

## Welcome to Waters Luncheon Seminar

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Your Feedback will be very much appreciated!



Please provide your feedback and you will get a gift set at reception!





Column-shaped pens



## Improving IEX Technology and IEX-MS Applications for Domain Specific Charge Variant Analysis of mAb





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#### mAb Charge Variants

Deamidation (+++) (-Asn-Gly- => Asp: +1 Da)

Racemization (++) (-Asp-Asp- => 0 Da) Succinimide (+++) (Asn/Asp => Suc: -17 Da)

Isomerization (+++) (-Asp-Gly- => IsoAsp: 0 Da)

CDF

Glycation (++) (Lys-Glc: +162 Da)

Acetone (+) (Lys-: +56 Da)

Aldimine (+) (Lys-: +38 Da)

C-term. Pro-amidation (+)

(Pro-OH => Pro-NH2: -1 Da)

N-term. Blocking (+)

(Gln/Glu => PyroGlu: -17/-18

Da)

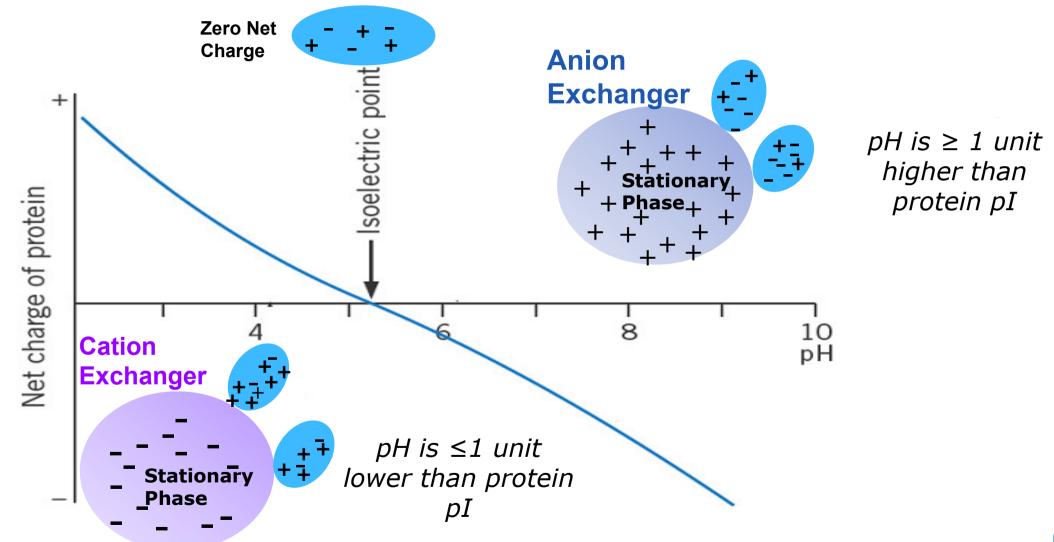
N-Glycosylation Major chemical Species Effect (Sialic acids) (++++) degradation pathways formed (NANA, NGNA) Acidic Sialylation COOH addition Deamidation **COOH** formation Acidic C-terminal lysine Loss of NH2 Acidic cleavage COOH formation Adduct formation Acidic or loss of NH2 Succinimide formation Loss of COOH Basic Methionine, cysteine, Conformational lysine, histidine, Basic Fc change tryptophan oxidation Conformational Disulfide-mediated Basic change C Asialylation (terminal H Loss of COOH Basic Galactose) C-term. clipping (+) C-terminal lysine and NH2 formation Basic (- Lys: -128 Da; - Gly: -57 Da) glycine amidation or loss of COOH

J Chromatogr. A. (2017) 1498:147-154.

