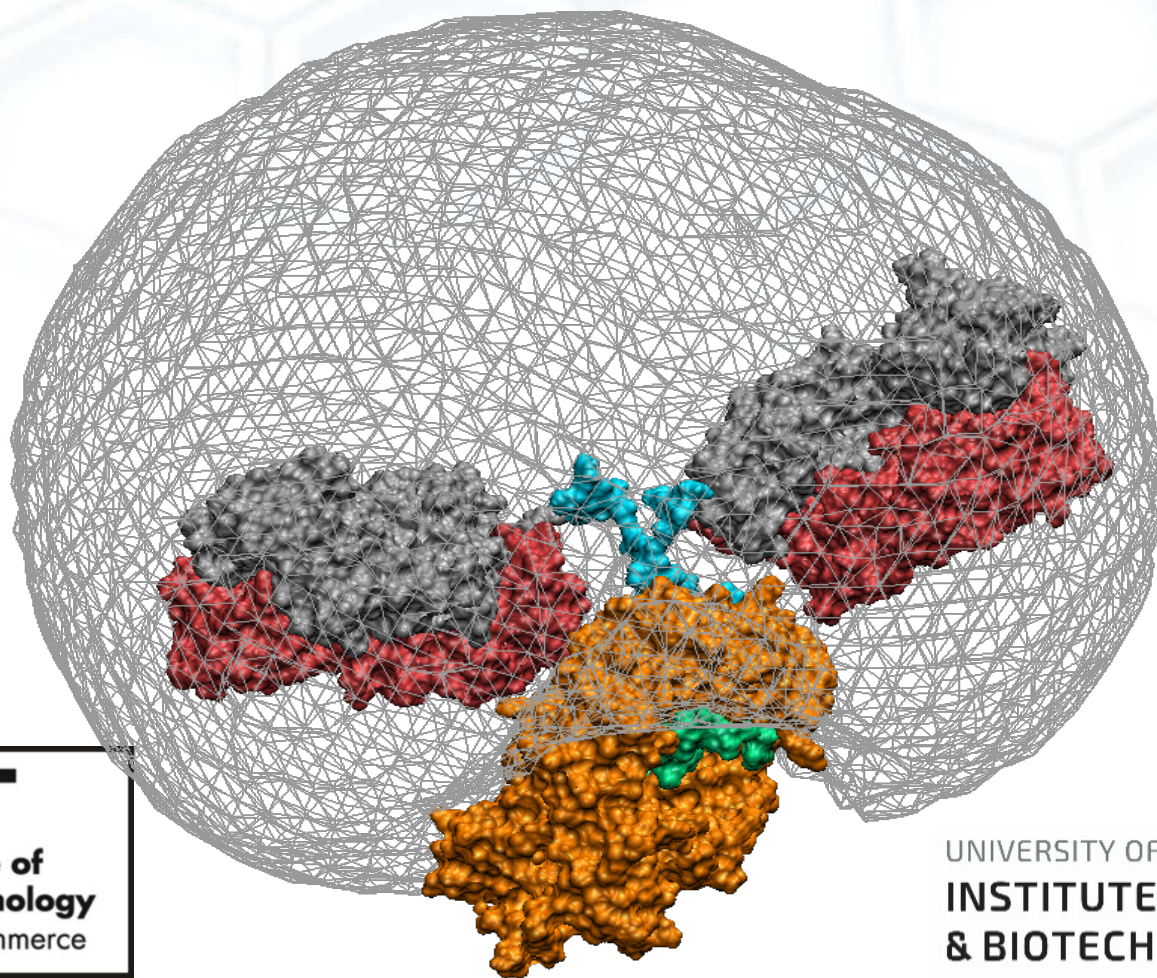


# Innovative Analytical Technologies and Biopharmaceutical Reference Materials

John Schiel, John Marino, Zvi Kelman, Jeff Hudgens, Robert Brinson, Luke Arbogast, Frank Delaglio, Trina Mouchahoir, Thomas Cleveland, Kyle Anderson, Michael Tarlov



