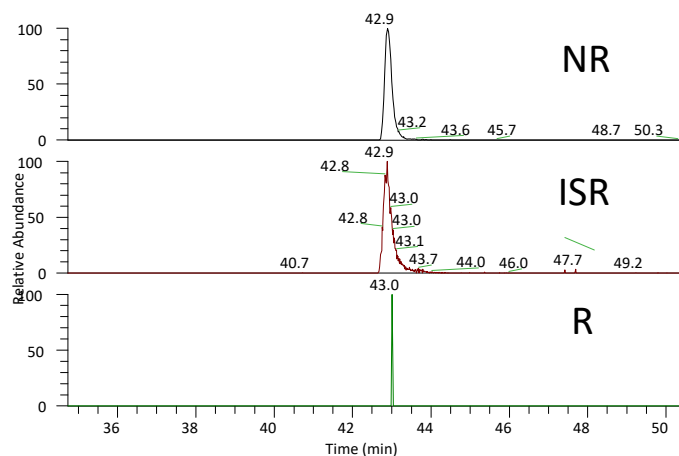


Confident ID of DS8# in the NR MS2



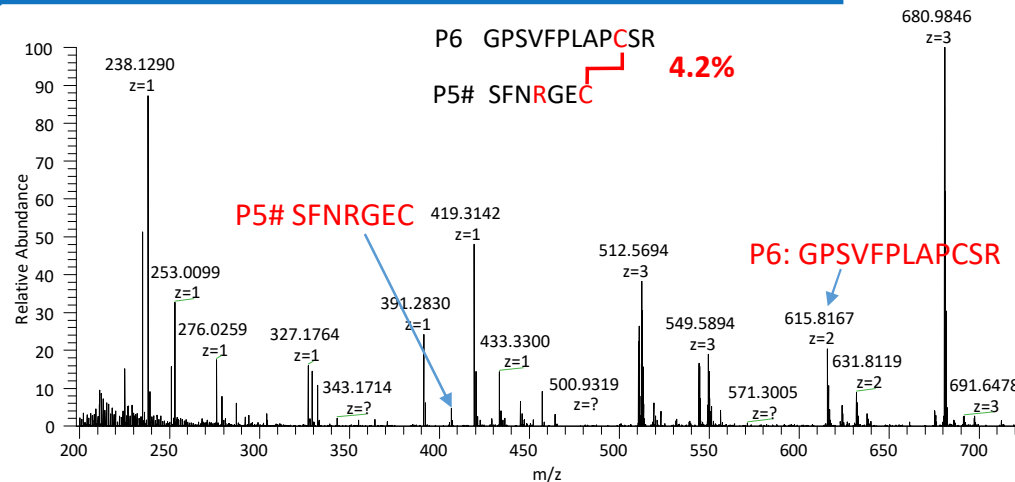
ISR-assisted identification of disulfide-linked peptides with missed cleavages

The EIC of precursor and in-source reduced peptides



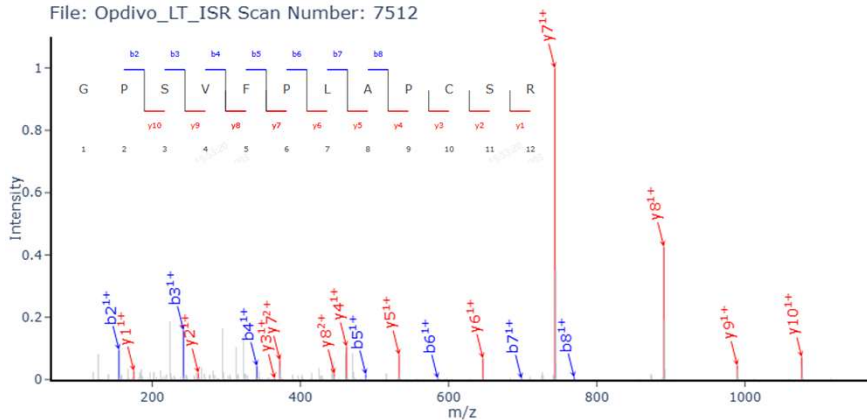
Highly reduced peptides observed in the ISR Dataset_42.9min