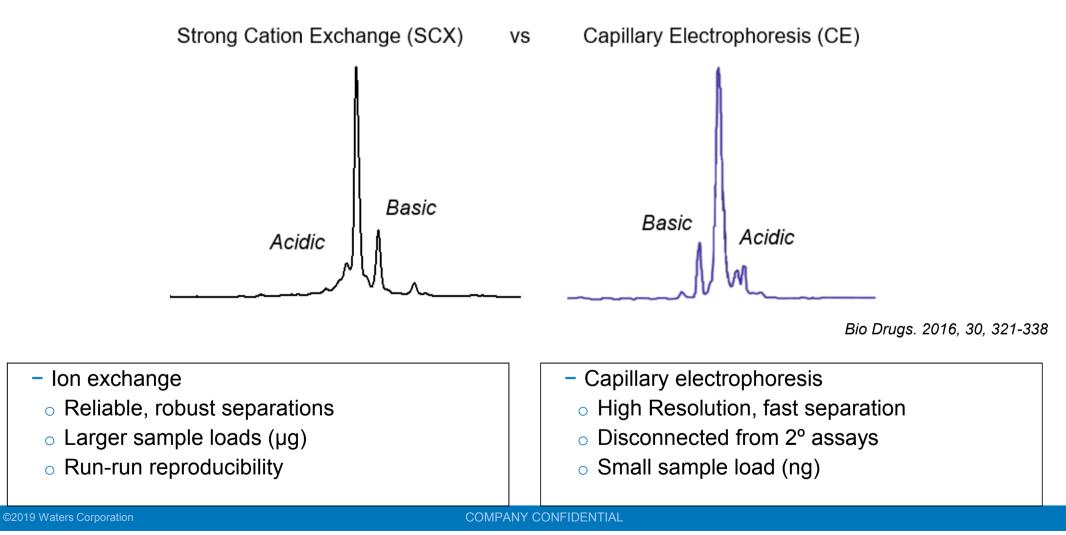


#### **Protein Isoelectric Points and IEX**



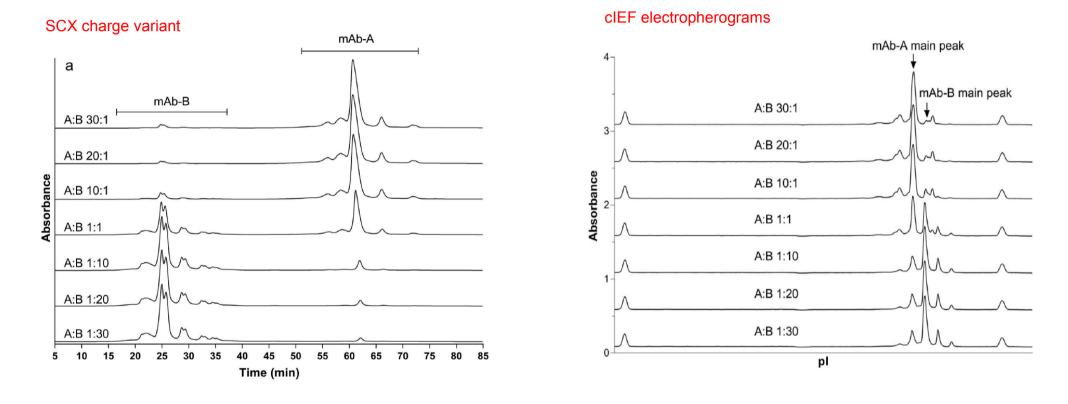


### **Charge Variant Profiling**



POSSTRUE

# cIEF and IEX as Orthogonal Methods for mAb Charge Variant Analysis

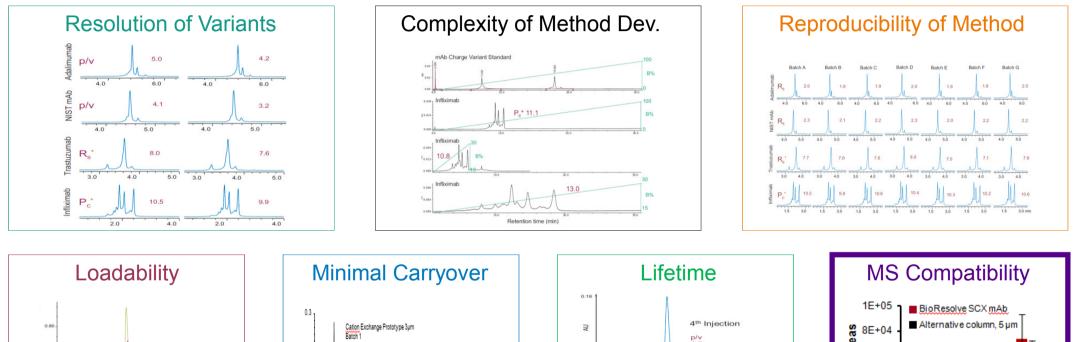


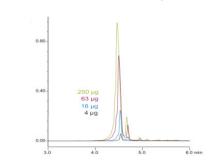
mAbs. 2019, 11, 3, 489-499

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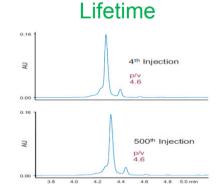
#### Challenges in IEX for mAb Charge Variant Analysis

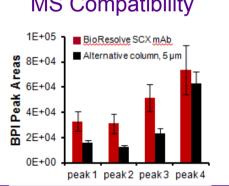










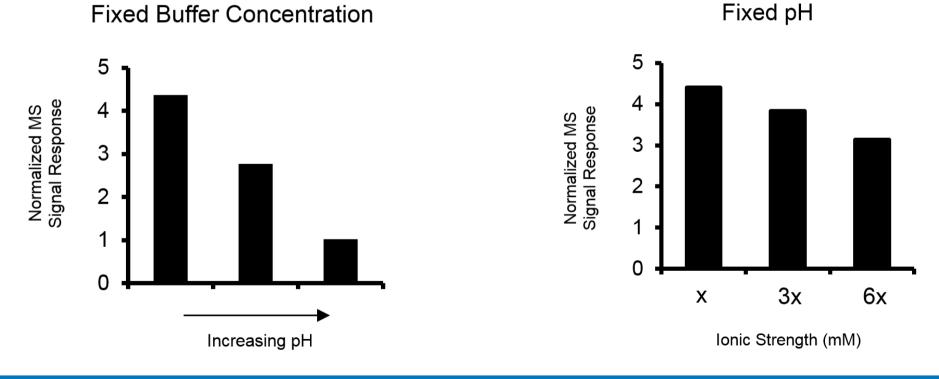


## Gradient Options for Online IEX-MS

- pH Gradient
  - Ionization efficiency challenges (High pH)



- Salt Gradient
  - MS burden
  - Metal contamination



## Mobile Phase Options for Online IEX-MS



Mobile Phase	рКа
Ammonium Formate	3.75, 9.25
Ammonium Acetate	4.75, 9.25
Ammonium Bicarbonate	6.40, 9.25

- Volatile mobile phase
  - MS-grade reagents
  - Trace metal certified

### Ammonium Bicarbonate for Online IEX-MS



#### Effects of Ammonium Bicarbonate on the Electrospray Mass Spectra of Proteins: Evidence for Bubble-Induced Unfolding

Jason B. Hedges, Siavash Vahidi, Xuanfeng Yue, and Lars Konermann\*

Department of Chemistry, The University of Western Ontario, London, Ontario, N6A 5B7, Canada

D

Е

F

17+

1000

- Supercharging
  - Protein Denaturation
- CO<sub>2</sub> adducts

acetate

Α

в

С

Normalized ESI-MS Intensity

9+

9+

9+

2000

pH instability

bicarbonate

9+

9+

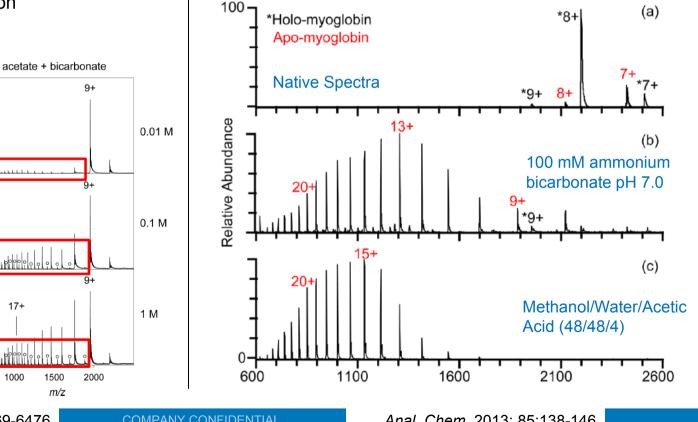
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#### Electrothermal Supercharging in Mass Spectrometry and Tandem Mass Spectrometry of Native Proteins