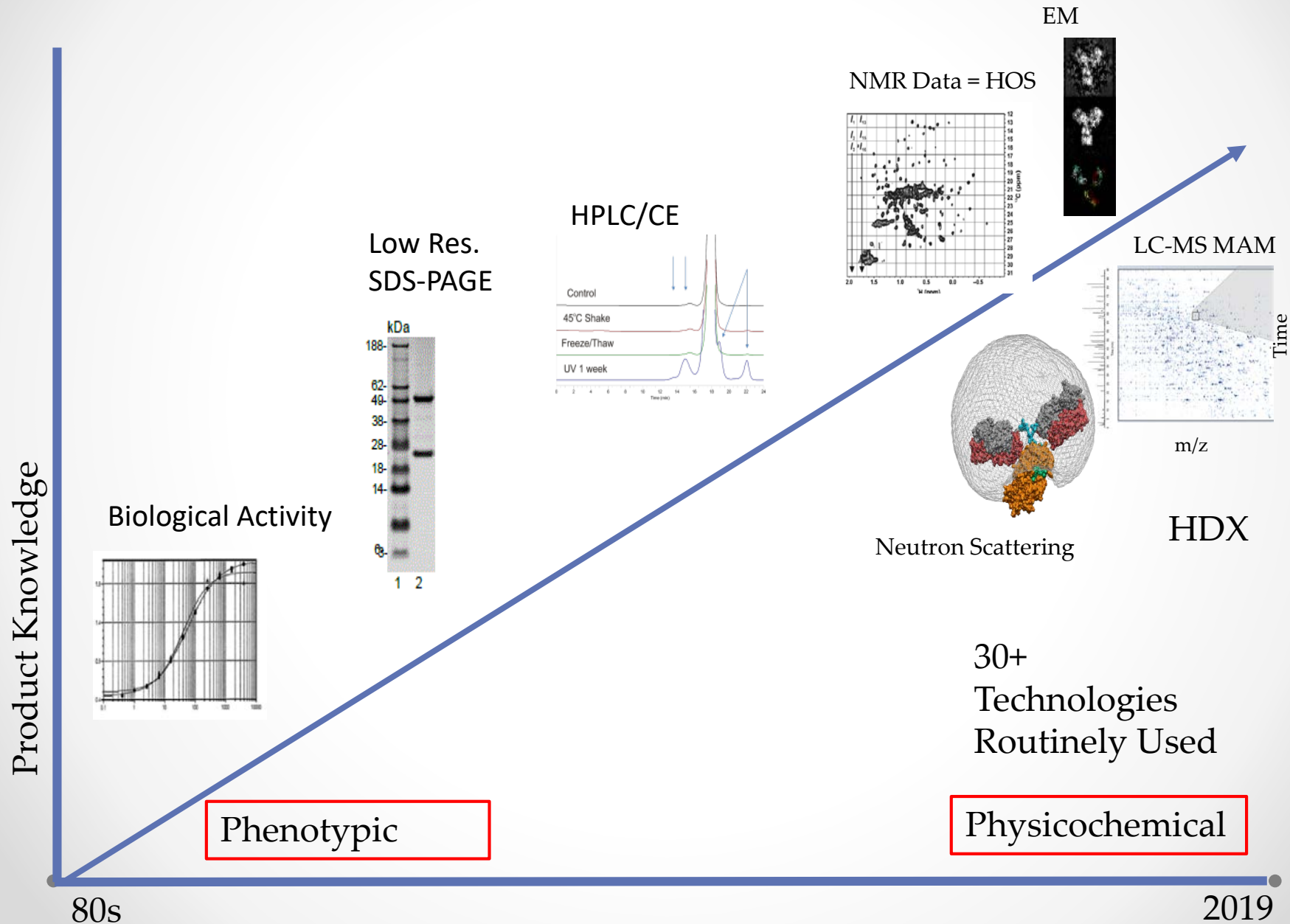
**NIST**  
National Institute of  
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U.S. Department of Commerce

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**INSTITUTE FOR BIOSCIENCE  
& BIOTECHNOLOGY RESEARCH**

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# Evolution of mAb Analytical Methods



# The toolbox is getting full

- Trend toward
  - Attribute-specific analytics (e.g MAM, CZE/cIEF-MS)
  - Higher-order structure with high resolution (NMR, HDX, etc.)
  - Conformational Ensembles (EM, Neutron and X-ray scattering, etc.)
- Replacement vs. addition = lower cost and speed
- Requirements for successful lifecycle appropriate implementation
  - Deep fundamental knowledge of analytical figures of merit
    - Nuances of validation, information content
  - Data analytics to completely harness information content of complex methods
    - Visual conformance to expectation can be a thing of the past
  - Ability to critically evaluate method suitability/fitness for purpose
    - A very good analytical technique can be performed sub-optimally

**Pre-competitive Reference Materials valuable to define state-of-the art and support evolution of Analytics and Control**



# National Institute of Standards and Technology

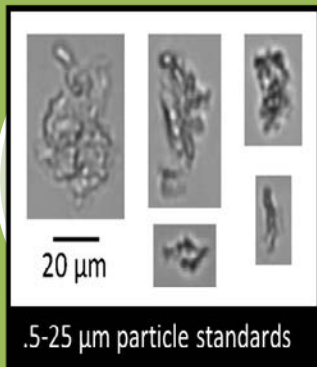
- Non-regulatory agency within U.S. Department of Commerce
- Founded in 1901 as National Bureau of Standards
- NIST responsible for US physical standards, test methods, & calibrations



