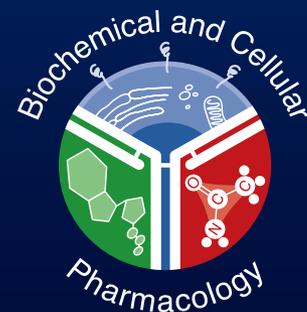


# A Holistic Strategy to Characterize the *In Vivo* Stability of Novel Modalities using Affinity Capture Coupled to LC-MS or CE-Based Methods

Cong Wu, Scientist

wu.cong@gene.com

CE Pharm, October 1<sup>st</sup> 2020



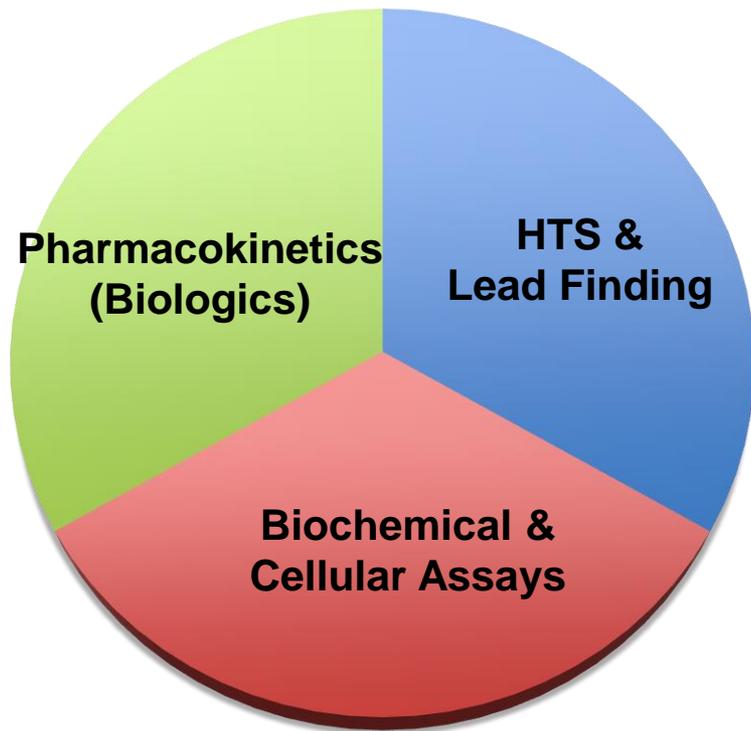
# Outline

- **Background**
  - LM BCP MS group overview
  - Novel large molecule modalities
  - Biotransformation
- **Analytical workflow for intact stability analysis**
  - Affinity capture + LC-MS
  - CE LIF
  - CE Western blot
- **Summary**

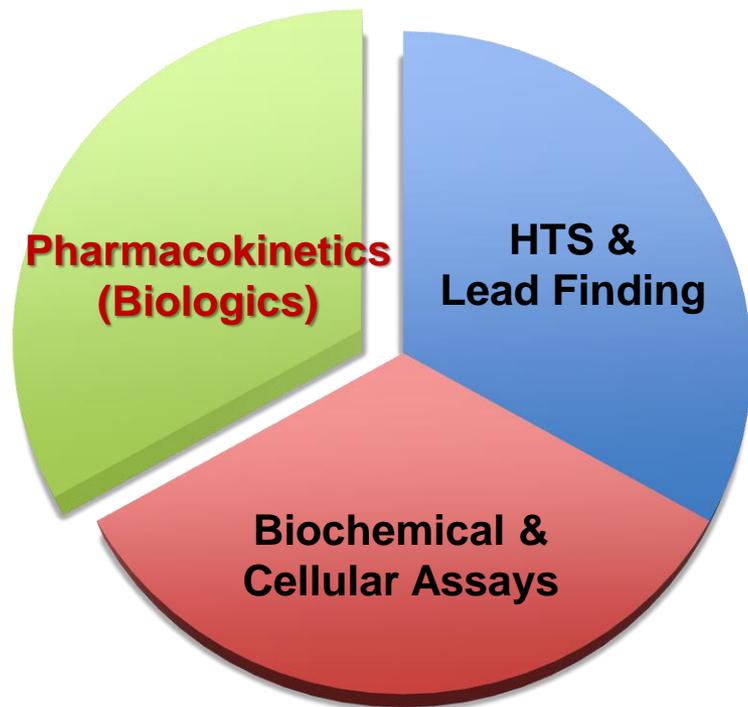
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# Large Molecule Biochemical and Cellular Pharmacology Mass Spec (LM BCP MS) group



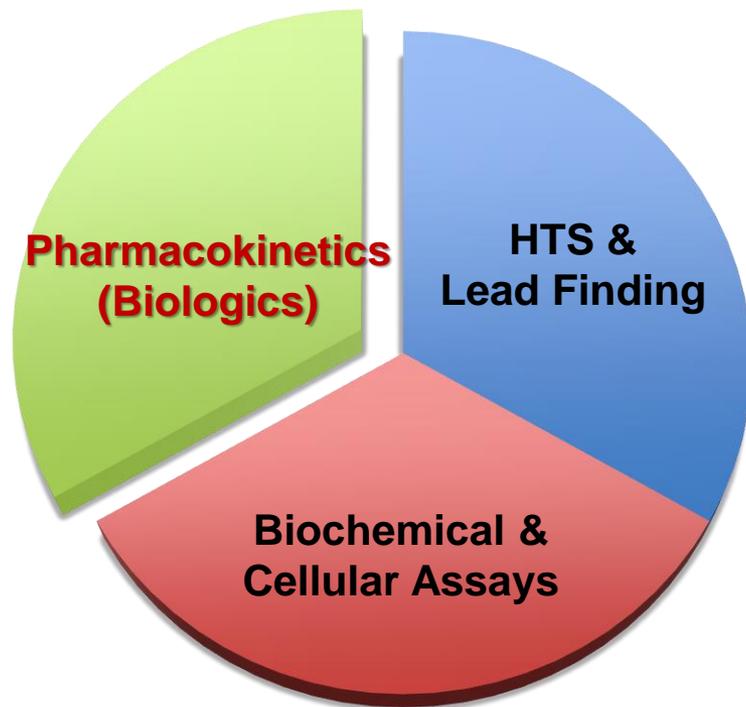
# Large Molecule Biochemical and Cellular Pharmacology Mass Spec (LM BCP MS) group