DS3#: P5#-P6



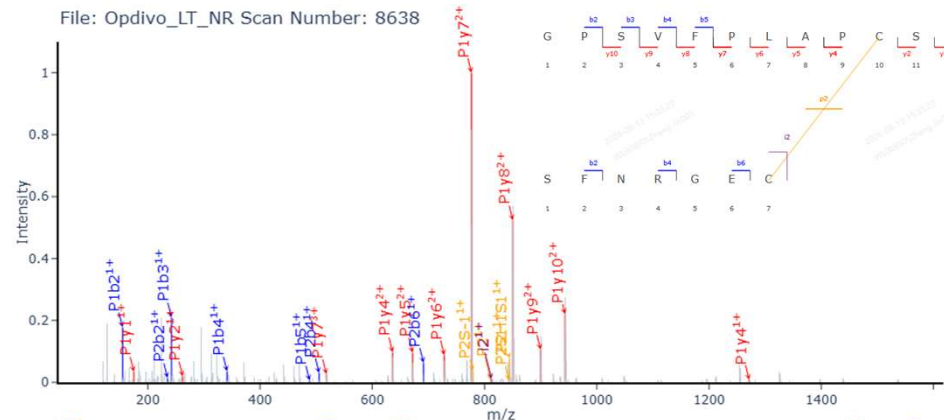
Only the P6 Was Confirmed by MS2

File: Opdivo_LT_ISR Scan Number: 7512



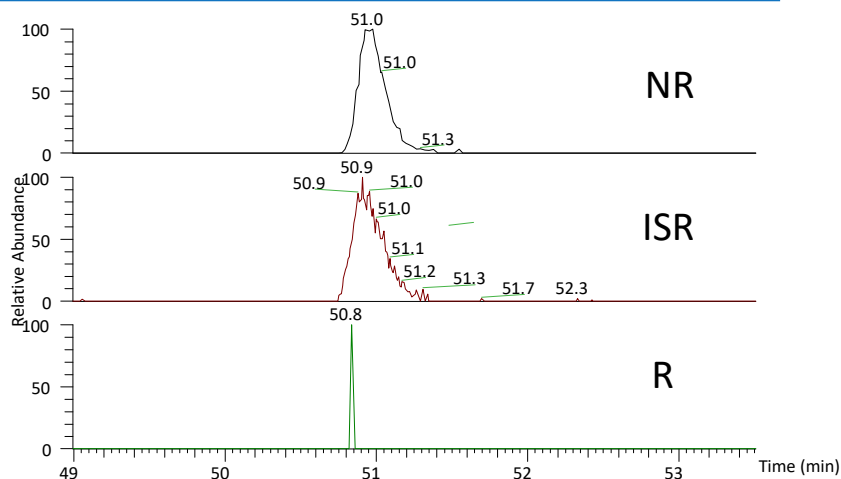
Confident ID of DS5# in the NR dataset

File: Opdivo_LT_NR Scan Number: 8638

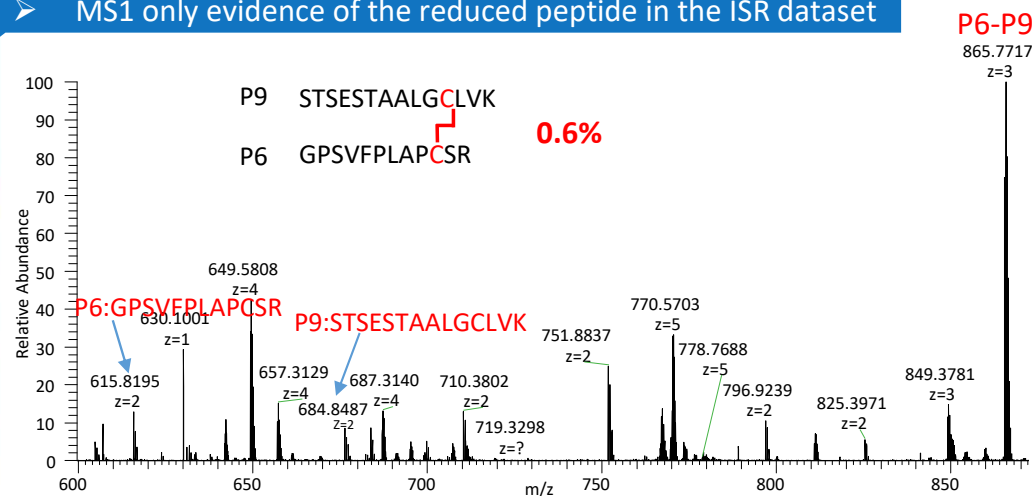


ISR-assisted identification of low-level peptides with disulfide scrambling

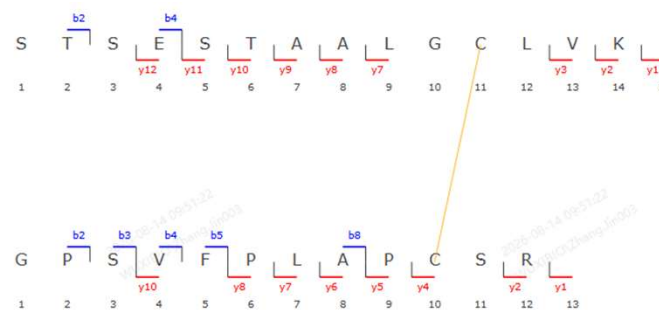
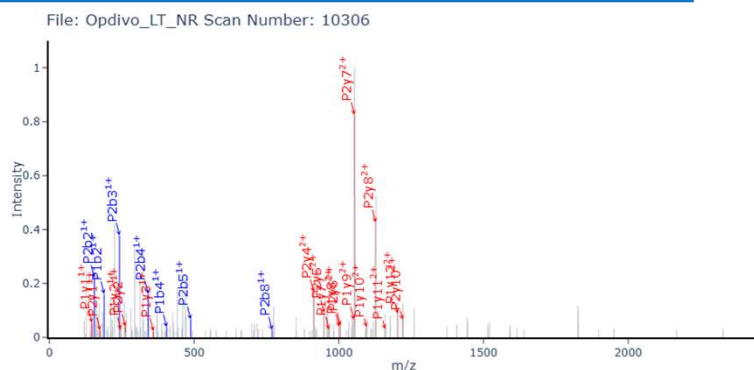
The EIC of precursor and in-source reduced peptides



MS1 only evidence of the reduced peptide in the ISR dataset



MS2 evidence of the P6-P9 in the NR dataset

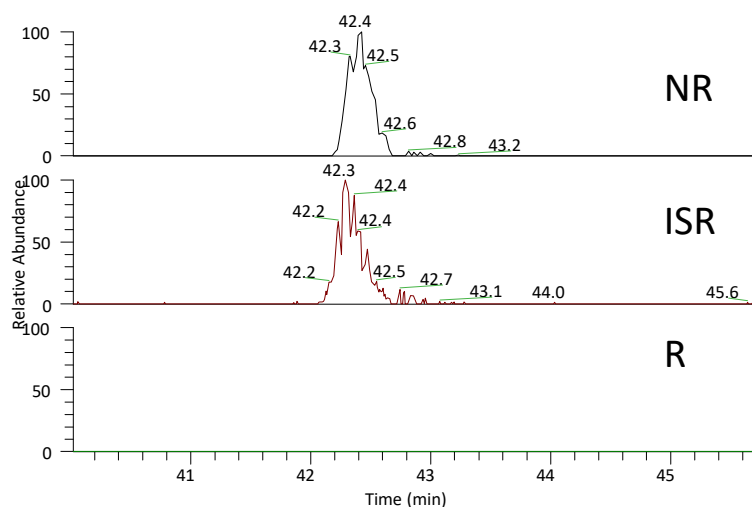




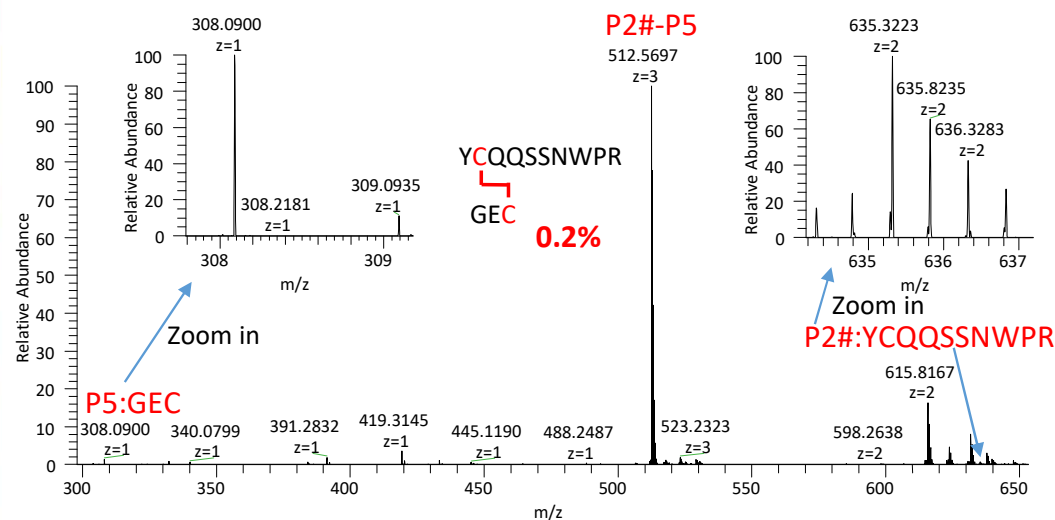
ISR-assisted identification of low-level peptides with disulfide scrambling

- No MS2 available for NR disulfide-linked peptide cluster
- Identification of low-level NR peptide based on ISR peptide MS1 and co-elution assessment

➤ The EIC of precursor and in-source reduced peptides

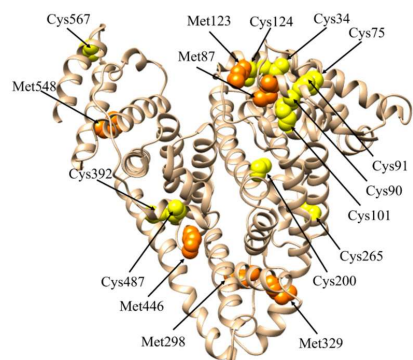


➤ MS1 only evidence of the reduced peptide in the ISR dataset



Human Serum Albumin (HSA)-disulfide mapping by tryptic digestion

Serum Albumin: A Multifaced Enzyme



Int J Mol Sci. 2021 Sep 18;22(18):10086.

Disulfide-containing species from a NR tryptic digestion of HSA

DS1: P1 TCVADESAENC DK

P2 LCTVATLR

DS2: P3 ETYGEMADCCAK

P4 NECFLQHK

P5 LVRPEVDVMCTAFHDNEETFLK

DS3: P6 AAFTECCQAADK

P7 AACLLPK

DS4: P8 CASLQK

P9 VHTECCHGDLLECADDR

P10 YICENQDSISSK

DS5: P11 ECCCKPLLEK

P12 SHCIAEVENDEMPADLPSLAADFVESK

DS6: P13 DVCK

P14 CCAAADPHECYAK

P15 QNCELFEQLGEYK

P16 CCK

DS7: P17 MPCAE DYLSVVLNQLCVLHEK

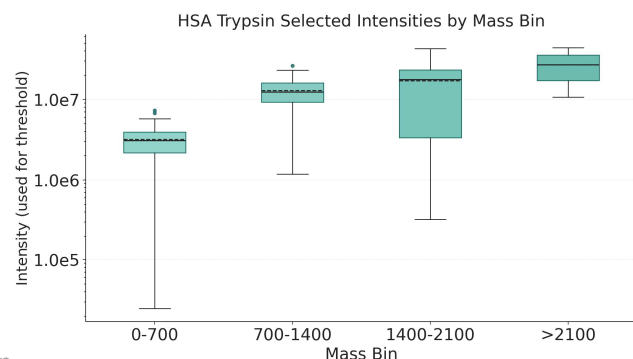
P18 CCTESLVNR

P19 RPCFSALEVDETYVPK

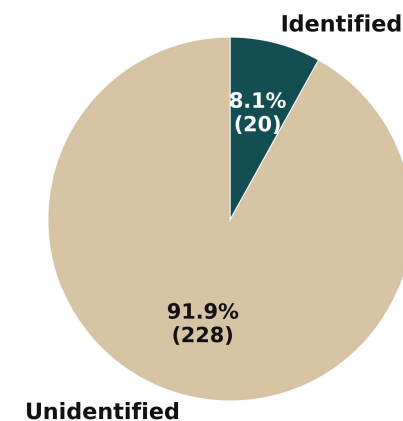
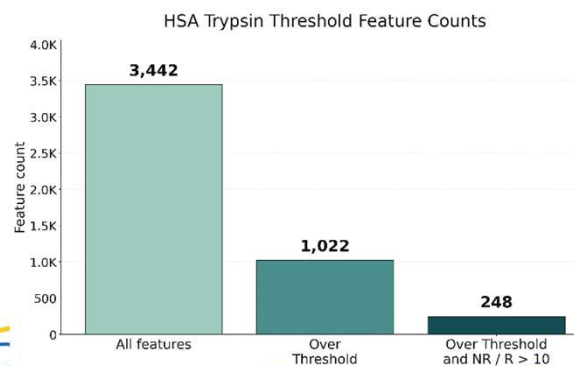
DS8: P20 EFNAETFTFHADICTLSEK