## **Unique Mission within the Federal Government**

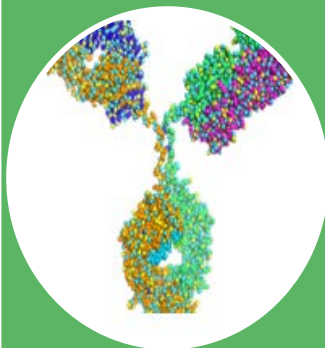
to promote innovation and industrial competitiveness by advancing  
**measurement science, standards, and technology**  
in ways that enhance economic security and improve our quality of life

# Example of NIST Reference Materials



Surrogate  
Protein  
Particle

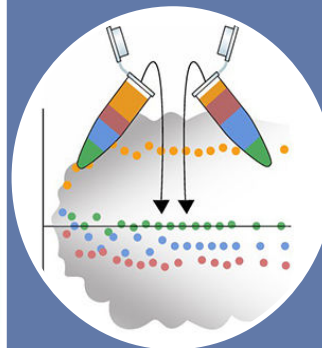
SRM 1989



NIST Monoclonal  
Antibody  
RM 8671



Genomic DNA  
Standard Standards  
for HER2  
Measurements  
Reference Material  
SRM<sup>®</sup> 2373



DNA Sequence  
Library for External  
RNA Controls  
SRM 2374



GIAB: Human  
DNA for Whole-  
Genome Variant  
Assessment

RM 8398  
RM 8391  
RM 8392  
RM 8393  
RM 8375

**Measurement Assurance**

# NISTmAb RM 8671

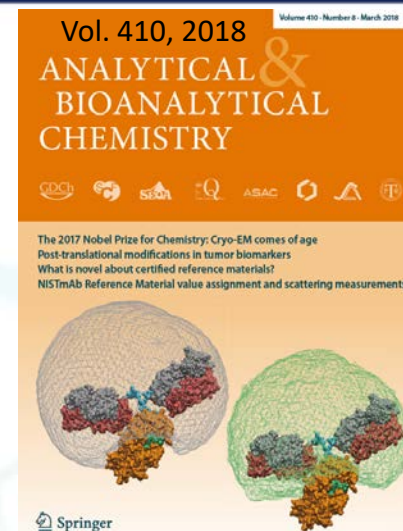
## NISTmAb Attributes:

- Publicly available “biopharmaceutical grade”
- Open Innovation Humanized mAb (IgG1κ)
  - Voluntary, pre-competitive, product neutral standard
  - Exhaustively characterized for physicochemical and biophysical attributes
  - Reference Values, stability, homogeneity assured through lifecycle plan

## Provides an industry-wide shared resource

- Novel technology development and de-risking
- Industry wide collaborative studies to
  - Address shared challenges
  - Advance analytical capabilities
  - Evaluate “regulatory readiness” and appropriate implementation points

NIST Inter-laboratory studies and analytical R&D have targeted emerging analytics expected to have broader impact in the coming 5-10 years



- LC-MS Multi-Attribute Method
- HOS: NMR, HDX, XRD
- EM
- Neutron scattering
- Intact, middle down MS
- Glycosylation Analysis
- LC: SEC, RP, IEX, HIC
- CE: cIEF, cSDS, CZE
- SDS-PAGE
- MS/MS library compilation
- Biophysical: CD, FTIR, DSC, DLS, AUC, SLS, DSF
- Protein particulates

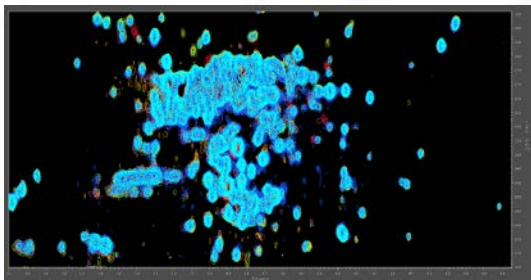
<http://pubs.acs.org/isbn/9780841230262>, <http://pubs.acs.org/isbn/9780841230293>, <http://pubs.acs.org/isbn/9780841230316>

# Interlaboratory Measurement Comparisons Using NISTmAb

- Assess variability between labs and analytical technologies
- Identifies potential technology gaps
- Informs development of potential NIST reference materials
- Fosters collaboration across global biopharma community