## Pharmacokinetics (PK):

- Biotransformation:
  - Intact stability (clipping)
  - Amino acid level modification
  - Chemical stability of conjugates
- Biodistribution:
  - Total drug concentration in circulation
  - In tissue

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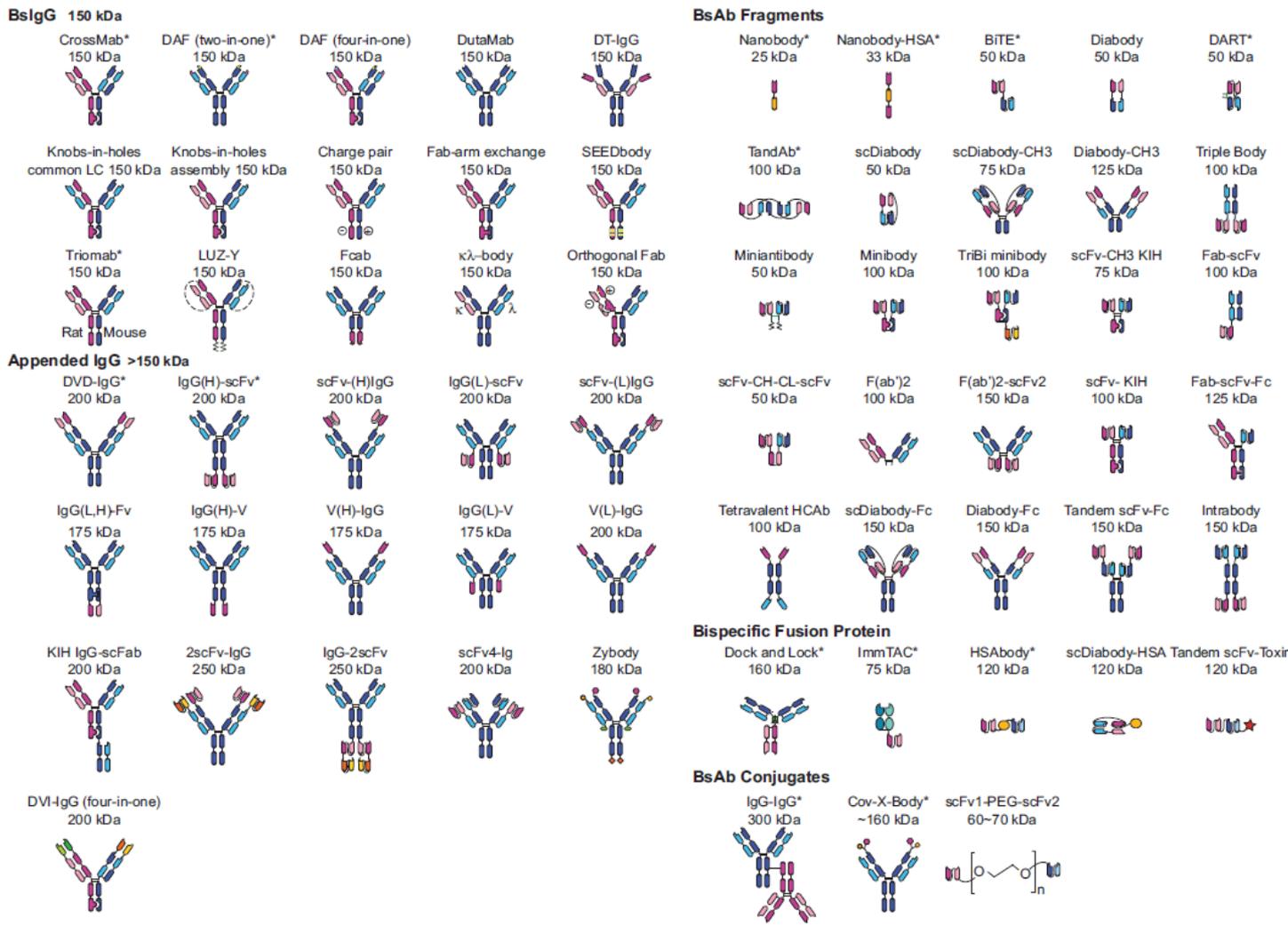
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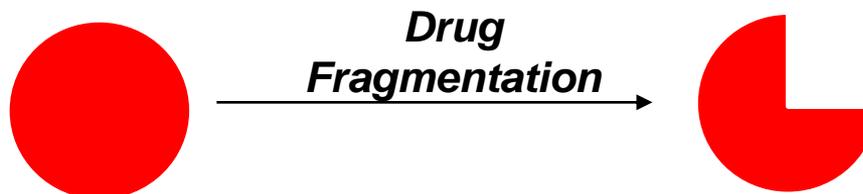
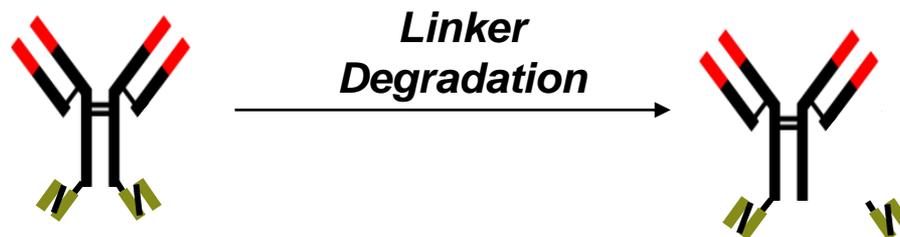
# Emerging new modalities aim to modulate challenging targets