P21 CCK

P22 ETCFAEEGK



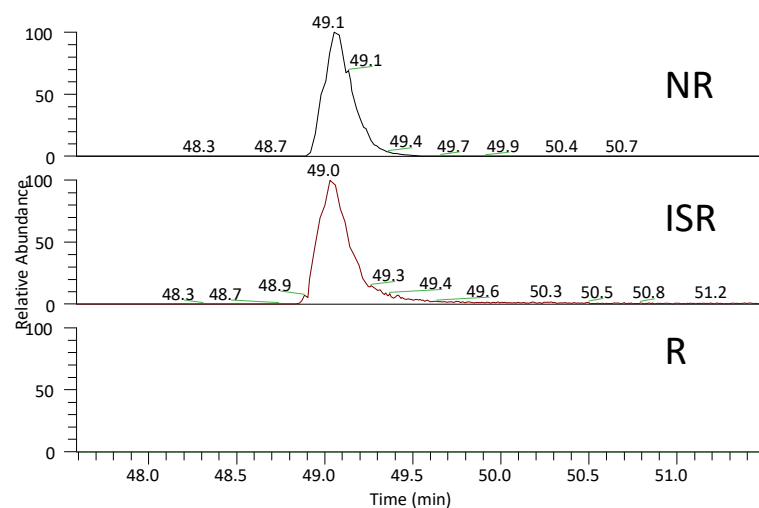
Confiden....



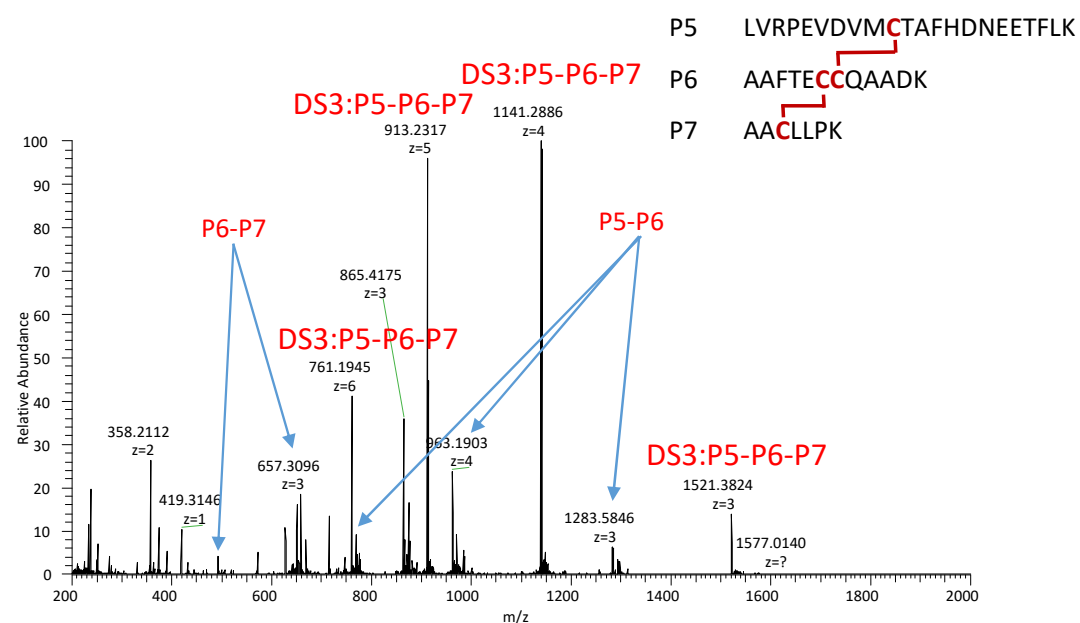


ISR-assisted identification of HSA-LT-DS3 (1+2+1 cluster)

➤ The EIC of precursor and in-source reduced peptides

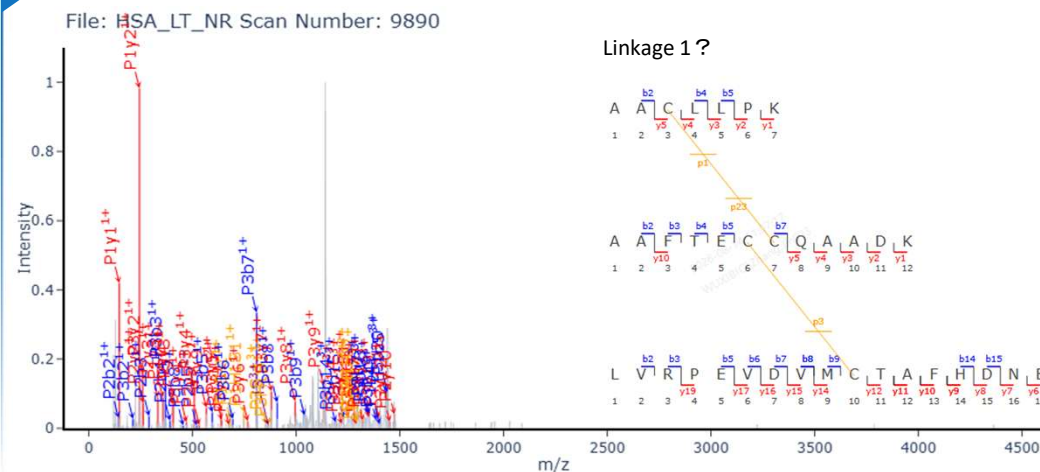


➤ Highly reduced peptides observed in the ISR Dataset

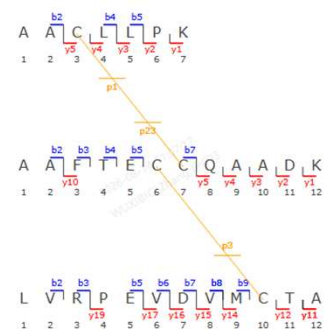


ISR-assisted identification of HSA-LT-DS3 (1+2+1 cluster)

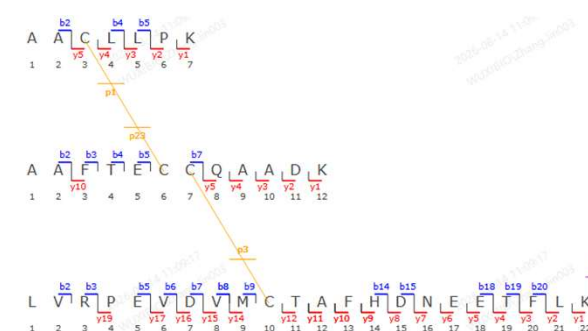
➤ NR MS2 Spectrum does not provide definitive linkage assignment



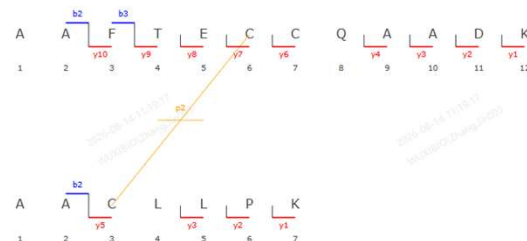
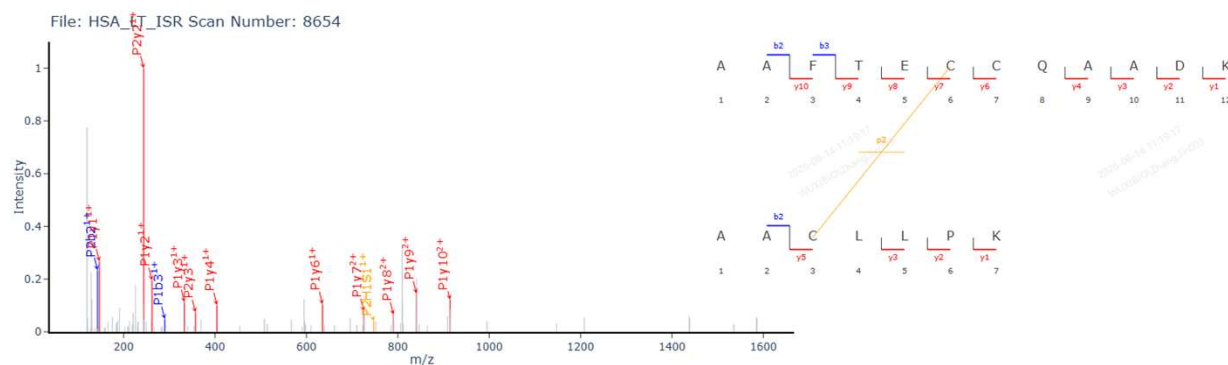
Linkage 1 ?



