

Characterization and Monitoring of mAb Charge Variants via Online IEX-MS

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Waters MS User Meeting ASMS 2019 Atlanta, GA June 1, 2019

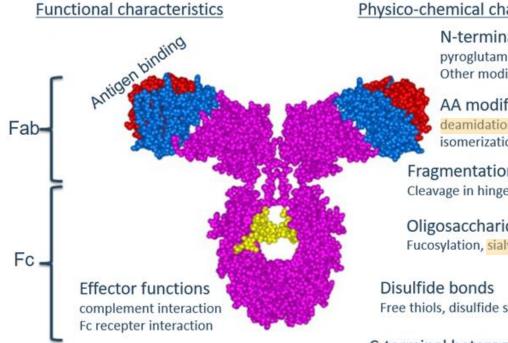




- 1. mAb CQA Characterization
- 2. Reverse Phase vs Ion Exchange Chromatography
- 3. Online IEX-MS: Considerations for Method Development
- 4. Case Studies
- 5. Summary and Q & A

Quality Attributes to Consider – Biotherapeutic Monoclonal Antibodies (mAb)





Physico-chemical characteristics

N-terminal heterogeneity pyroglutamate formation Other modifications

AA modifications deamidation, oxidation, glycation, isomerization

Fragmentation Cleavage in hinge region, Asp-Pro

Oligosaccharides Fucosylation, sialyation, galactosylation...

Free thiols, disulfide shuffling, thioether

C-terminal heterogeneity Lysine processing, proline amidation

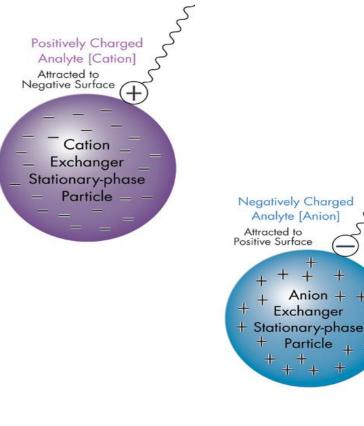
Reverse Phase vs Ion Exchange Chromatography

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	Reverse Phase (RP)	Ion Exchange (IEX)
Separation Based On	Hydrophobicity	Protein Surface Charge
Conditions	Denaturing	Native
Common Variants Separated	OxidationClipping (LMW)	 Deamidation Sialic acid & other N-glycan variants C-terminal lysine variants Sulfation/phosphorylation
Advantages	Easy MS-compatibility	Ability to collect fractions and test functionality of variants
Gaps	 Method destroys folding and functionality Cannot separate deamidation / isomerization species or N-glycan variants 	 Traditional IEX mobile phases are not MS-compatible Tedious fraction collection is required for simple peak identification

Ion Exchange Chromatography

- Separation according to differences in their surface charge
- Most mAbs have pl > 7, so cation exchange (CEX) is more common
- CEX separation strategies:
 - **pH gradient** (increase of pH, altering protein surface charge)
 - Salt gradient (increase ionic strength, altering protein binding to stationary phase)

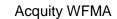


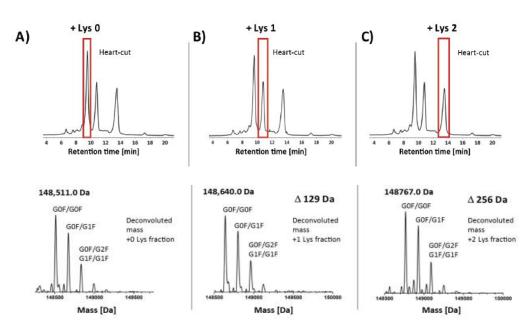


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Charge Variant Identification with Traditional IEX

- Fraction Collection & MS Analysis
 - Intact or subunit analysis
 - Peptide Mapping





Birdsall, R. et al "Characterization of Biotherapeutics: ACQUITY UPLC H-Class Bio with 2D Part 2 of 3: Rendering a Viable Interface for IEX with ESI-MS Analysis"

2D-LC/MS



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Why Should We Couple IEX to MS Directly?