Catherine A. Cassou, Harry J. Sterling, Anna C. Susa, and Evan R. Williams\*

Department of Chemistry, University of California, Berkeley, California 94720-1460, United States



1500

m/z

1000

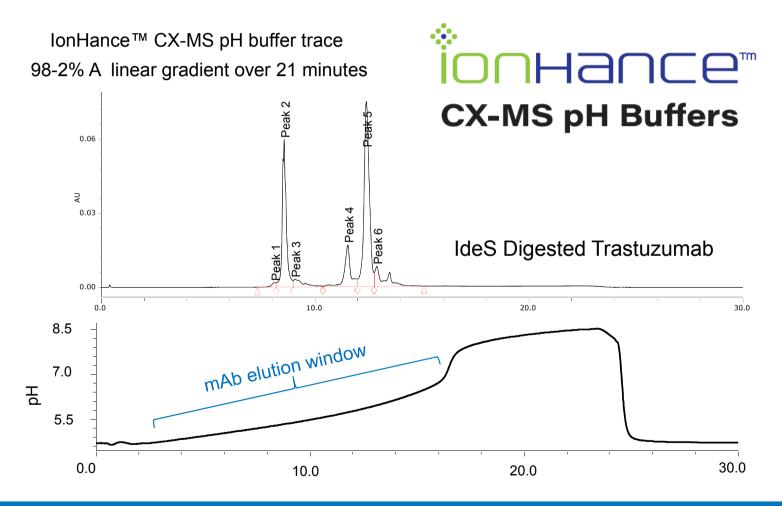
Anal. Chem. 2013; 85:16469-6476

2000

1500

m/z

#### Ammonium Acetate Mobile Phase for Online IEX-MS



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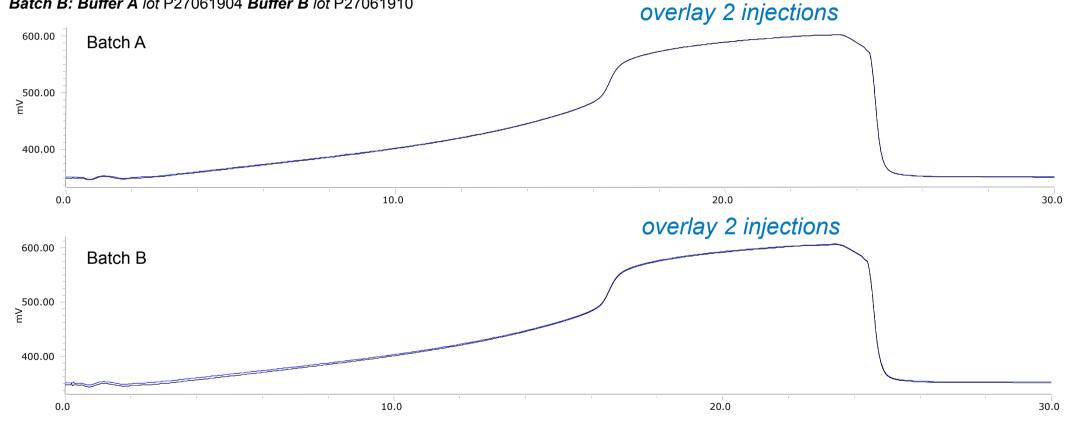
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#### IonHance<sup>™</sup> CX-MS pH Buffer Reproducibility Linear pH Gradients



Linear pri Gradients

Batch A: Buffer A lot P27061902 Buffer B lot P27061908 Batch B: Buffer A lot P27061904 Buffer B lot P27061910



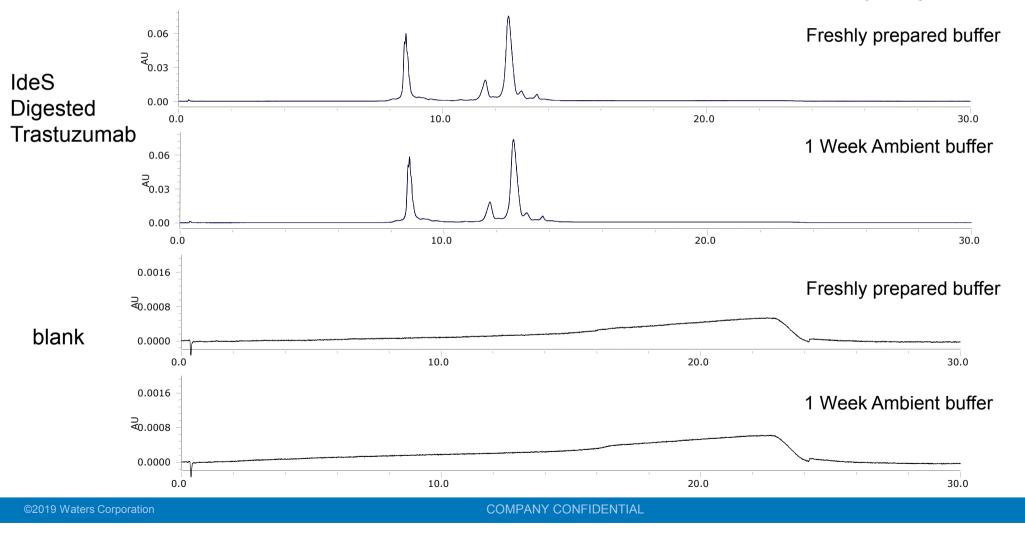
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#### IonHance<sup>™</sup> CX-MS pH buffer 1-Week Buffer Stability Tests