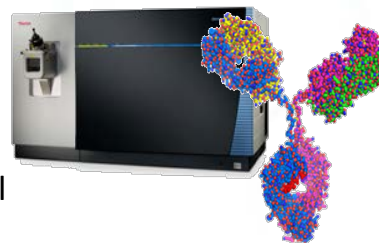
## 2D-NMR of NISTmAb Fab

- 30 participants, ~ 11 industrial
- Rob Brinson



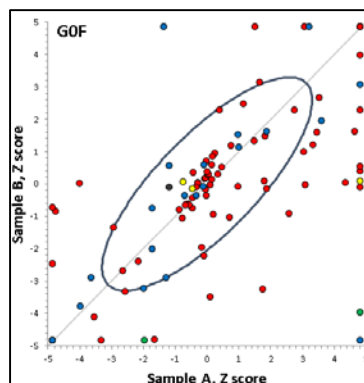
## Multi-Attribute Method Consortium

- 30 industrial participants
- submitted



## Glycoanalysis of NISTmAb

- 108 participants, ~ 50 industrial
- Lorna DeLeoz



## HDX-MS of NISTmAb Fab

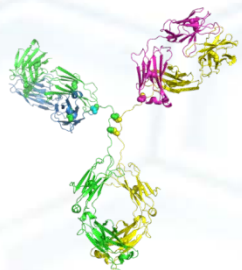
- 22 participants, ~ 8 industrial
- Jeffrey Hudgens



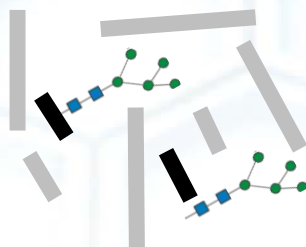


# Multi-Attribute Method

- Enables attribute-specific monitoring
- Enables comprehensive detection of process/product impurities