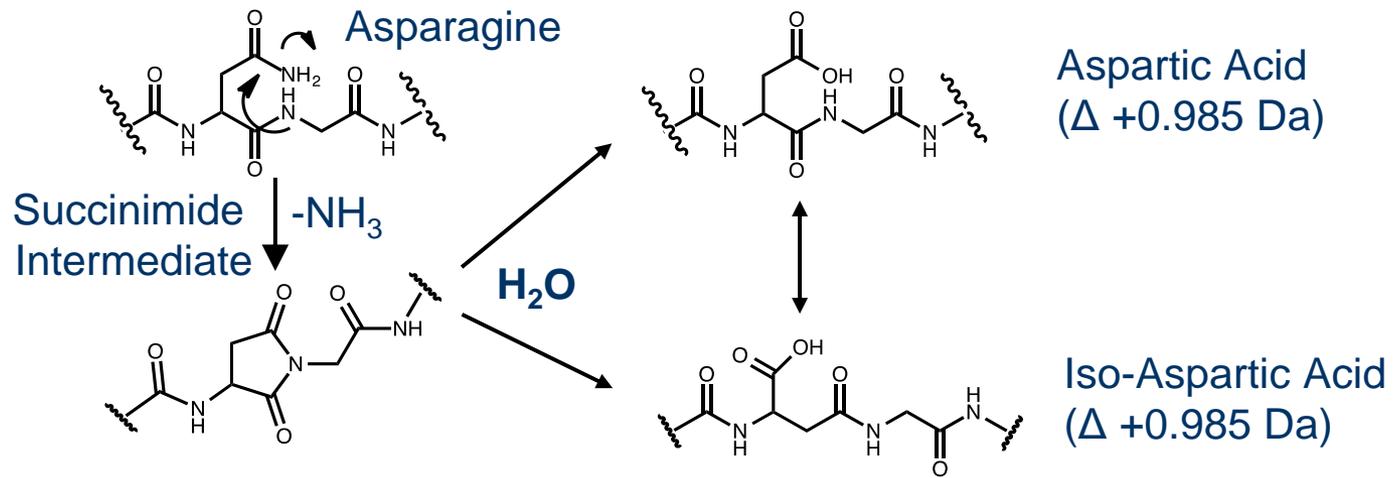
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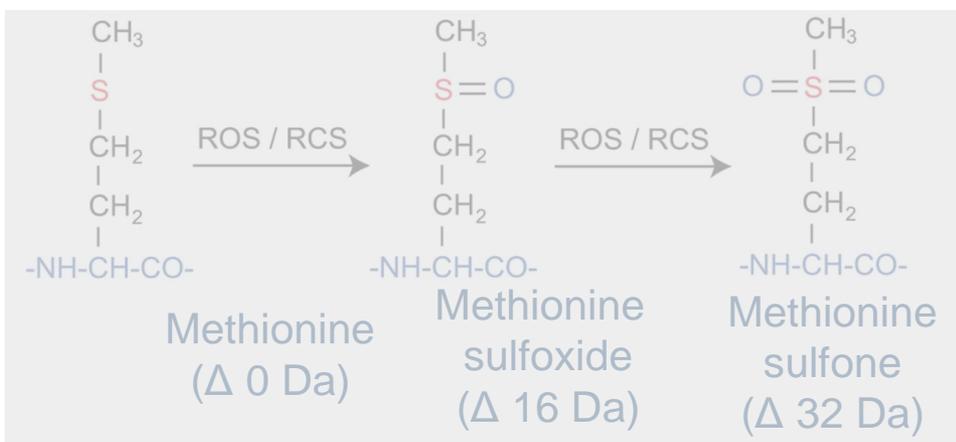
# Biotransformation – *in vivo* intact stability