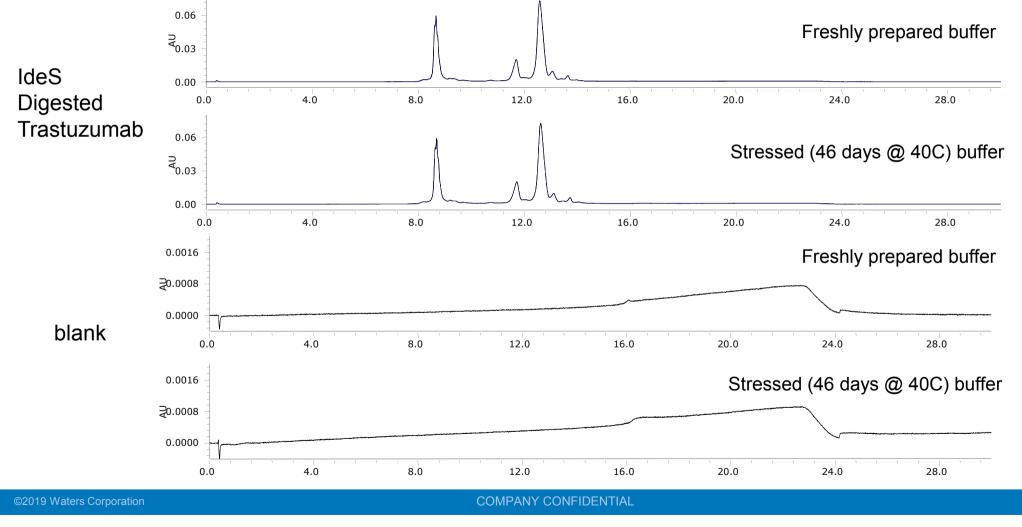
#### overlay 2 injections



#### IonHance<sup>™</sup> CX-MS pH buffer Long Term Buffer Stability



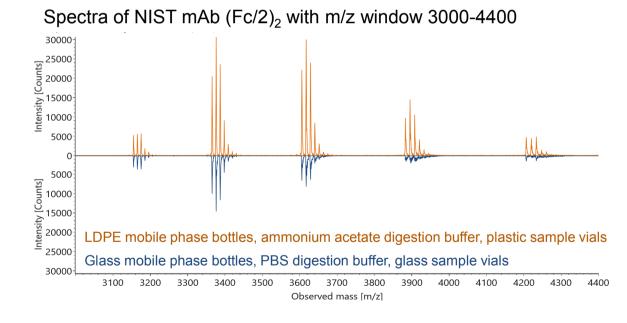
overlay 2 injections



#### **MS Quality: Eluent Considerations**



- Use Plastic
  - CX-MS in trace metal certified LDPE
  - 18.2 M $\Omega$  H<sub>2</sub>O, not MS-grade H<sub>2</sub>O in glass
  - Graduated cylinders, beakers, etc



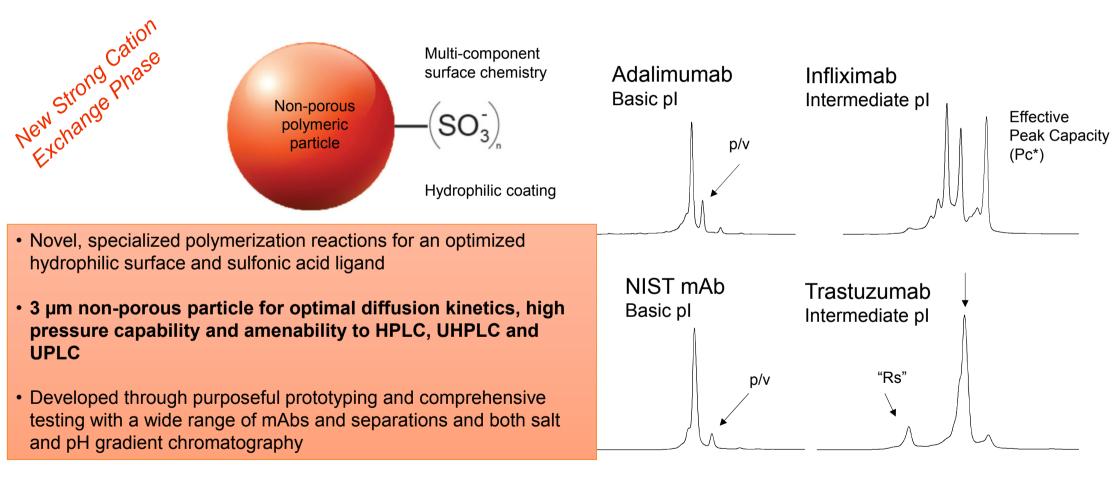
- Avoid unnecessary contamination
  - Concentrates are trace metal certified
  - Digest without Na, K, Ca

#### 10X Concentrate ICP-MS report

Sample	Replicate	Potassium (K) (ppbw)	Sodium (Na) (ppbw)
IEX MS Buffer B P27061912A	1	23	152
	2	24	160
	3	23	160
	Average	23	157
	Measurement Uncertainty (2δ)	2	9
IEX MS Buffer A P27061904A	1	42	106
	2	49	113
	3	47	110
	Average	46	110
	Measurement Uncertainty (2δ)	6	7

#### **Novel Stationary Phase**





 See: "Designing a New Particle Technology for Robust Charge Variant

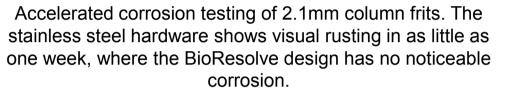
 Analysis of mAbs" Waters Application Note: 720006475EN (January 2019)