Digestion

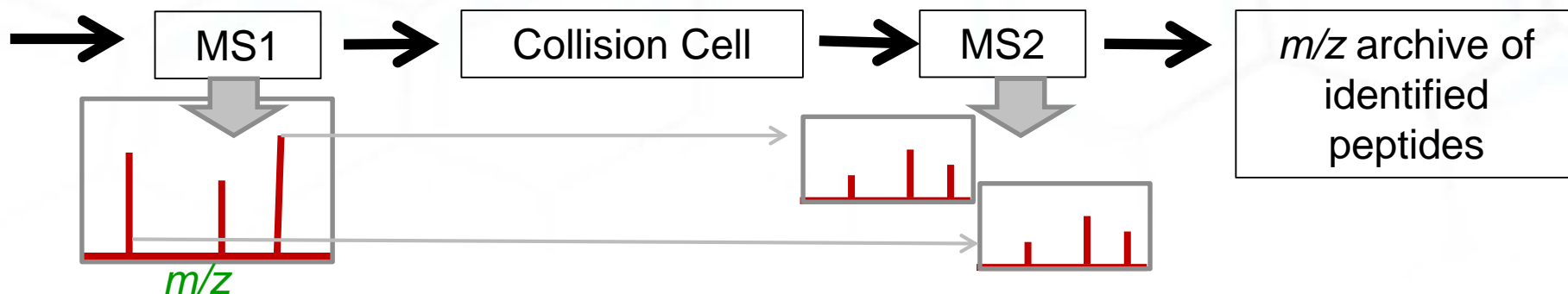


LC-MS/MS

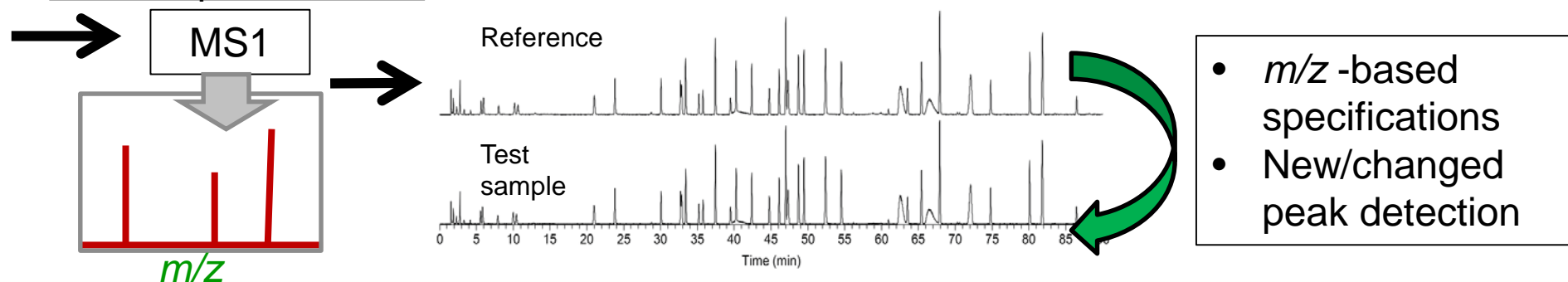
## High Resolution LC-ESI-MS

- Primary sequence confirmation
- PTMs
- Site-specific glycan identification

## MAM Development



## MAM Implementation



- *m/z* -based specifications
- New/changed peak detection

# MAM Consortium NPD Round Robin

Trina Mouchahoir, Rich Rogers, John Schiel



## Purpose

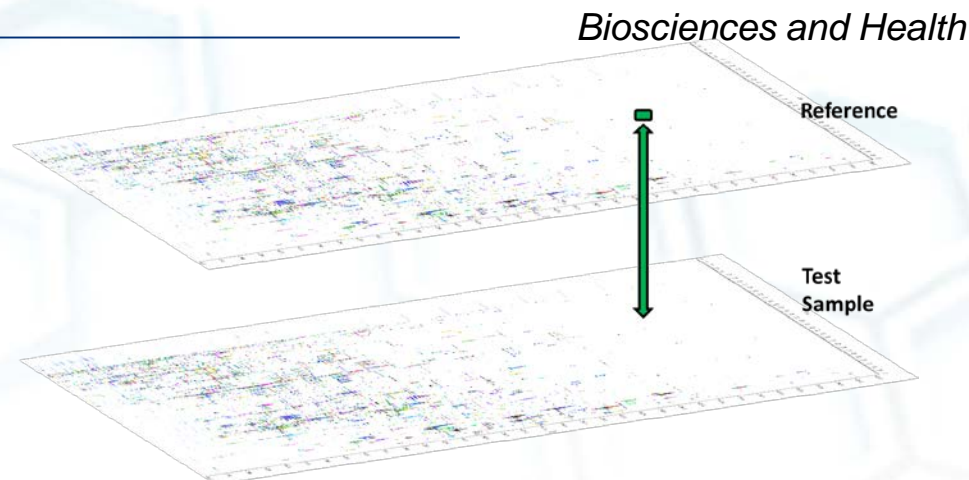
- Evaluate industry-wide new peak detection performance metrics

## Results

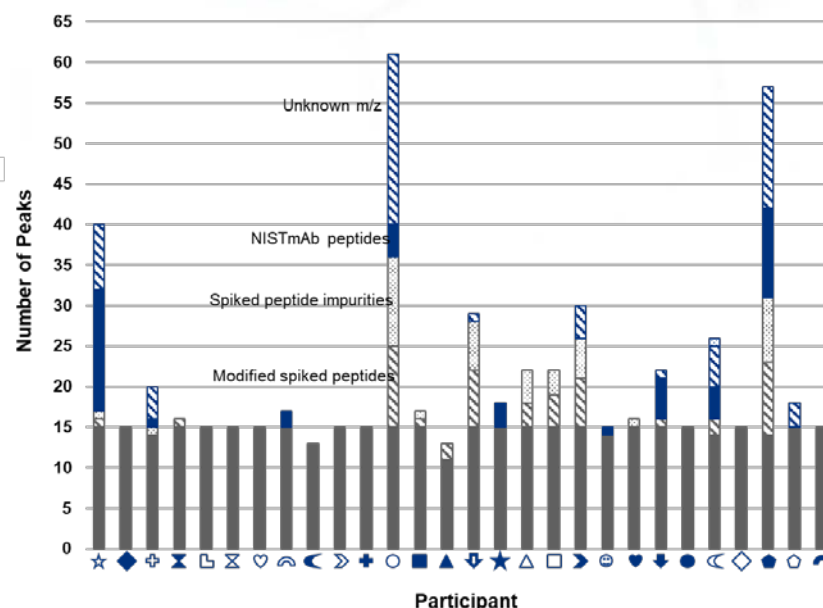
- 28 Industry/Instrument Vendor/Government Participants
- New peak detection is sensitive impurity test
- NPD criteria are being set within performance metrics of current instrumentation
- False positives and false negatives can be mitigated with proper controls. Common pitfalls were identified and explained