Enable quick decision-making

Reduce the need for tedious fraction collection

Easily distinguish desired product from impurities

Avoid complex 2D-LC setups







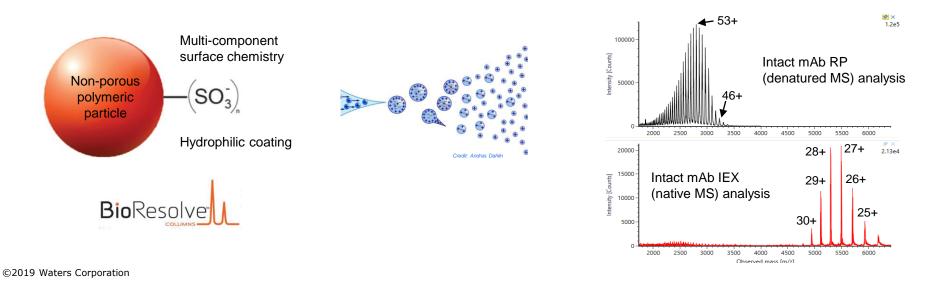




Considerations for Online IEX-MS

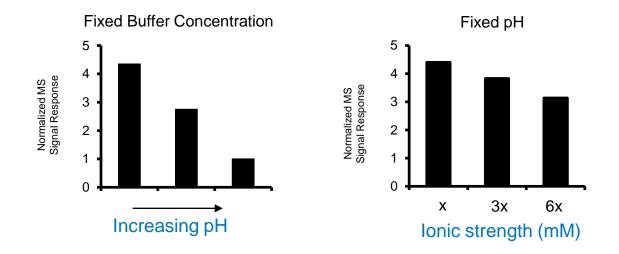


- Optimal chromatographic separation with volatile salts allowing for ESI ionization
 - BioResolve SCX column
 - Ammonium-based dual salt / pH gradient mechanism for optimal separation
 - Native MS analysis



SEC-MS to Study pH and Ionic Strength Effect on MS Signal Intact NIST mAb

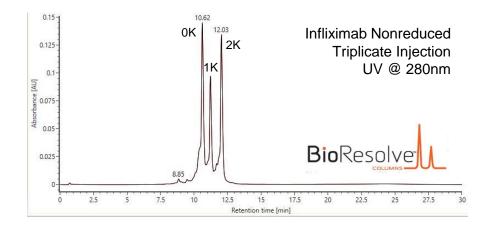




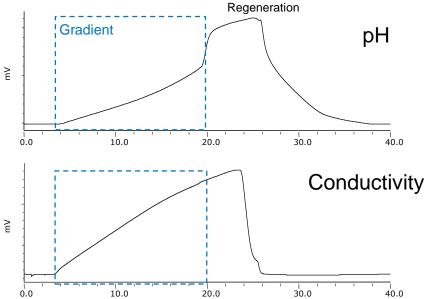
- SEC-MS to observe MS response vs. mobile phase pH and ionic strength
- PH impacts signal more than increases in ionic strength, yet it is still desirable to reduce salt content to not overburden the MS

A Robust and Reproducible IEX Method

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- Column: BioResolve SCX, 3µm, 2.1 x 50 mm @ 30 °C
- MP: Ammonium-based dual salt/pH gradient
- Flow Rate: 0.1 mL/min
- Injection Volume: 5-10 μg on column



Online pH & conductivity traces confirm desired linear gradient

Is The Separation Generic?

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Column: BioResolve SCX 3µm, 2.1 x 100 mm @ 30 °C

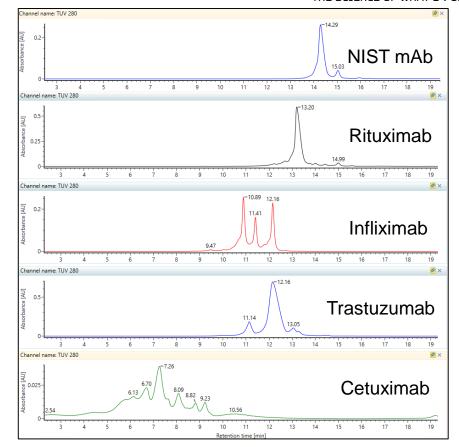
Mobile Phases: Ammonium-based dual salt / pH gradient

Flow Rate: 0.1 mL/min

Gradient: 40-98% B in 20 min



One single gradient works for a wide range of mAbs!