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**Patent Pending** 

#### BioResolve SCX mAb Column Hardware Design Mitigate corrosion risk, while maintaining UPLC pressure compatibility, column packing performance, and repeatability

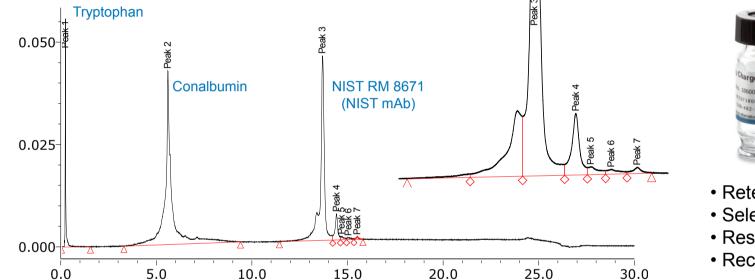


Shelf life testing of the improved design has also shown no degradation in separation performance. Columns were evaluated with salt gradients, flushed, and stored for 1 month.





#### mAb Charge Variant Standard A Mixture of Tryptophan, Conalbumin, and NIST mAb



pF

COMPANY C



- Selectivity
- Resolution

Curve

Initial

6

6

6

6

6

Recovery

%B

0

0

100

100

0

0

Column dimension 4.6 × 50 mm

%A

100

100

0

0

100

100

Flow

(mL/min)

- QC batch testing for a rigorous check on suitability for biopharm applications
- Available for proficiency checks and system suitability

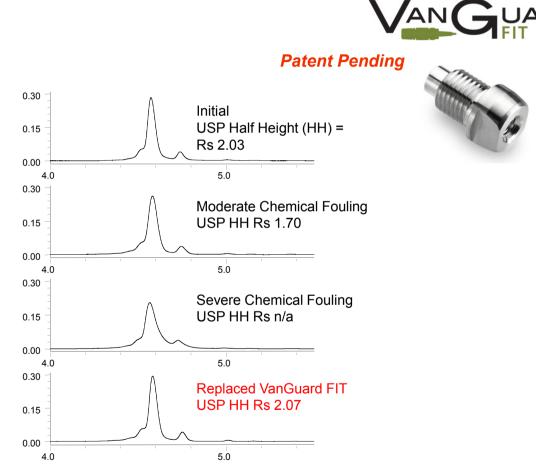
	Initial	1.44
	1.0	1.44
	23.6	1.44
I Gradient	24.6	1.44
	25.6	1.44
example	30.0	1.44
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Time

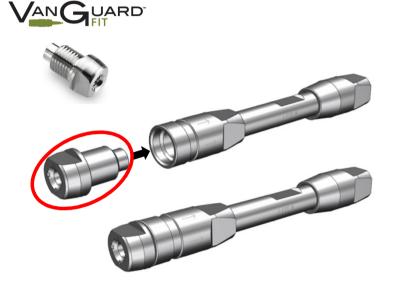
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#### Lifetime is Important Recovering from Particulate and Chemical Fouling

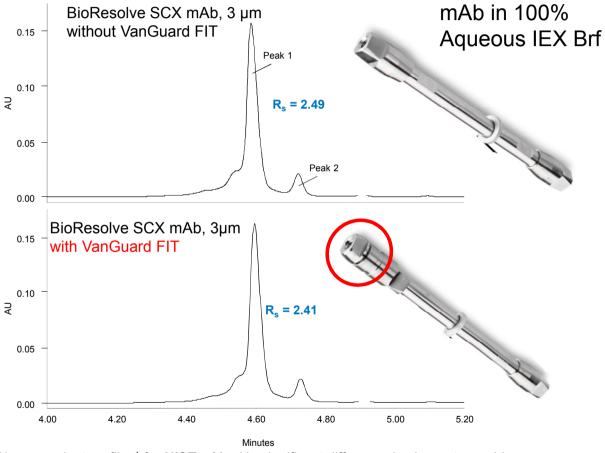
- Problem Statement
  - The injection of column fouling excipients (e.g., polysorbate) and particles (e.g., insoluble sample or microbes) are well known causes of premature failure of columns.
  - Traditional guard columns help protect the analytical column. However, they are relatively expensive and introduce compromising levels of additional dispersion
- Purposefully Designed Solution
  - VanGuard FIT (Fully Integrated Technology) guard column is a new, simplified guard column design that maximizes column life without degrading biomolecule component resolution.



#### No Compromise Column Protection and Extended Lifetimes with the Use of VanGuard FIT Cartridges



BioResolve SCX mAb Column, 4.6 x 50 mm column with integrated VanGuard FIT. Replaceable cartridge screws directly into the column inlet end nut. Optimal installation has never been easier nor more efficient in terms of maintaining analytical columns resolving power.



Charge variant profiles<sup>1</sup> for **NISTmAb**. No significant difference in chromatographic performance on BioResolve SCX mAb columns without (top) or with (bottom) VanGuard FIT.

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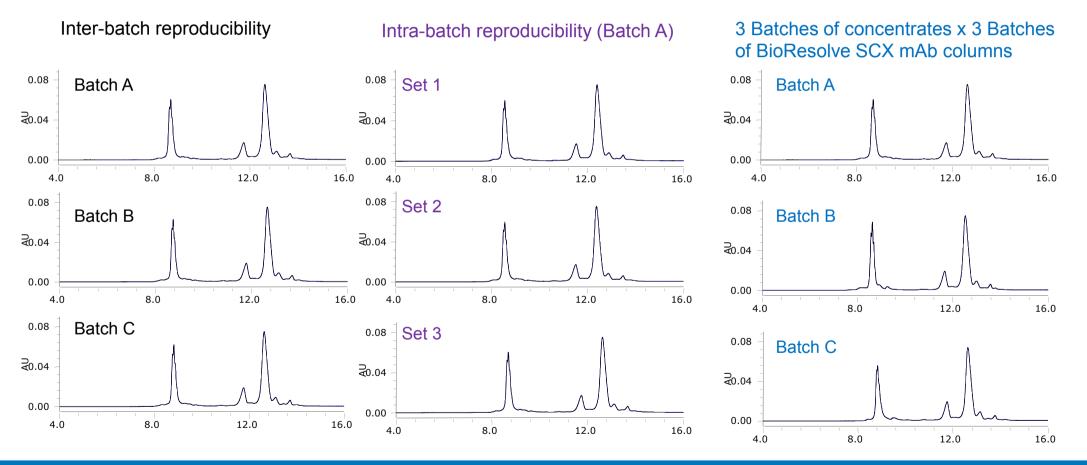
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## IonHance<sup>™</sup> CX-MS pH Buffer Reproducibility



overlay 2 injections

#### IdeS Digested Trastuzumab



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#### BioResolve SCX mAb Portfolio Developed through Comprehensive Testing and Purposeful Prototyping