## Future Perspective

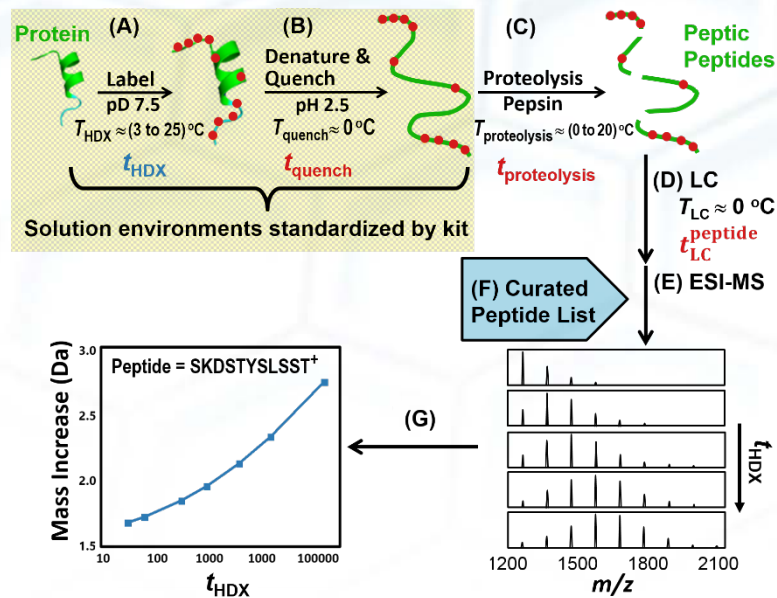
- MAM-specific validation criteria, including NPD analysis, are the next step toward robust QC
- Empirical process/product-specific NPD criteria will be critical to success
- Likely to see broader implementation of MAM
  - QC, process development, comparability, biosimilarity



NISTmAb digest spiked with 15 synthetic peptides (0.5 pmol each)



# Protein Structural Dynamics Measured by H/D Exchange Mass Spectrometry (HDX-MS)



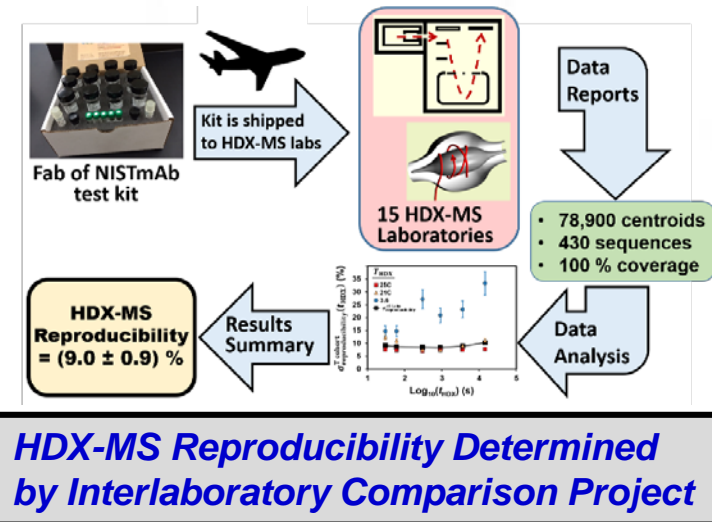
## Method

- HDX-MS measures H/D exchange rates that are governed by protein 3D structure and ligand-protein interactions.
- Until recently, HDX-MS is mostly used for epitope mapping and for protecting IP.
- HDX-MS is very sensitive to PTMs.
- HDX-MS can resolve dynamics of IgG1 glycoforms

## NIST Interlaboratory Comparison Project

- The study analyzed 78,900 measurements on Fab of NISTmAb, reported by 15 labs in 4 countries, resulting in the first determination of HDX-MS reproducibility
- HDX was demonstrated to be reproducible, potential areas for improvement identified

Hudgens, et. Al. Anal Chem. 2019 Jun 4;91(11):7336-7345



# HDX-MS Technology Advancements

Drs. Kyle Anderson, Jeffrey W. Hudgens

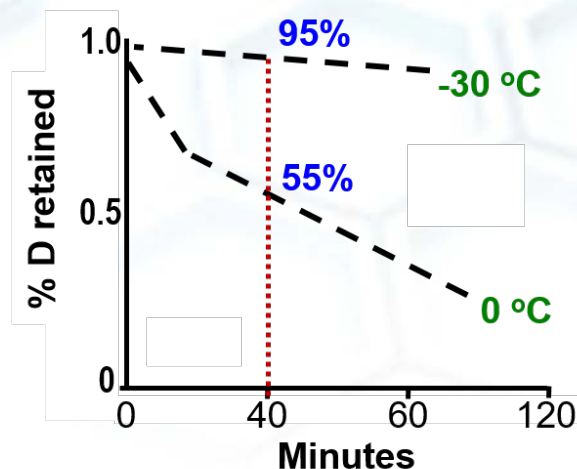
## Future Perspective

- Additional hardware/software innovations will further improve resolution, dynamic range, and reproducibility of HDX-MS.
- HDX-MS implementation will continue to grow
  - Novel modalities
  - More routinely used throughout drug development lifecycle

## Ongoing Projects : Examples

- Developed an ultra-cold (-30 °C) proteolysis-chromatographic system, which suppresses data-corrupting back-exchange by >7x.
- Reported a robotic lipid removal method for HDX-MS—promptly adopted by industry—that facilitates pharmaceutical studies of membrane proteins.