## Deamidation – N, Q, Isomerization – D, E



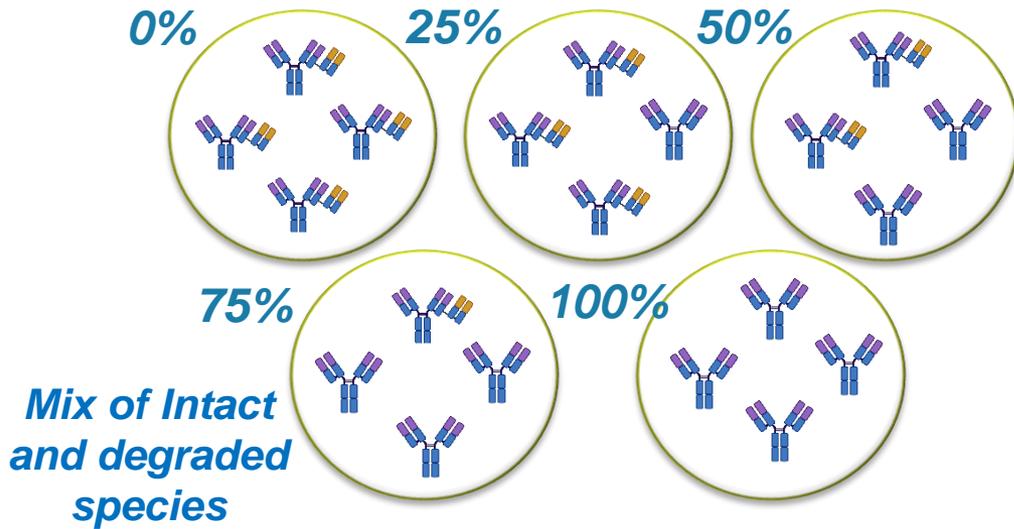
## Oxidation – M,W



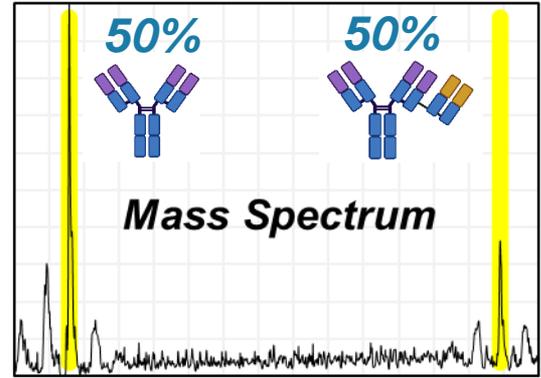
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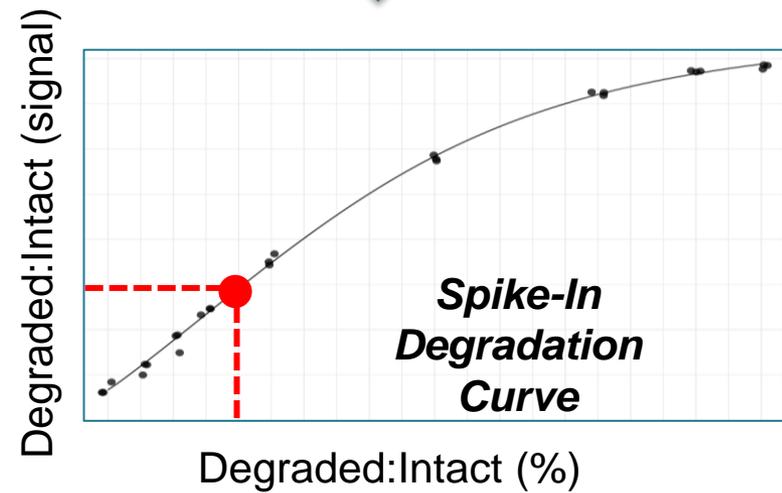
# Affinity capture + LC-MS workflow for intact stability analysis



Affinity Capture



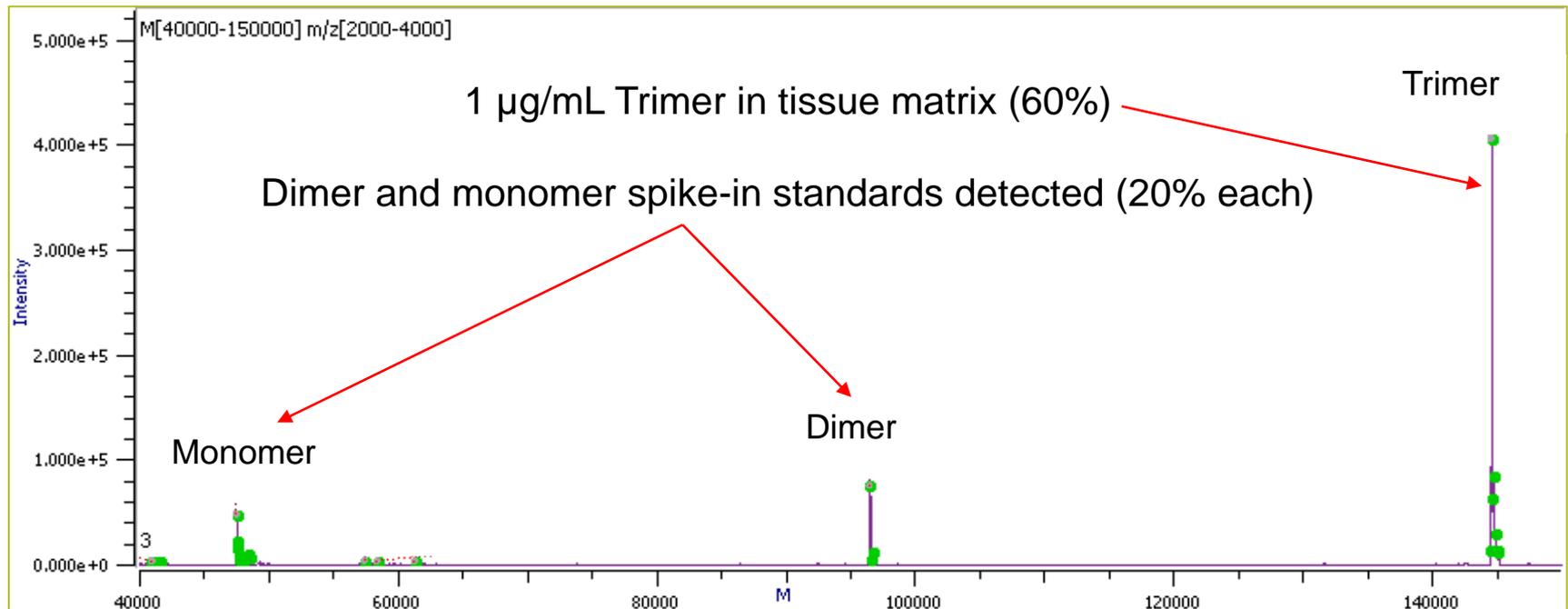
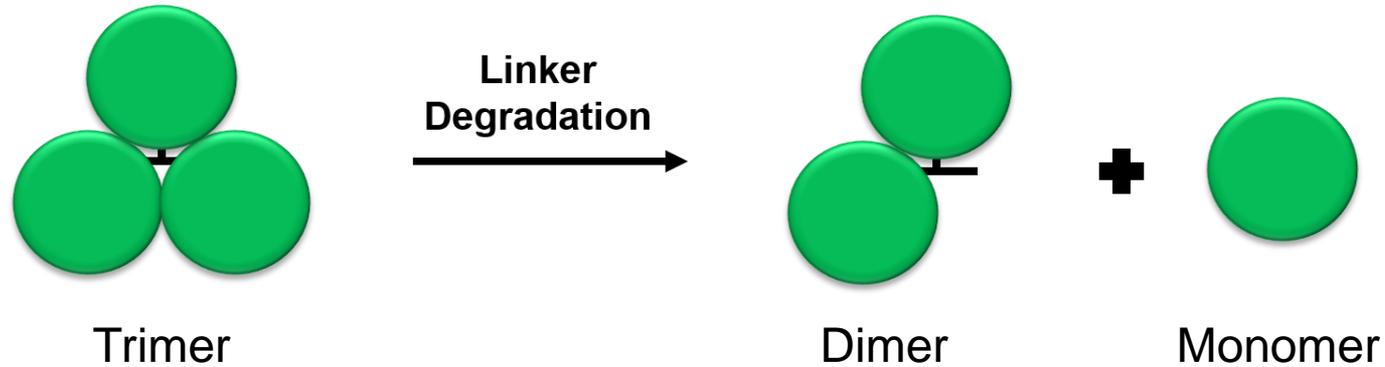
Calibration curve