- BioResolve SCX mAB Columns
- VanGuard FIT (Fully Integrated Technology)
- mAb Charge Variant Standard
- BioResolve pH Gradient Buffer Concentrates (Optical Only: Non-MS compatible)



# Mass Spectrometry (MS) – an Important Tool for Biopharmaceutical Characterization and Analysis





#### A Retrospective Evaluation of the Use of Mass Spectrometry in FDA Biologics License Applications

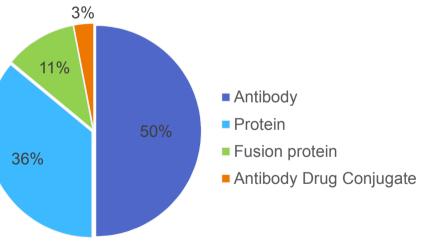
Sarah Rogstad,<sup>1</sup> Anneliese Faustino,<sup>1</sup> Ashley Ruth,<sup>2</sup> David Keire,<sup>1</sup> Michael Boyne,<sup>2</sup> Jun Park<sup>3</sup>

<sup>1</sup>Division of Pharmaceutical Analysis, Office of Testing and Research, Center for Drug Evaluation and Research, U.S. Food and Drug Administration, Silver Spring, MD 20993, USA

<sup>2</sup>Biotechlogic, Inc., Glenview, IL 60025, USA

<sup>3</sup>Office of Biotechnology Products, Center for Drug Evaluation and Research, U.S. Food and Drug Administration, Silver Spring, MD 20993, USA

- From 2000-2015 there were 80 approved electronic BLAs
- 79 used MS for protein or impurity characterization



Rogstad et al. A Retrospective Evaluation of the Use of Mass Spectrometry in FDA Biologics License Applications. J. Am. Soc. Mass Spectrom. 2017, 28, 786-794

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#### MS in regulatory filings steadily increasing over time

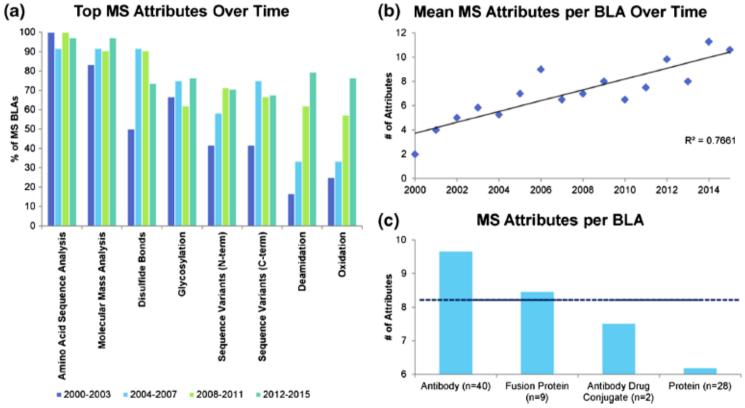


Figure 2. MS attribute analysis. (a) Top eight MS attributes over time. BLAs were binned by year with four-year increments. The percentages of BLAs that examined the top eight MS attributes are shown for each bin. Percentages are based on the total number of electronic BLAs that used MS. (b) The mean number of MS attributes analyzed per BLAs per year. (c) The mean number of MS attributes per BLA is shown based on product type

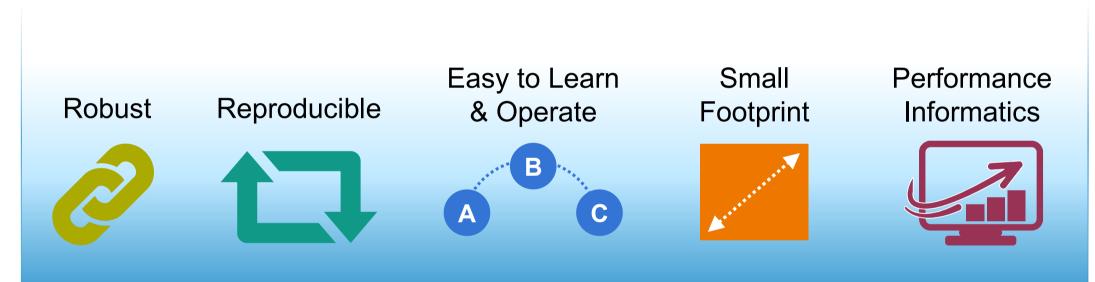
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Rogstad et al. A Retrospective Evaluation of the Use of Mass Spectrometry in FDA Biologics License Applications. J. Am. Soc. Mass Spectrom. 2017, 28, 786-794 25

## Top Unmet Needs for Broader Deployment of LC/MS



Compiled from Hundreds of Surveys and Interviews with Biopharmaceutical Scientists