Linkage 2 ?



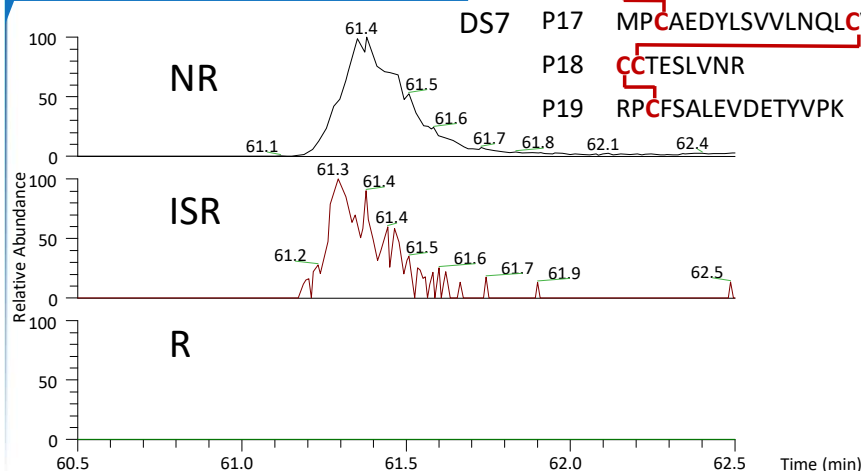
➤ ISR MS2 enabled linkage assignment through identification of a partially reduced disulfide-linked peptide



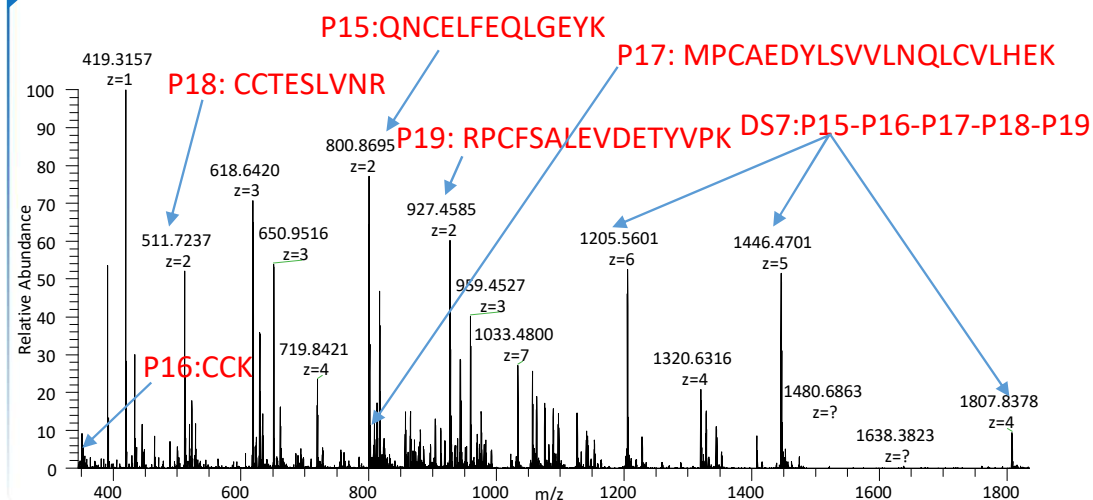
ISR-assisted identification of HSA-LT-DS7 1+2+2+2+1