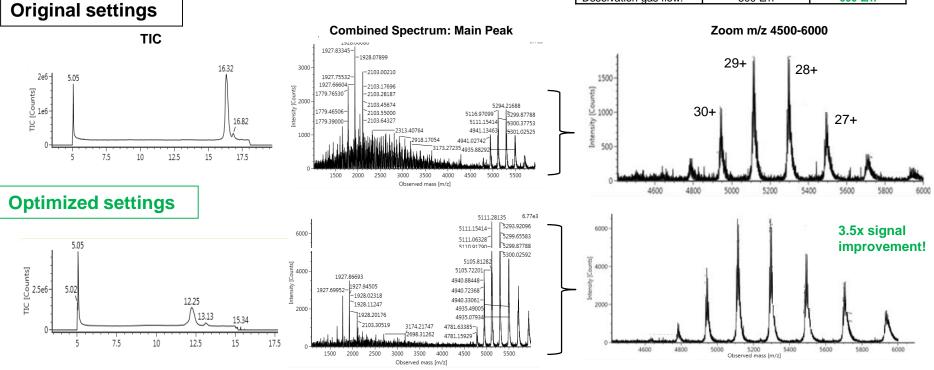


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Considerations for MS Signal Optimization NIST mAb, Vion IMS QTof

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Parameter	Original	Optimized
Source temp.:	135 °C	120 °C
Desolvation temp.:	500 °C	350 °C
Cone gas flow:	300 L/h	100 L/h
Desolvation gas flow:	800 L/h	600 L/h



Considerations for MS Optimization *Quality of Reagents*

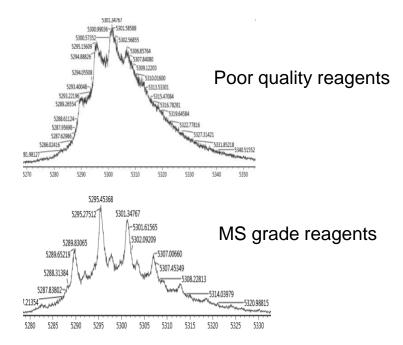
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Quality of reagents and mobile phase preparation will have an impact...

...on quality of results

...on cleanliness of the instrument

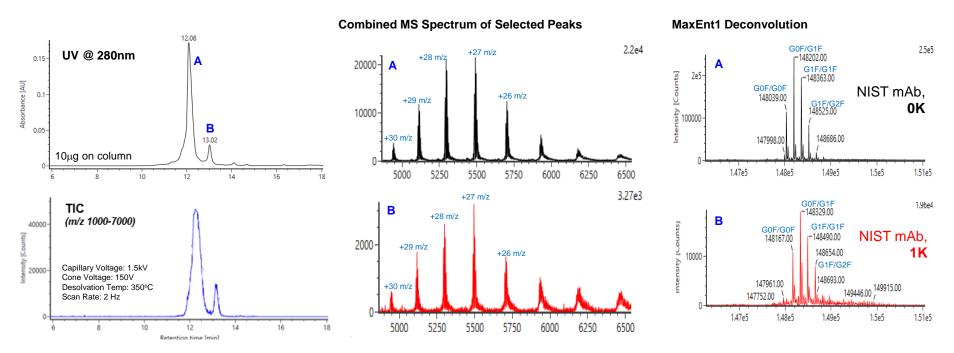
[Intact NIST mAb] 28+



NIST mAb C-terminal Lysine Variant Evaluation on BioAccord System





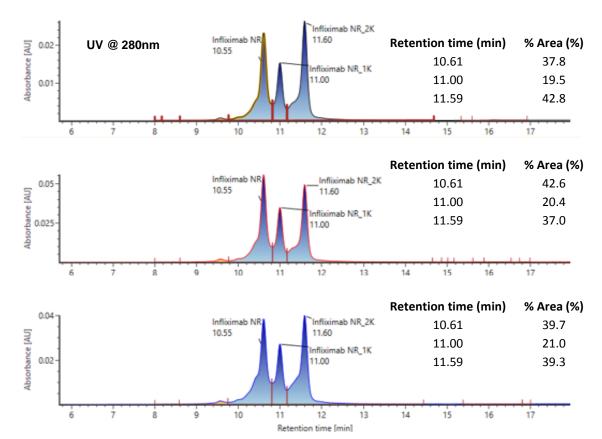


Expected Mass: 148,036.6 Da (G0F/G0F, 2 x pQ1)