Without compromising the fidelity of the LC/MS data

#### **BioAccord System Integrates Full Waters Portfolio**





#### Service & Support

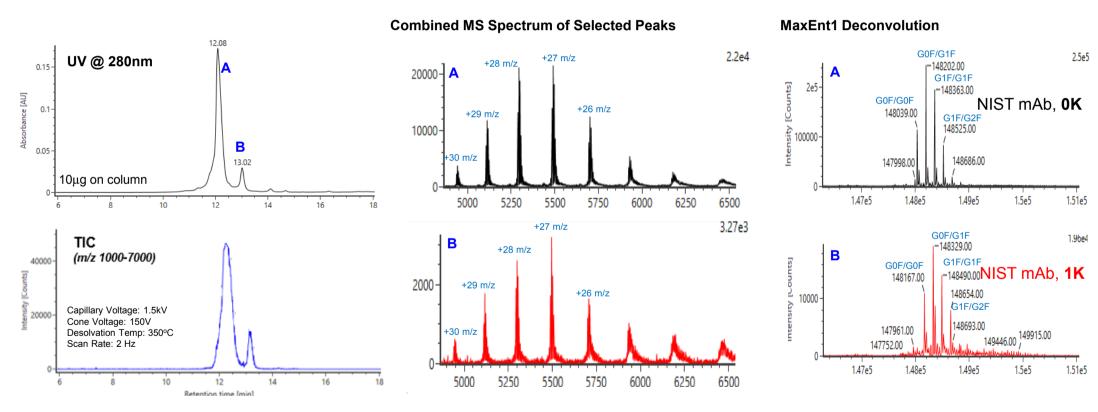
- NEW app-specific system install
- NEW app-specific customer training
- **NEW** system qualification

#### **Scientific Content**

- NEW application notes to demonstrate system performance and benefits
- NEW example data & method templates to assist new users with getting started

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#### NIST mAb C-terminal Lysine Variant Evaluation on BioAccord System



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

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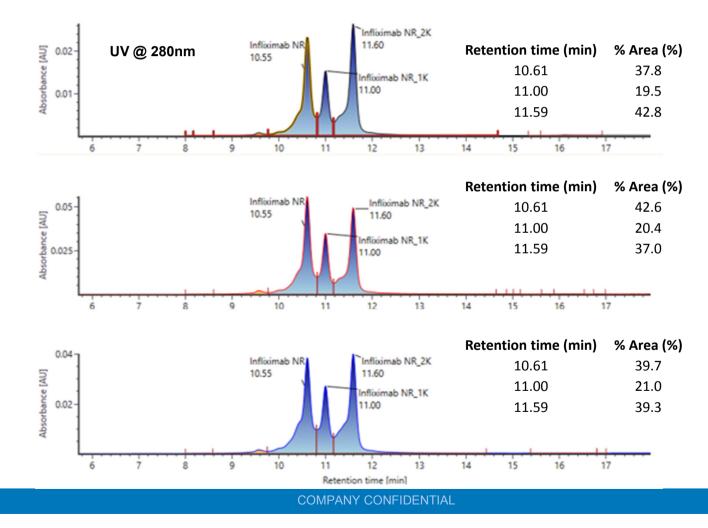
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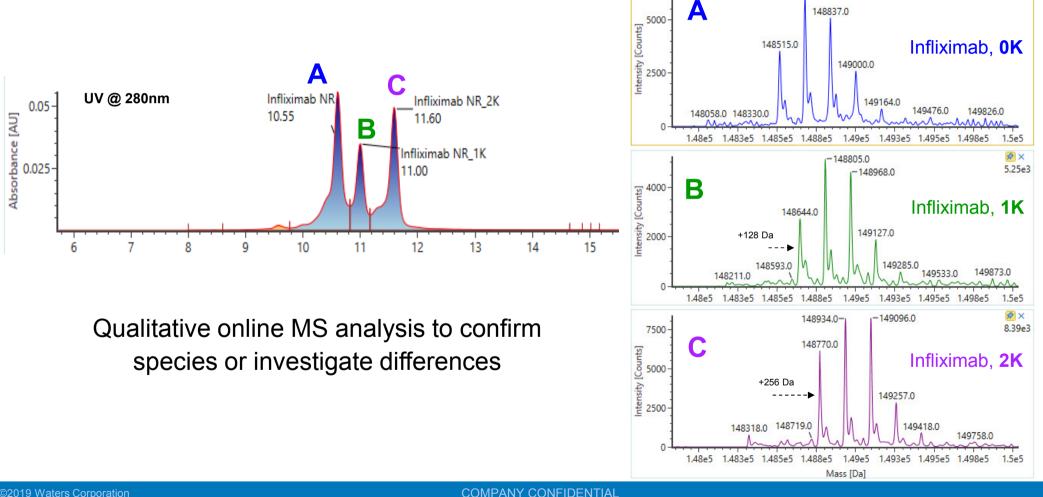
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## Case Study 1: Infliximab Biosimilar Analysis



UV integration for quantitative comparison charge variant profiles





### Case Study 1: Infliximab Biosimilar Analysis

**MaxEnt1 Deconvolution** 

148676.0

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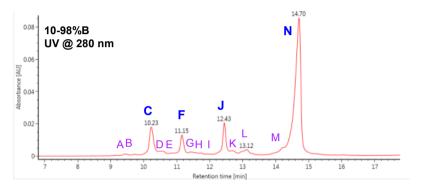
X

6.33e3



#### IEX-MS Analysis of Infliximab IdeS Subunits

Peak	Lysine Variant	Species Detected
А	0K	Possible G0F-G2F deamidation; G2FS1/ G0-G2
В	0K	Possible G0F-G2F deamidation;
С	0K	Main 0K species G0F-G2F
D	0K 1K	G0F-N/G0F, G0F-N/G1F, G0F-N/G0 (0K) Possible G0F-G2F deamidation (1K)
E	0K	Man5/Man5, Man5/G0F
F	1K	Main 1K species G0F-G2F
G	1K 2K	G0F-N/G0F, G0F-N/G1F, G0F-N/G0 Possible G0F-G2F deamidation (2K)
Н	1K 2K	Man5/Man5 G2FS1) / G0-G2
I	2K	⊶ • → / G0F-G2F
J	2K	Main 2K species G0F-G2F
К	2K	G0F-N/G0F, G0F-N/G1F, G1F-N/G1F, G0F-N/G0
L	2K (Fab) <sub>2</sub>	Man5/Man5, Man5/Man5+HexNAc Possible (Fab)2 deamidation
М	(Fab) <sub>2</sub>	Possible (Fab)2 deamidation
Ν	(Fab) <sub>2</sub>	Main (Fab)2 species