## Reduced Back-exchange at -30 °C



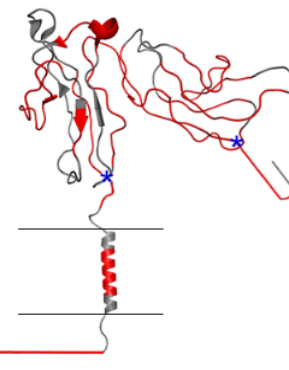
## New biochemical system

Signal Peptide

10 20 30 40  
MTMETQMSQHVCPRLWLLQPLTVLLLLASADSQAAPPKA  
50 60 70 80  
VLKLEPPWINVLQEDSVTLTCQGARS PESDSIQWFHNGNL  
90 100 110 120  
IPTHTQPSYRFKANNDSGEYTCQTGQTSLSDPVHLTVLS  
130 140 150 160  
EWLVLTQTPHLEFQEGETIMLRCHSWKDKPLVKVTFQNGK  
170 180 190 200  
SQKFSLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPV

Transmembrane

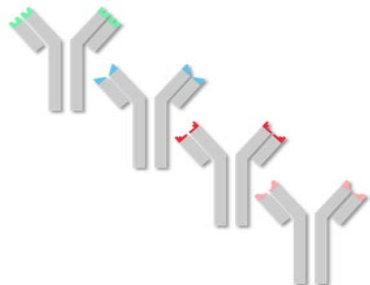
210 220 230 240  
TITVQVPSMGSSSPMGVIVAVVIATAVAAIYAVALIYC  
250 260 270 280  
RKKRISANSTDPVKAQFEPGRQMIAIRKRQLEETNNDY  
290 300 310  
ETADGGYMTLNPRAPTDODDKNIYLTLPNDHVSNN



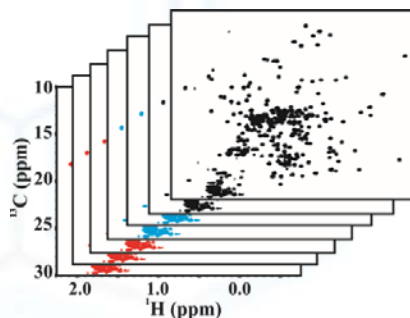
Sequence coverage of FcγRIIa entrained in a bilipid matrix.



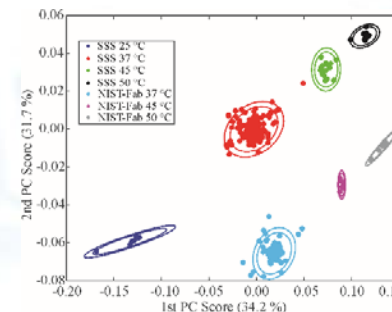
## mAb Therapeutic Samples



## 2D NMR Fingerprints



## Statistical Analysis



## Purpose

- Establish a community standard for the measurement of the higher order structure (HOS) critical quality attribute (CQA) by the 2D-NMR method at atomic resolution.

## Results

- Database of spectra from 26 laboratories in nine countries, with equal representation from industry, government, and academia.
- 2D-NMR spectral fingerprinting method is both **repeatable** and **reproducible**.
- Peak position is a **robust** measurement. The same answer is obtained regardless of hardware, field strength, or experimental set-up.
- All data and scripts available at: <https://www.ibbr.umd.edu/groups/nistmab-nmr>

## Future Perspective

- Assurances that the structures of two proteins are highly similar is generally considered to be highly indicative of similar function. Therefore, the ability to precisely and accurately compare structural attributes of two proteins could be key pieces of information that inform the degree of clinical data necessary to confirm safety and efficacy.

Brinson, et. Al. MABs. 2019 Jan;11(1):94-105.