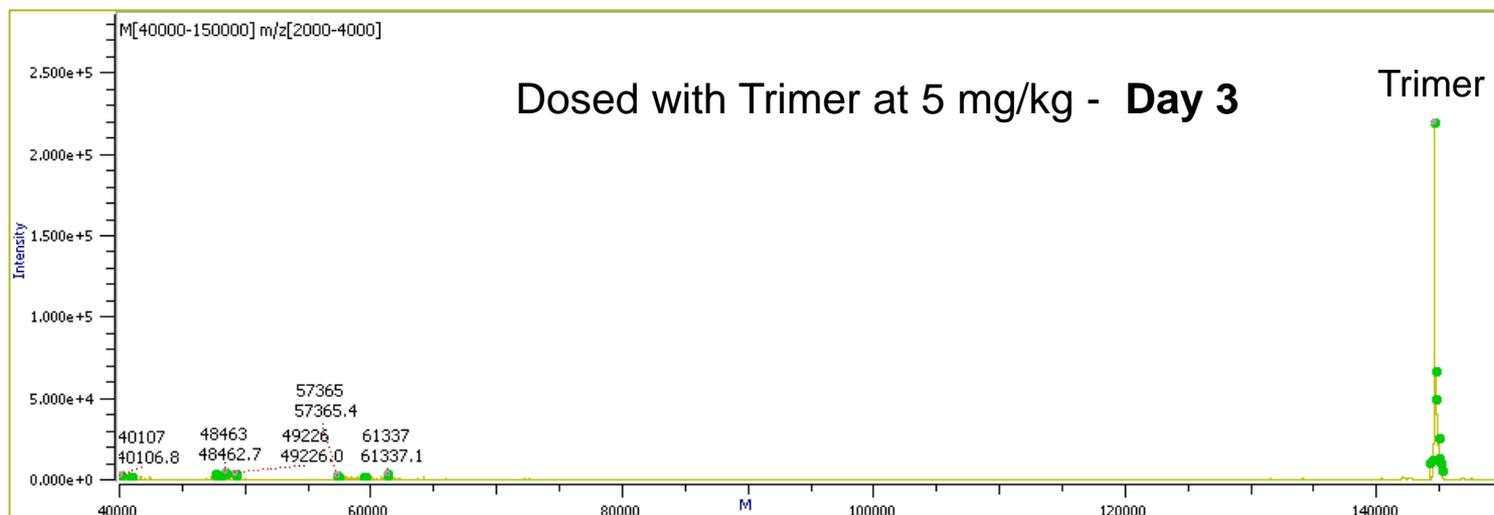
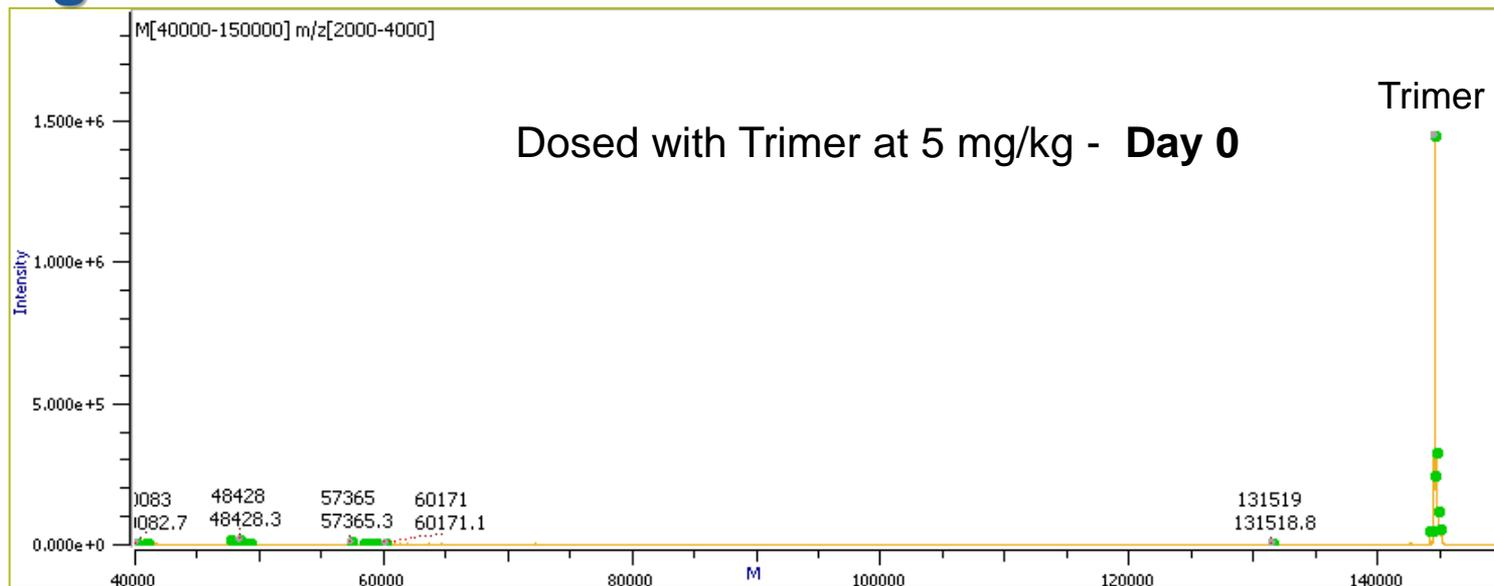
Relative Degradation in vivo / ex vivo