The EIC of precursor and in-source reduced peptides

P15 QNCELFEQLGEYK
P16 CCK
P17 MPCEADYLSVVLNQLCVLHEK
P18 CCTESLVNR
P19 RPCFSALEVDETYVPK

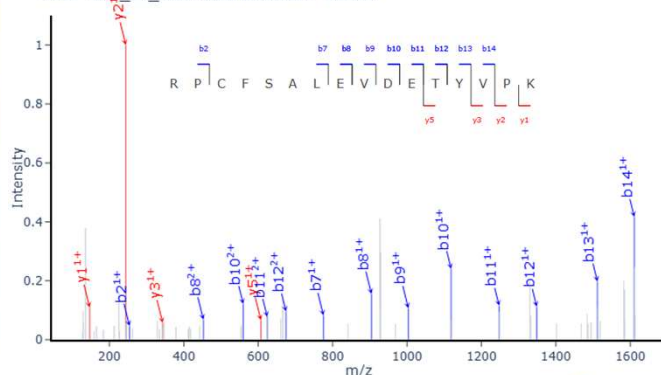


Highly reduced peptides observed in the ISR Dataset

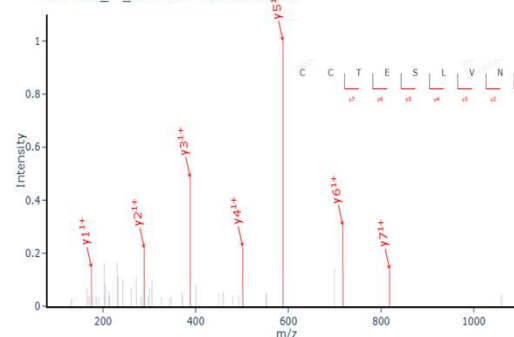


ISR MS2-assisted confirmation

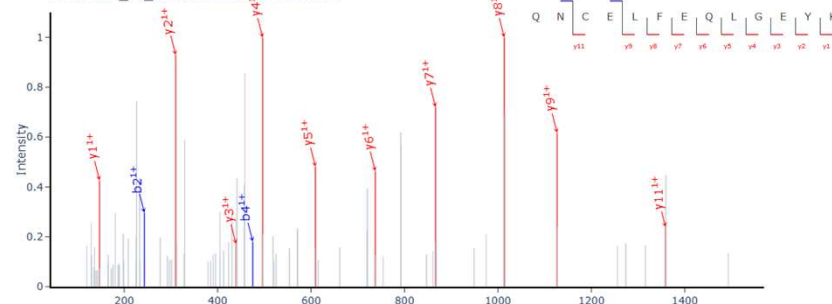
File: HSA_LT_ISR Scan Number: 10923



File: HSA_LT_ISR Scan Number: 10889

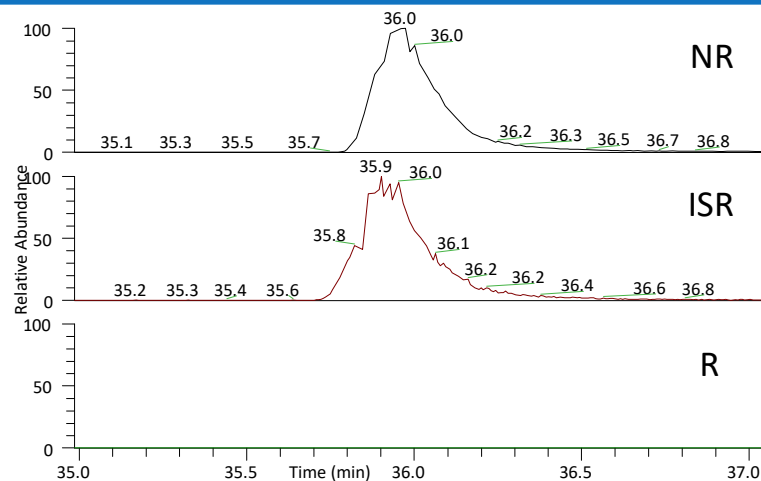


File: HSA_LT_ISR Scan Number: 10921

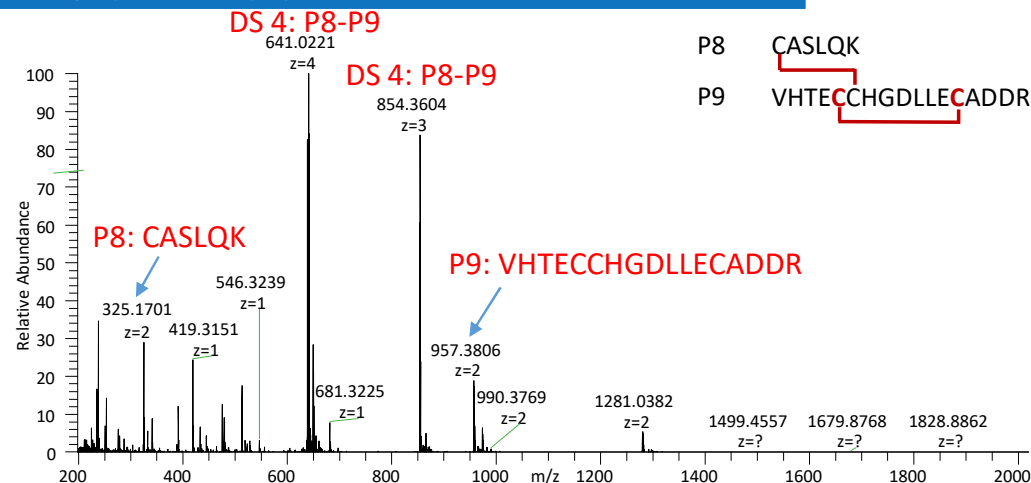


ISR-assisted identification of HSA-LT-DS4 1+3

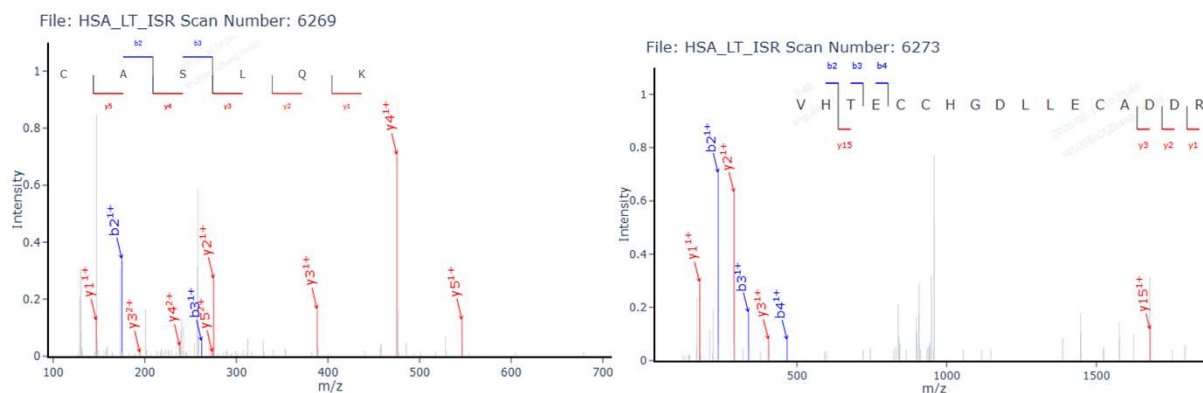
➤ The EIC of precursor and in-source reduced peptides



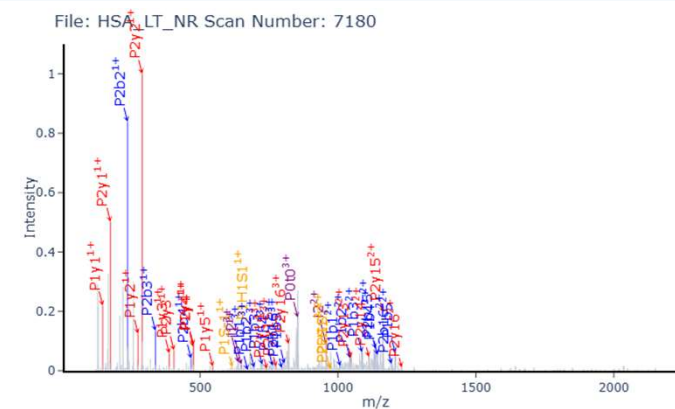
➤ Highly reduced peptides observed in the ISR Dataset



➤ ISR MS2 of P8 and P9

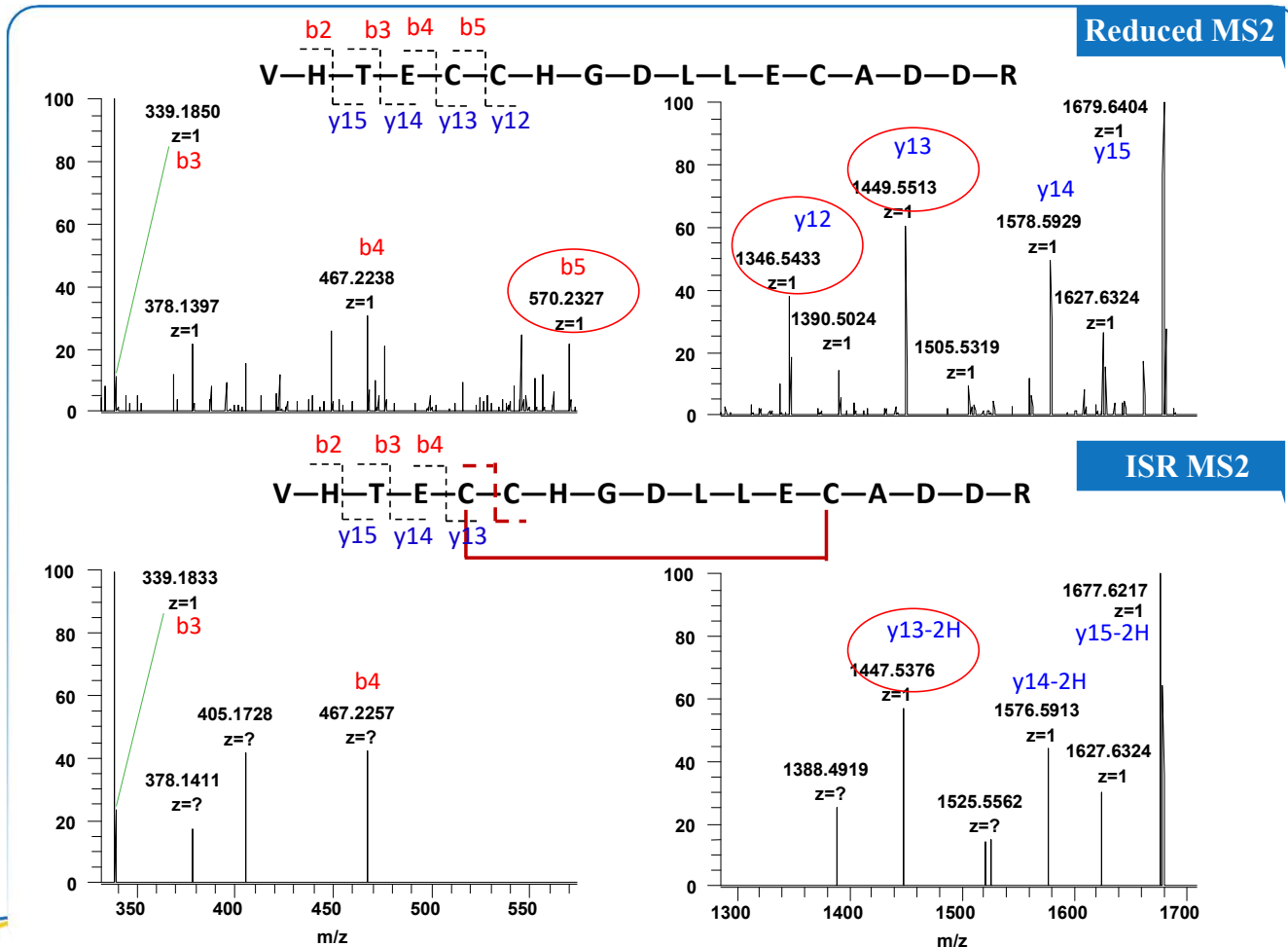
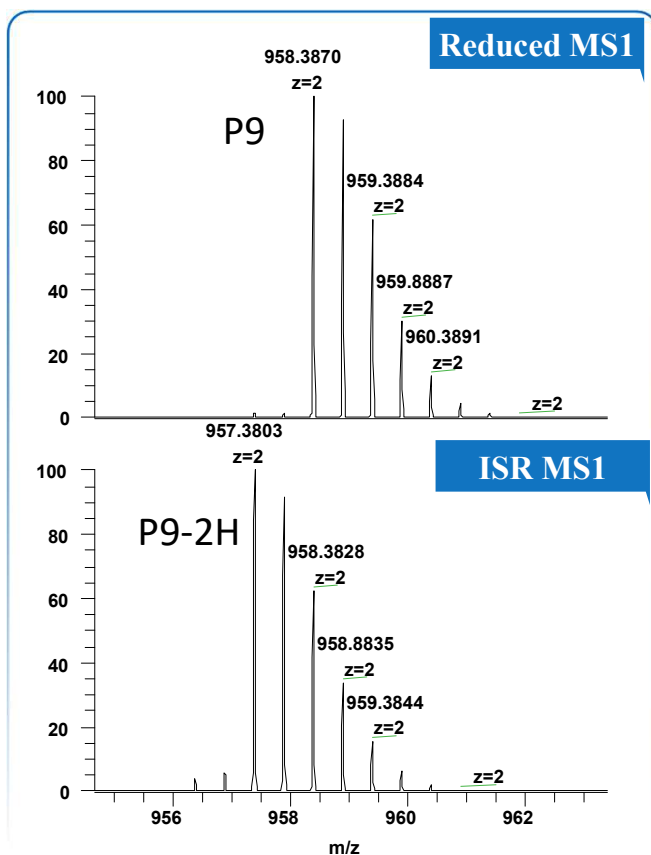