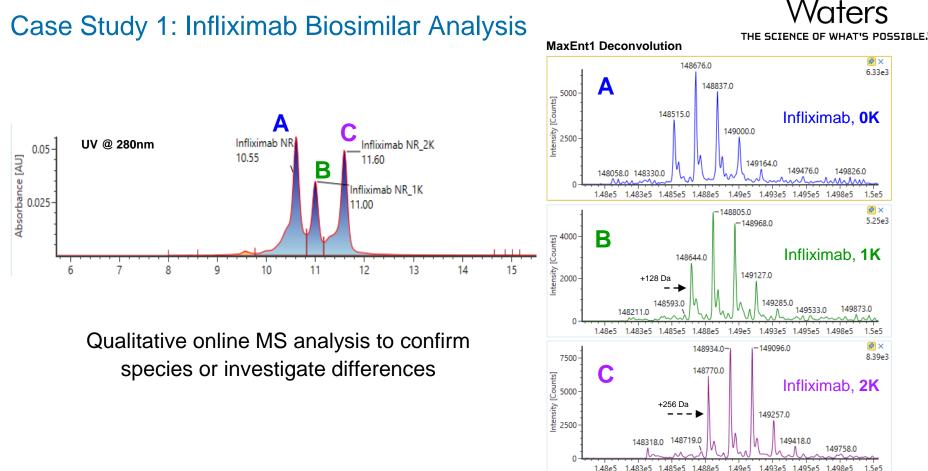
Case Study 1: Infliximab Biosimilar Analysis

UV integration for quantitative comparison charge variant profiles

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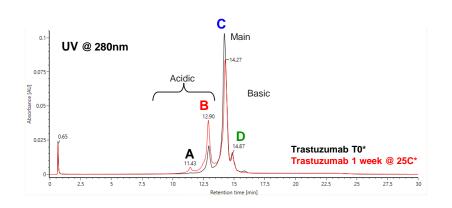
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Mass [Da]

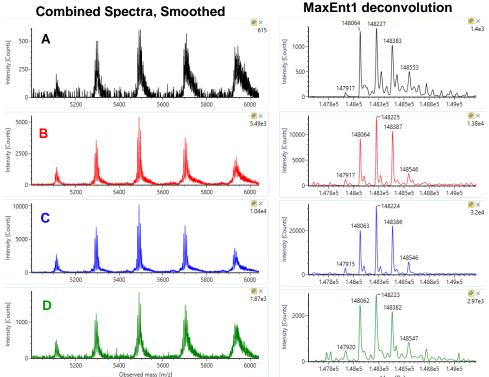
Case Study 2: Forced Degradation Study Trastuzumab, pH 8.0 Stress

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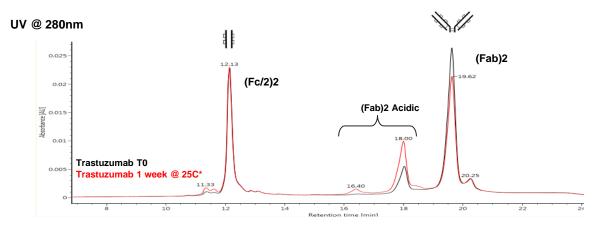
Mass [Da]



	Acidic	Main	Basic
ТО	14.0%	74.7%	11.3%
1wk25C	32.7%	58.3%	9.0%
Δ	+18.7%	-16.4%	-2.3%



Forced Degradation Study Trastuzumab: IdeS Digested Samples



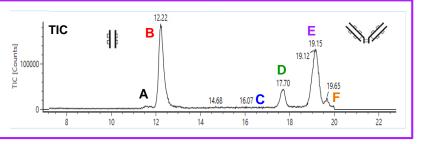
(Fc/2)2	Acidic	Main	Basic
ТО	7.1%	84.4%	8.5%
1wk25C	11.6%	81.2%	7.2%
Δ	+4.5%	-3.2%	-1.3%