Quantification

# Case study of a trimeric molecule stability in tissue



# PK samples from Day 0 vs Day 3 showed no detectable degradation



No degradation products were observed up to Day 3

# Comparison of bioanalytical tools for *in vivo* clipping characterization and quantitation



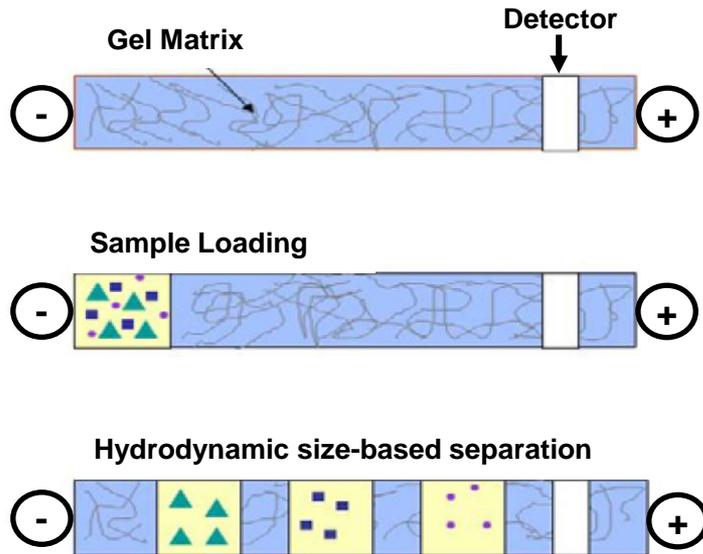
	LC-MS	CE-SDS LIF	CE-Western Blot
<b>Specificity</b>	High		
<b>Sensitivity</b>	Medium with MW bias		
<b>Relative quantitation ability</b>	Standards and calibration curve required		
<b>Resolution</b>	Single amino acid resolution		
<b>Robustness</b>	Medium		

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# Capillary Electrophoresis SDS Laser Induced Fluorescence (CE – SDS LIF)