➤ NR MS2 of data quality was insufficient for linkage ID



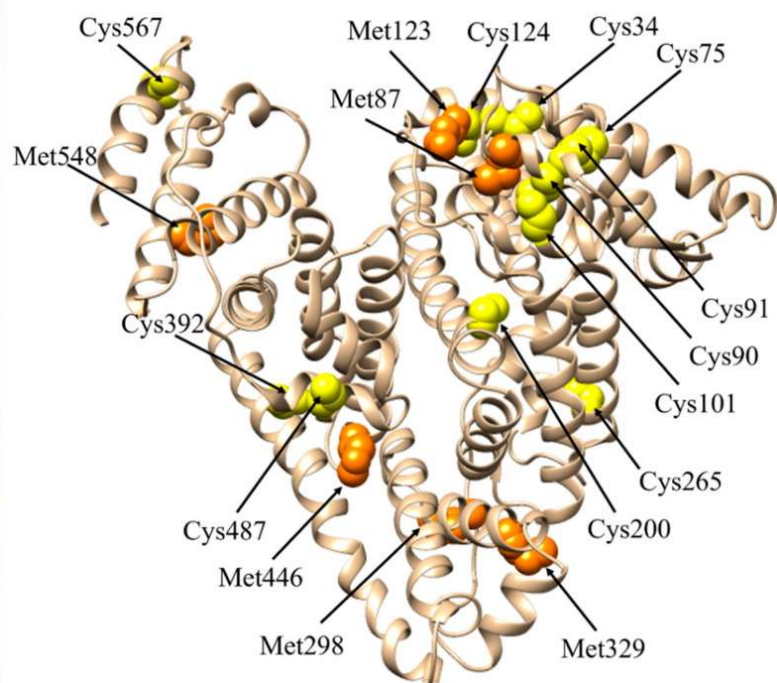
ISR-assisted identification of HSA-LT-DS4 1+3

The connectivity of "1+3" disulfide cluster may be assigned by comparing MS2 of reduced and ISR peptides

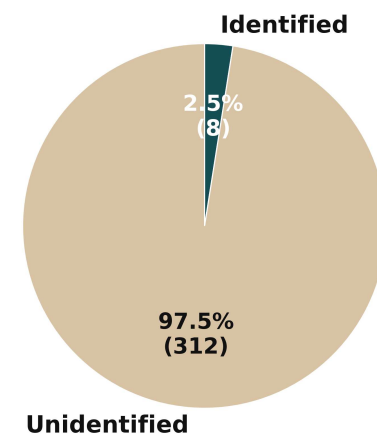
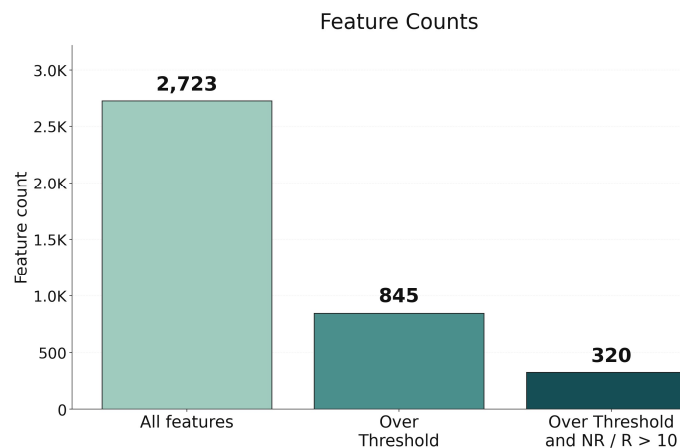
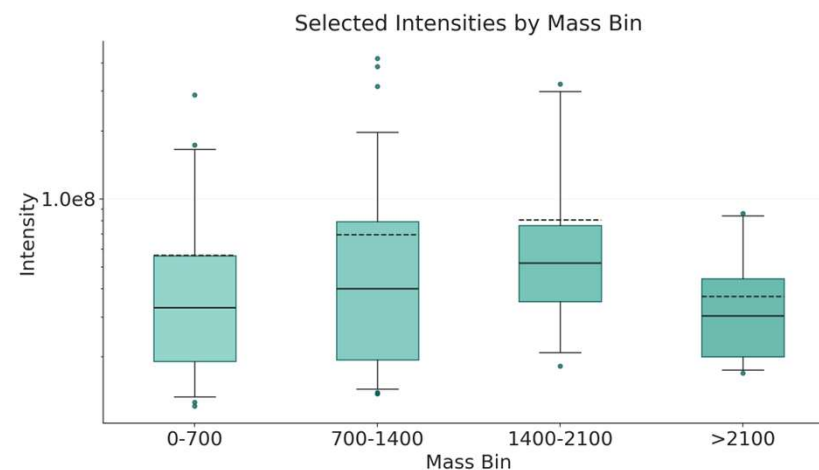


Human Serum Albumin (HSA)-disulfide mapping by non-specific enzyme digestion (pepsin)

Serum Albumin: A Multifaced Enzyme



Int J Mol Sci. 2021 Sep 18;22(18):10086.