# Measurement Science to Evaluate Conformational Ensembles

Tom Cleveland, John Marino



**Protein therapeutics do not have “a” static structure**

**Mechanism of Action:**  
Structure contributes to understanding of drug mechanism

**Potency:** Dynamics may govern interactions

**Harmful Side Effects:**  
Structural flexibility correlate with stability?

NISTmAb Negative Stain EM

Safety and Efficacy

Manufacturing

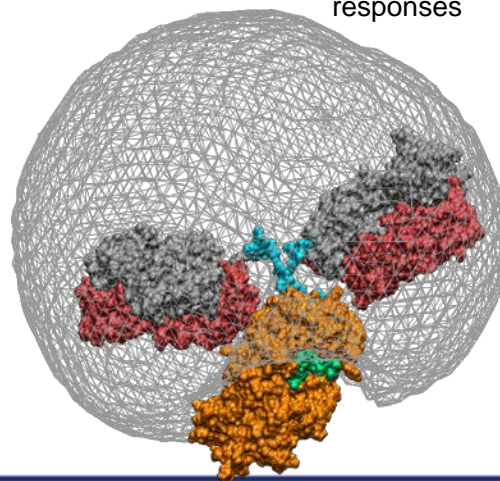
**Delivery/Formulation:**  
Structure contributes to formulation stability and solution viscosity

**Aggregation:** Some structures can lead to drug aggregation and dangerous immune responses

Lei, ..., **Cleveland, Marino**, Ren. 2019. *Scientific Reports* 9:1-15.

Castellanos MM, Howell SC, Gallagher DT, **Curtis JE**. *Anal Bioanal Chem*. 2018 Mar;410(8):2141-2159.

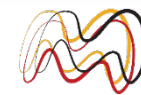
Xu AY, Castellanos MM, Mattison K, Krueger S, **Curtis JE**. *Mol Pharm*. 2019 Oct 7;16(10):4319-4338.



Neutron Scattering and X-ray scattering combined with modeling offer insights into dynamics

# NISTmAb non-originator cell lines

Zvi Kelman, Lila Kashi, William Odell

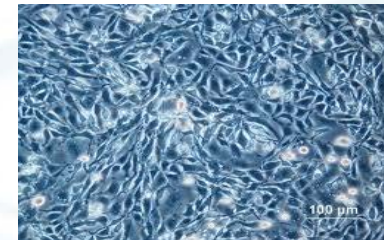


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BIOTECHNOLOGY  
RESEARCH

*Biosciences and Health*

## Need

- Pre-competitive cell line to
  - Evaluate innovative process technology
  - Advance PAT, downstream, etc.
  - Continuous processing/real time release test case
  - Platform to demonstrate novel engineering biology approaches



## Current Status

- Non-originator cell lines expressing NISTmAb under development
- Preliminary method development from NISTmAb to be ported to non-originators



## Future Perspectives

- Data collected may extend open innovation concept to entirety of drug development lifecycle
- “Living” RMs may have substantial impact

Kashi, Yandofski, Preson, Arbogast, Giddens, Marino, Schiel, Kelman. 2018 Aug/Sep;10(6):922-933.

# Public Partnership → Limitless Potential

## **VISION: Utilize RMs to accelerate**

*Full utilization of emerging technology data for holistic product quality assessment*

*Emphasis on analytics for attribute-specific product optimization and control*

*Mechanisms for inter-assay data integration and/or replacement*



Predicting clinical performance and feedback to manufacturing

**Computational Tools, Models & Analytics**

Lifecycle appropriate analytical technologies

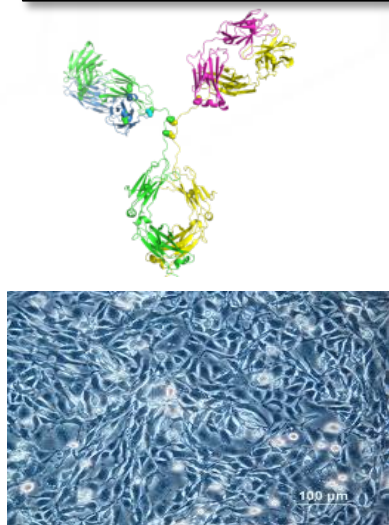
**Process Analytics & Manufacturing**

**Machine Learning/AI**

**Advanced Analytical Technologies**

Reference materials & qualified methods

**Reference Materials**



Maturation over time



Regulatory Opportunity!



# Acknowledgements

## ➤ NISTmAb Team

- Katharina Yandrofski
- John Giddens
- Trina Mouchahoir



## ➤ NPD Round Robin

- Rich Rogers (JUST)
- Trina Mouchahoir

## ➤ NMR Round Robin

- Robert Brinson
- John Marino
- Frank Delaglio
- Like Arbogast

## ➤ HDX Round Robin

- Jeff Hudgens
- Kyle Anderson

## ➤ EM

- John Marino
- Thomas Cleveland

## ➤ Non-originator cell lines

- Zvi Kelman
- Lila Kashi
- William O'Dell

## ➤ Biomanufacturing Coordinator

- Michael Tarlov



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