- Calibration curve – LIF signal is directly quantitative



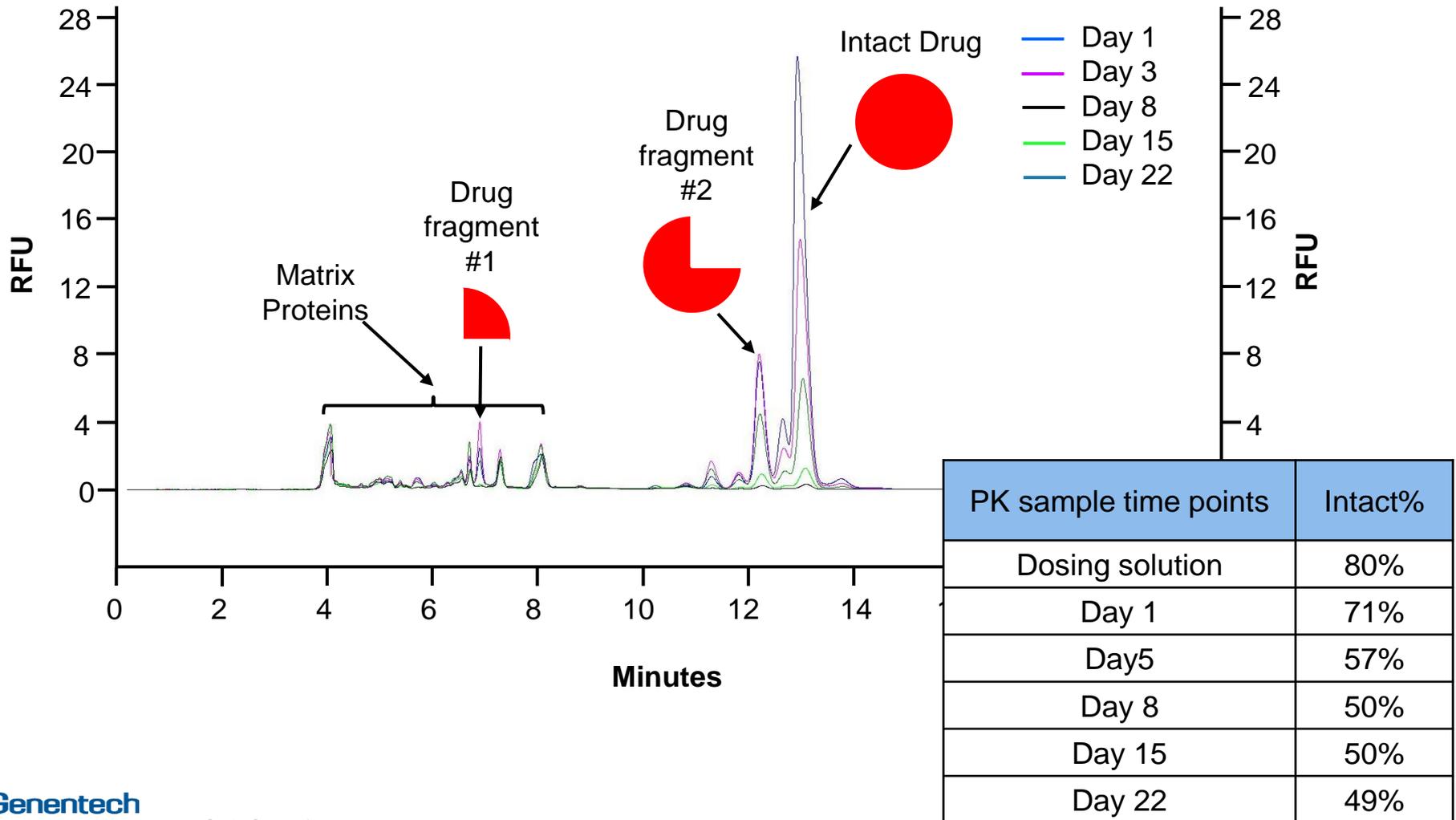
Fundamental steps of CE-SDS separation



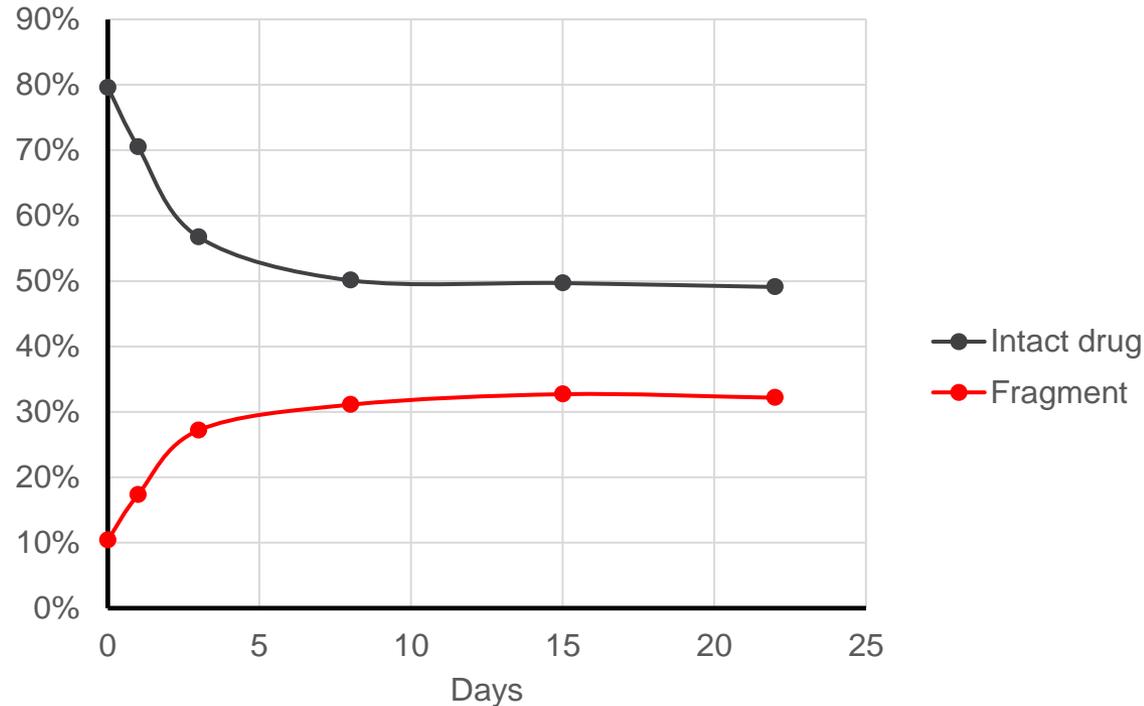
Sciex PA800 plus

1. Denature samples with SDS (and DTT for reduced CE-SDS)
2. Fluorescently label samples with FQ dye
3. Signal detection at 600 nm upon excitation at 488 nm

# Case study of a multimeric drug in a PK study



# Case study of a multimeric drug in a PK study



- Fragmentation of intact drug was significant in the first ~8 days after single dose injection
- The relative percentages of intact and fragmented drugs remained the same after Day 8

# Comparison of bioanalytical tools for *in vivo* clipping characterization and quantitation



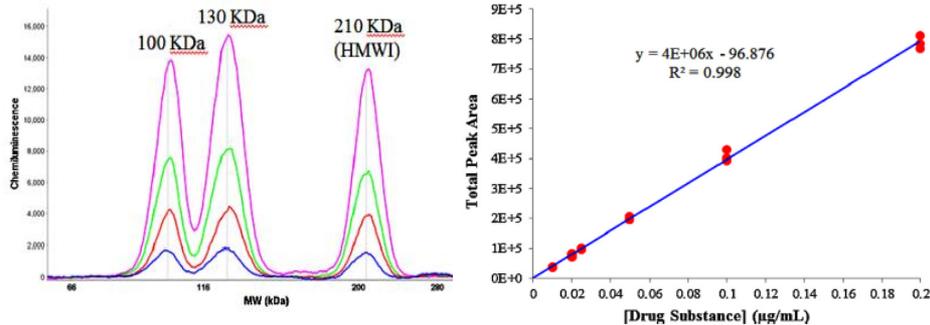
	LC-MS	CE-SDS LIF	CE-Western Blot
<b>Specificity</b>	High	Low	
<b>Sensitivity</b>	Medium with MW bias	Medium non-biased	
<b>Relative quantitation ability</b>	Standards and calibration curve required	LIF signal directly quantitative	
<b>Resolution</b>	Single amino acid resolution	Chain level resolution	
<b>Robustness</b>	Medium	High	