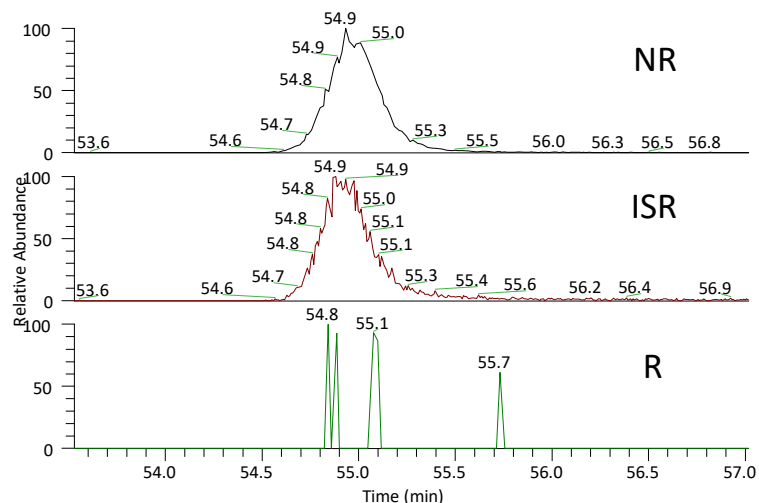


ISR-assisted identification of peptide cluster with 2 intra-disulfide bonds

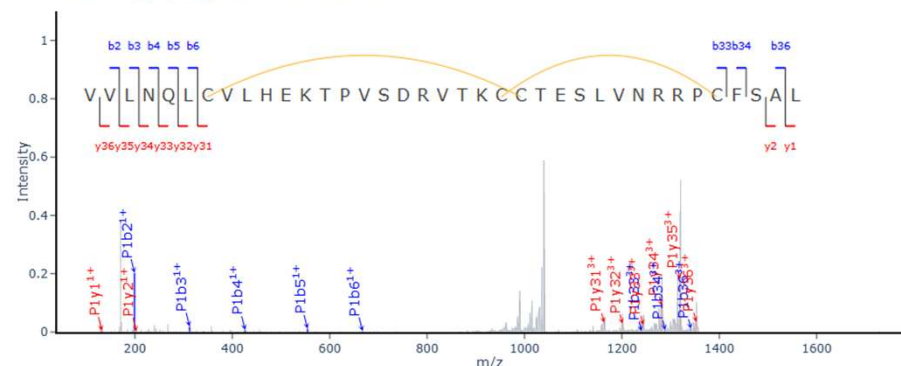
Internal peptide

VVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSAL

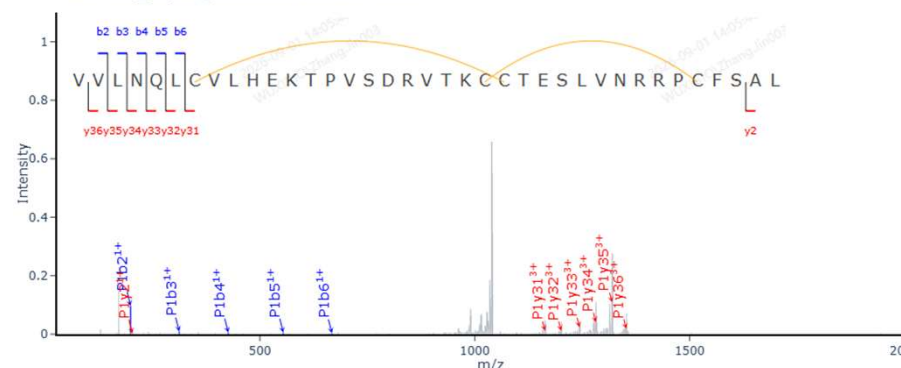
EIC of m/z 1039.2837z



File: HSA_Pepsin_NR Scan Number: 10995

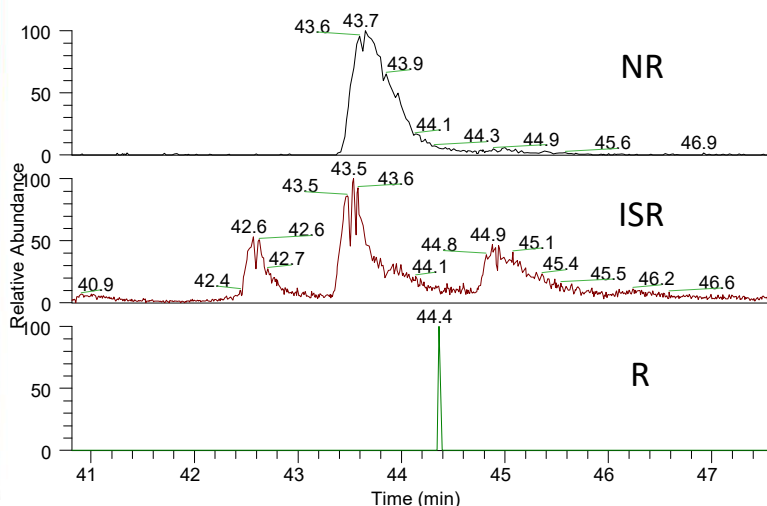


File: HSA_Pepsin_ISR Scan Number: 9587

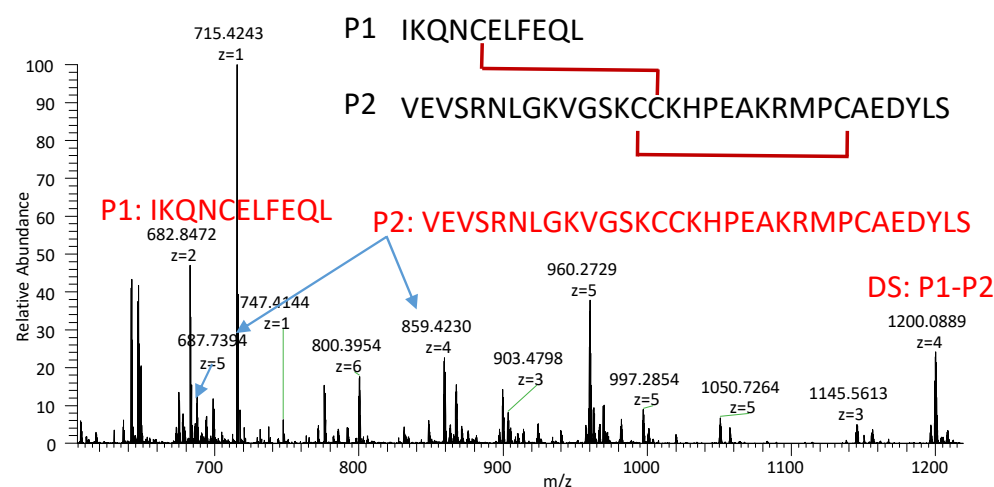


ISR-assisted identification of peptide cluster 1+3

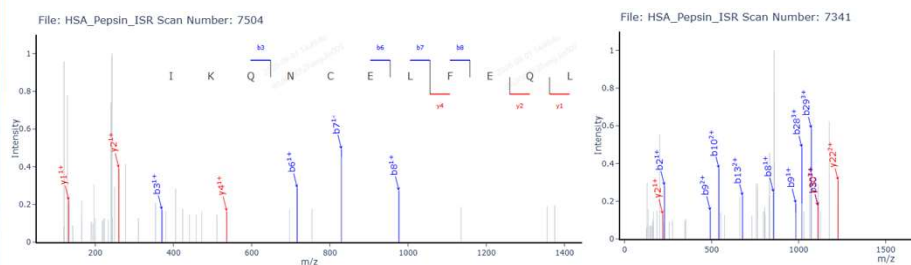
The EIC of precursor and in-source reduced peptides



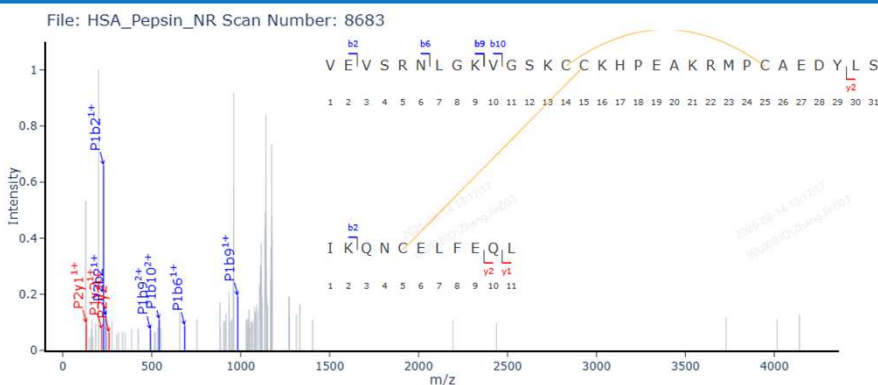
Highly reduced peptides observed in the ISR Dataset