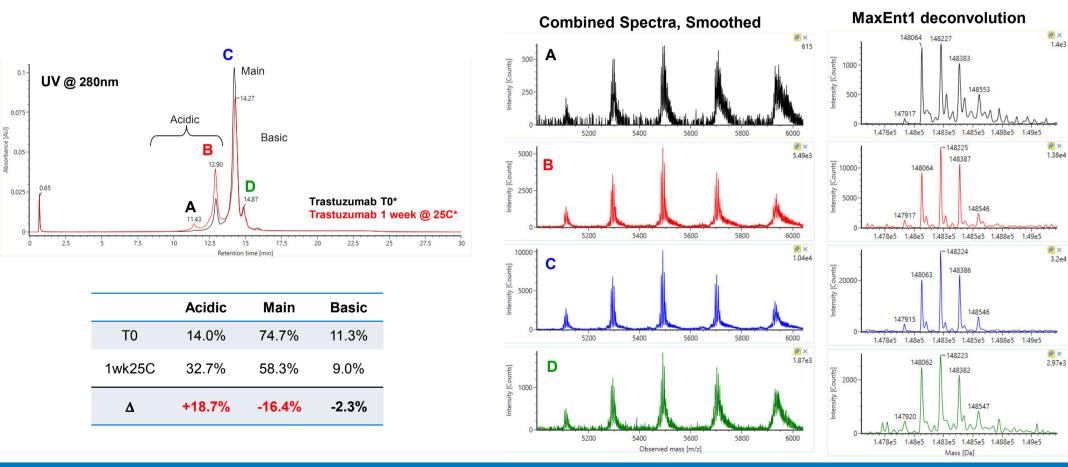


Peaks A-L: Fc-related species, including N-glycoforms containing sialic acid and Man5 N-glycans for each of the 3 C-terminal lysine variants

(Fab)2 acidic variant (likely deamidation) is also detected

Waters

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

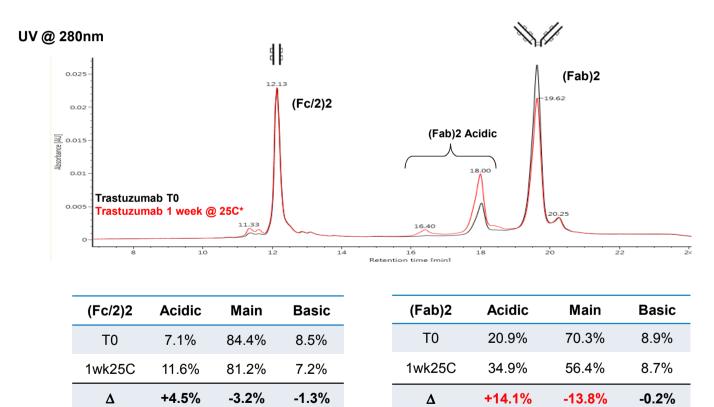


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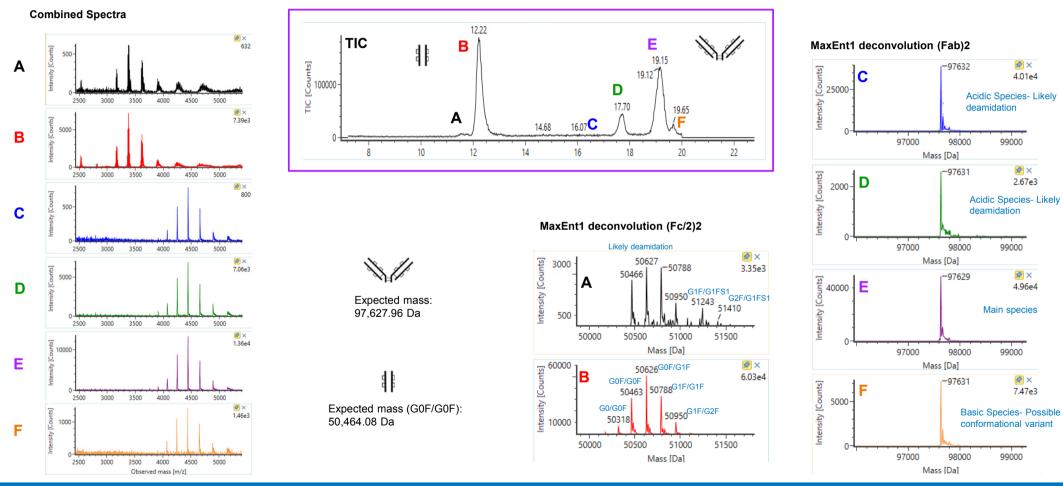
#### Forced Degradation Study Trastuzumab: IdeS Digested Samples



- 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



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## Summary

- Charge variants are considered critical quality attributes that need to be monitored throughout the life cycle of a drug
- IEX-MS is capable of providing robust, reproducible separations coupled to real time MS data acquisition for peak identification
  - Considerations include buffers, MS settings, reagent and consumable quality
  - IonHance CX-MS buffers provide a flexible platform for easy high quality IEX-MS
  - Applicable to intact and subunit characterization and charge variant monitoring
- Oral Presentation Funai Hall, OR21, 4:50-5:05pm
  - Mechanism of Unusually High Particle Diameter Dependence of Column Backpressure with SCX Polymer Particles, Ed Bouvier
- Please visit PT-2011
  - Improving Online Ion Exchange Chromatography-Mass Spectrometry for Domain Specific Charge Variant Analysis of Monoclonal Antibodies

Your Feedback will be very much appreciated!



Please provide your feedback and you will get a gift set at reception!





Column-shaped pens