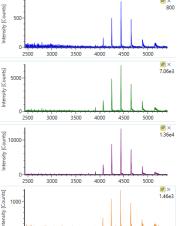
(Fab)2	Acidic	Main	Basic
Т0	20.9%	70.3%	8.9%
1wk25C	34.9%	56.4%	8.7%
Δ	+14.1%	-13.8%	-0.2%



- Further localize the increase in acidic variants to the Fab region
- Good correlation to intact mAb analysis via UV integration
- IdeS digest analysis gives better mass accuracy and greater confidence in assignments

Forced Degradation Study Trastuzumab: IdeS Digested Samples





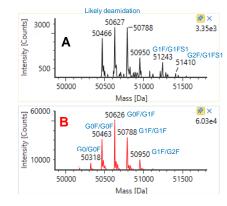


97.627.96 Da

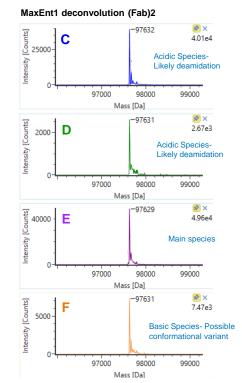
q

Expected mass (G0F/G0F): 50.464.08 Da

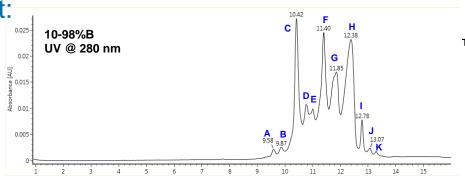
MaxEnt1 deconvolution (Fc/2)2



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Cetuximab IdeS Digest: Charge Variants

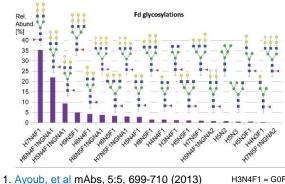


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System: Vion MS QToF Capillary Voltage: 3.0kV Cone Voltage: 150V Source Temperature: 120 °C Desolvation Gas: 350 °C Cone Gas flow: 100L/h Desolvation Gas flow: 600L/hr

Peak	(Fab)2 or (Fc/2)2	Species Detected
A,B	(Fc/2)2	G0F/G0F-G1F/G2F Deamidation
С	(Fc/2)2	G0F/G0F-G1F/G2F
D	(Fc/2)2	G0F/Man5; G1F/Man5; G0F/G0F, 1K Deamidation
E	(Fc/2)2	Man5/Man5
F	(Fc/2)2 & (Fab)2	Fc: G0F/G0F-G1F/G2F, 1K Fab: H6N4F1+NGNA / H6N4F1+NGNA; H6N4F1+NGNA / H8N5F1+NGNA
G	(Fc/2)2 & (Fab)2	Fc: G0F/Man5, 1K; G1F/Man5, 1K; Fab: H7N4F1/H6N4F1+NGNA; H9N5F1/H6N4F1+NGNA
н	(Fab)2	H7N4F1/H7N4F1; H7N4F1/H9N5F1
I	(Fc/2)2	G0F/G0F-G1F/G2F, 2K
J	(Fc/2)2	G0F/Man5, 2K; G1F/Man5, 2K
К	(Fc/2)2	Man5/Man5, 2K

Released Glycan analysis1: orthogonal support for IEX-MS peak assignments



H3N4F1 = G0FH4N4F1 = G1FH5N4F1 = G2FH5N2 = Man5



- IEX is used to monitor native state protein charge heterogeneity, and isolate charge variants for structural and functional analyses
- We have separated and identified mAb charge variants using IEX-MS with a combined salt (volatile) and pH gradient separation
- The ability of online IEX-MS to simplify charge variant characterization should reduce dependency on traditional fractionation-based workflows over time

Acknowledgements

- Matt Lauber
- Ying Qing Yu
- Qi Wang
- Henry Shion
- Steve Koza
- Hua Yang
- Weibin Chen
- Min Du
- Bill Warren

Thank you for your attention! Thank you for your attention! Any questions, please ask!

Tuesday Poster # T003: 10:30-11:30am & 12:30-2:30pm

"Online IEX-MS Characterization and Monitoring of mAb Charge Heterogeneity Using an Optimized Cation Exchange Resin and Compact TOF Mass Spectrometer"



Backup Slides

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