ISR MS2 of P1

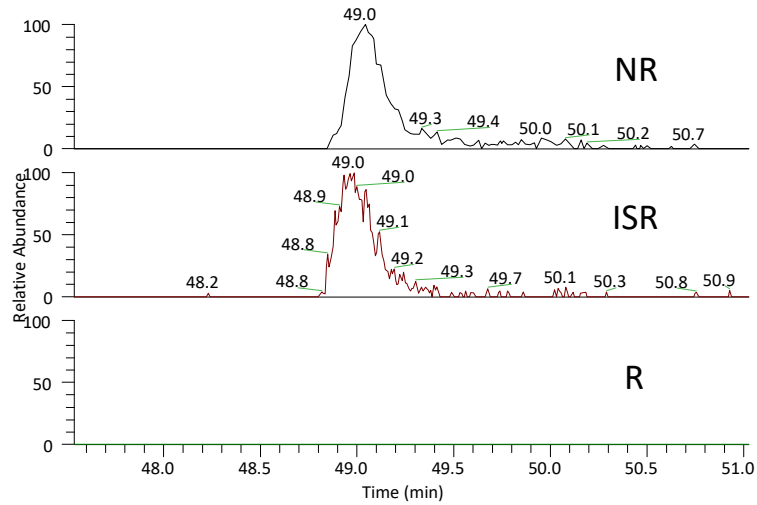


NR MS2 of P1-P2, data quality was insufficient for confident ID

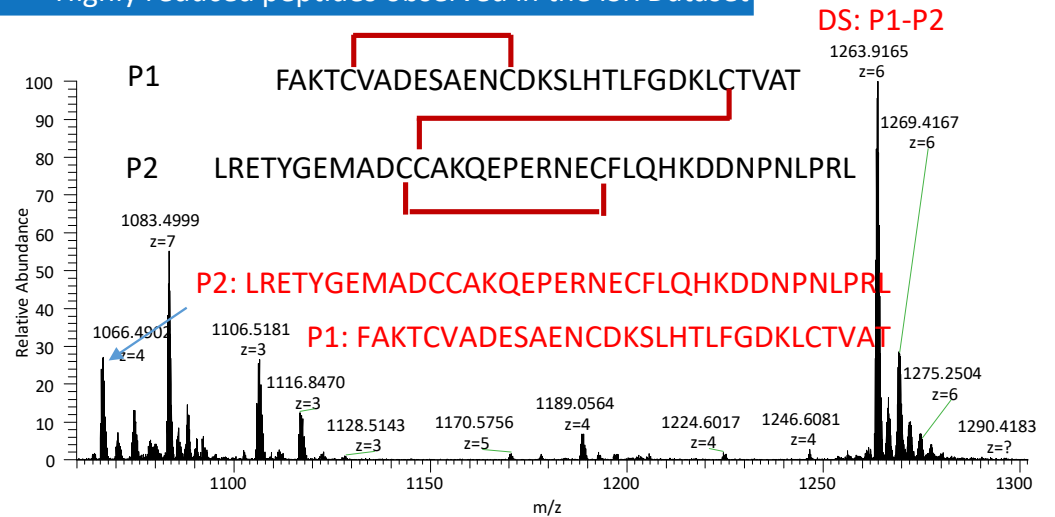


ISR-assisted identification of peptide cluster 3+3

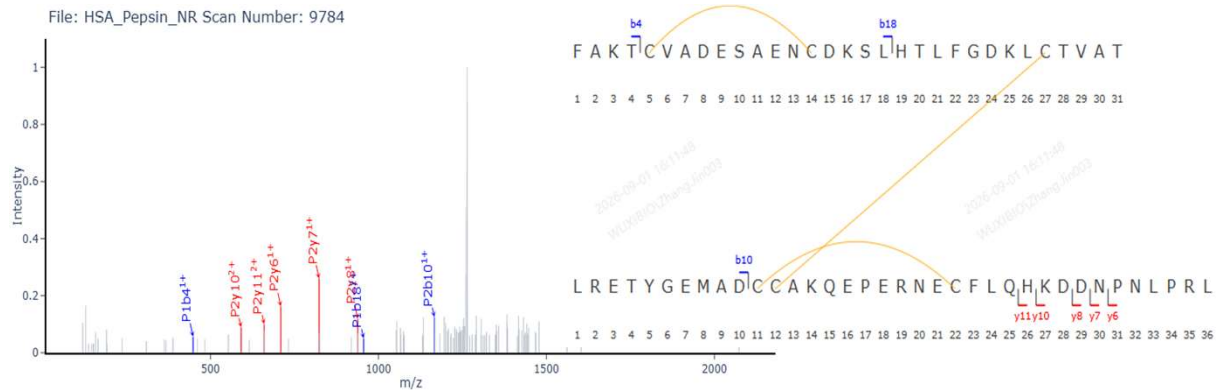
➤ The EIC of precursor and in-source reduced peptides



➤ Highly reduced peptides observed in the ISR Dataset



➤ NR MS2 of DS(P1-P2)



The background features a soft, out-of-focus blue and white bokeh. Overlaid on this is a complex, multi-colored molecular or cellular structure in shades of blue, purple, and teal. Several thin, wavy lines in blue, green, and yellow arc across the scene, creating a sense of movement and depth.

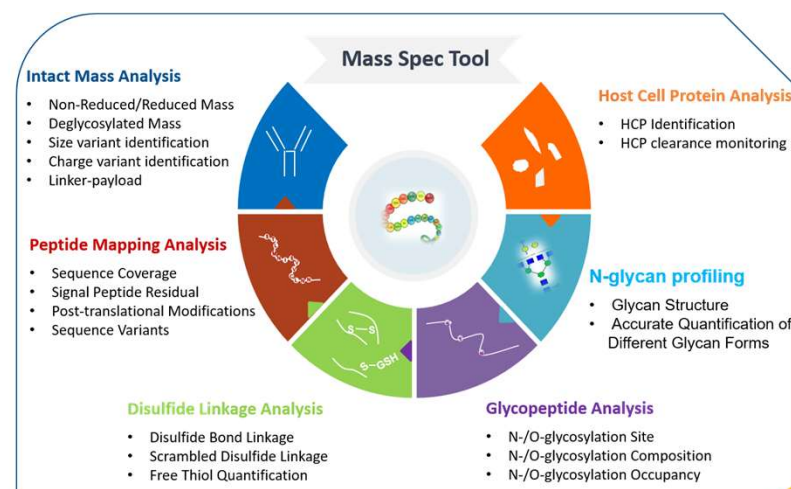
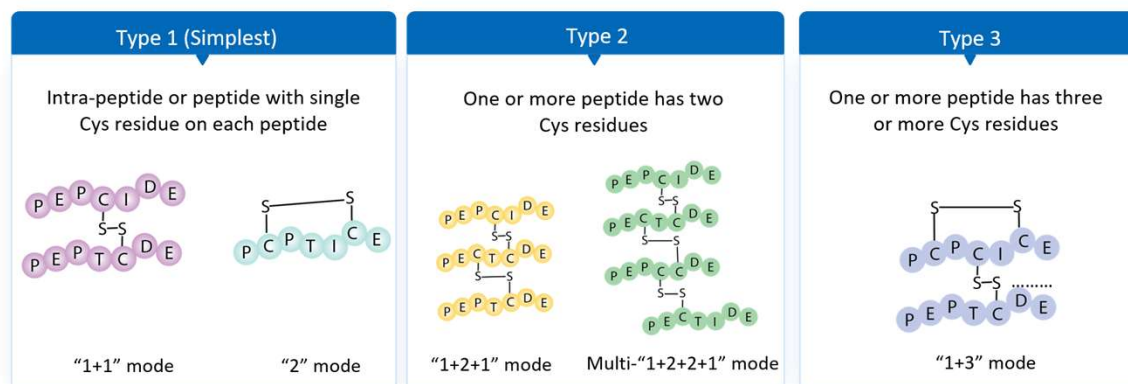
05

Summary

Summary

This ISR-assisted integrated workflow has the potential to totally transform conventional disulfide mapping by significantly simplifying the process and making it as straightforward as routine reduced peptide mapping.

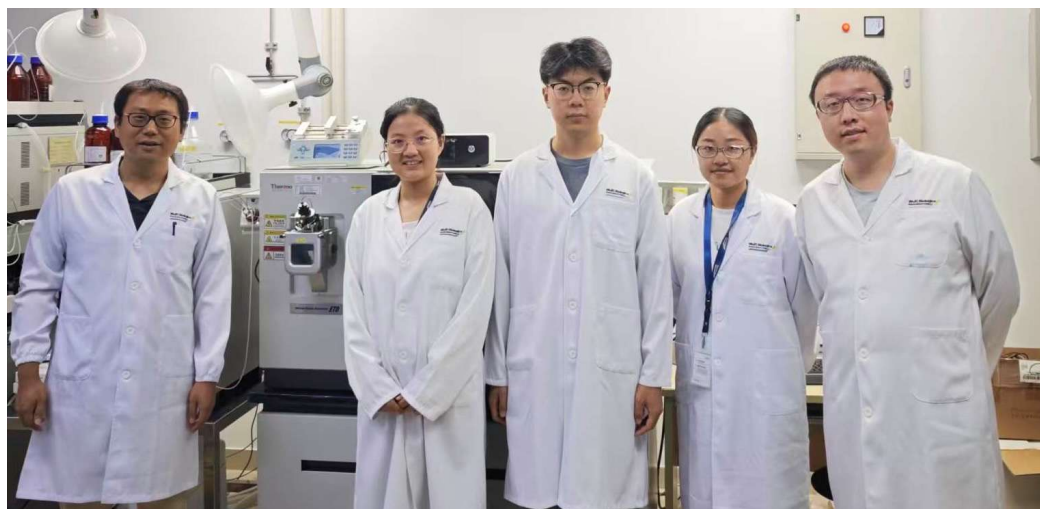
The same principle can be applied to tackle 'dark matter' in other LC-MS based protein characterization such as intact mass and peptide mapping analysis.



Acknowledgements

WuXi Biologics

- BioDev Wuxi Process Development



CASSS Mass Spec Organizers and Session Chairs

Audiences and Attendees

Thank You