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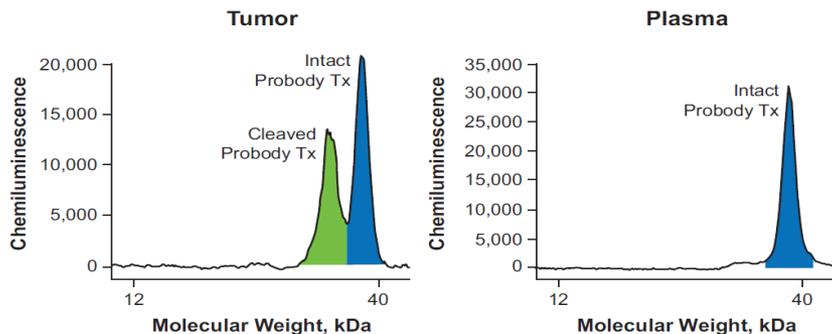
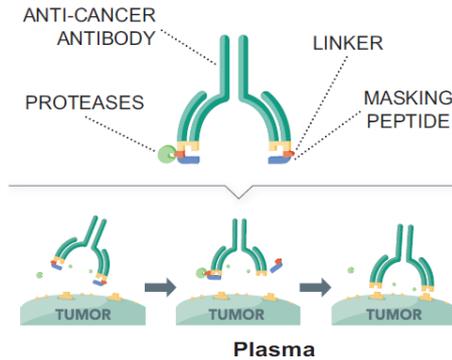
# Rationale for biotransformation

## Size-based separation for clipping

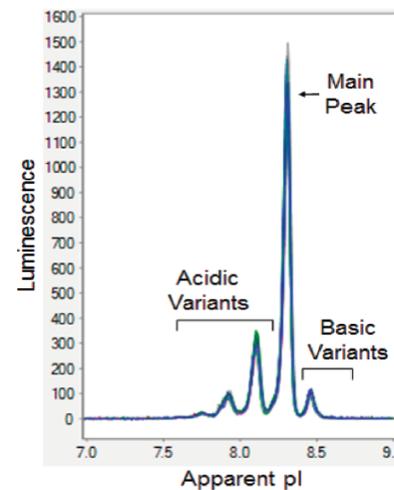


Xu *et al.* *J Phar Biomed Anal* (2012)

Poster TPS3107  
presented by  
CytomX Therapeutics,  
**ASCO 2017**



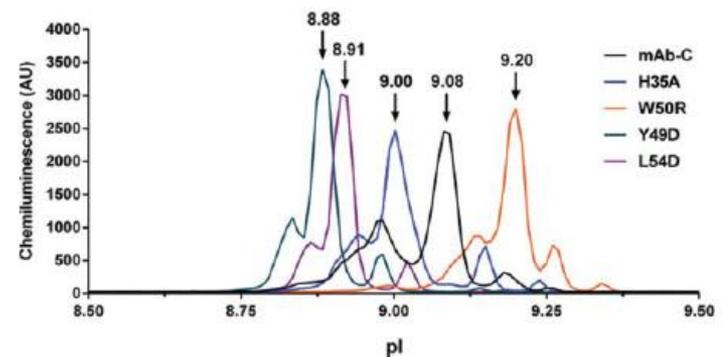
## Charge-based separation for deamidation



- 12 injection overlays showed high repeatability
- Limit of detection (S/N = 3) : 6 ng/mL (2 pg/capillary)
- Dynamic range: 12.5 ng/mL – 2  $\mu\text{g/mL}$
- Samples directly loaded from cell culture supernatant

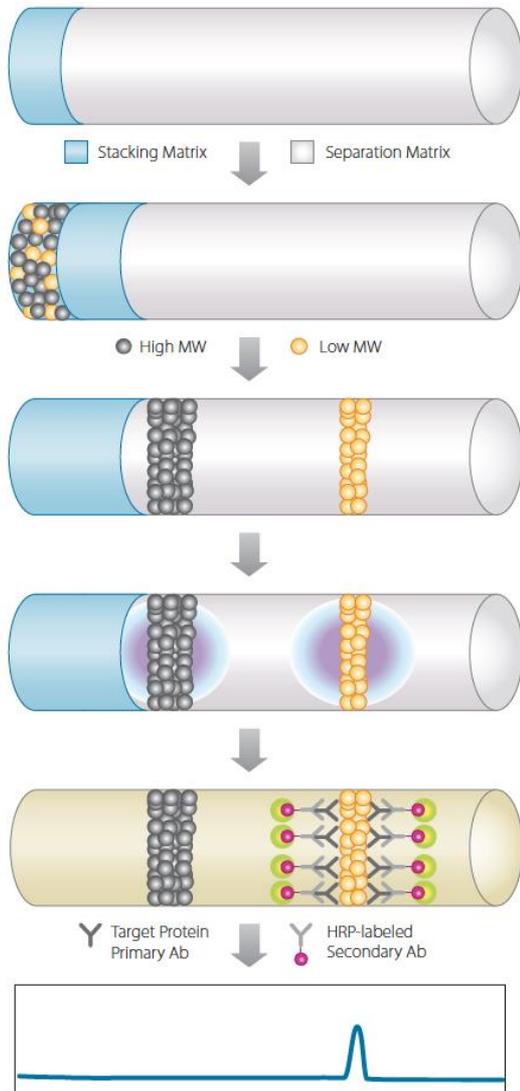
Michels *et al.* *Analytical Chemistry* (2012)

A



Geoghegan *et al.* *mAbs* (2016)

# BACKGROUND ON CE WESTERN BLOT



**Load matrices**  
(up to 12 channels)



**Load samples**  
(reduced and denatured)



**Separate based on**  
**MW (or pI)**



**Immobilize via UV**



**Immunoblot**



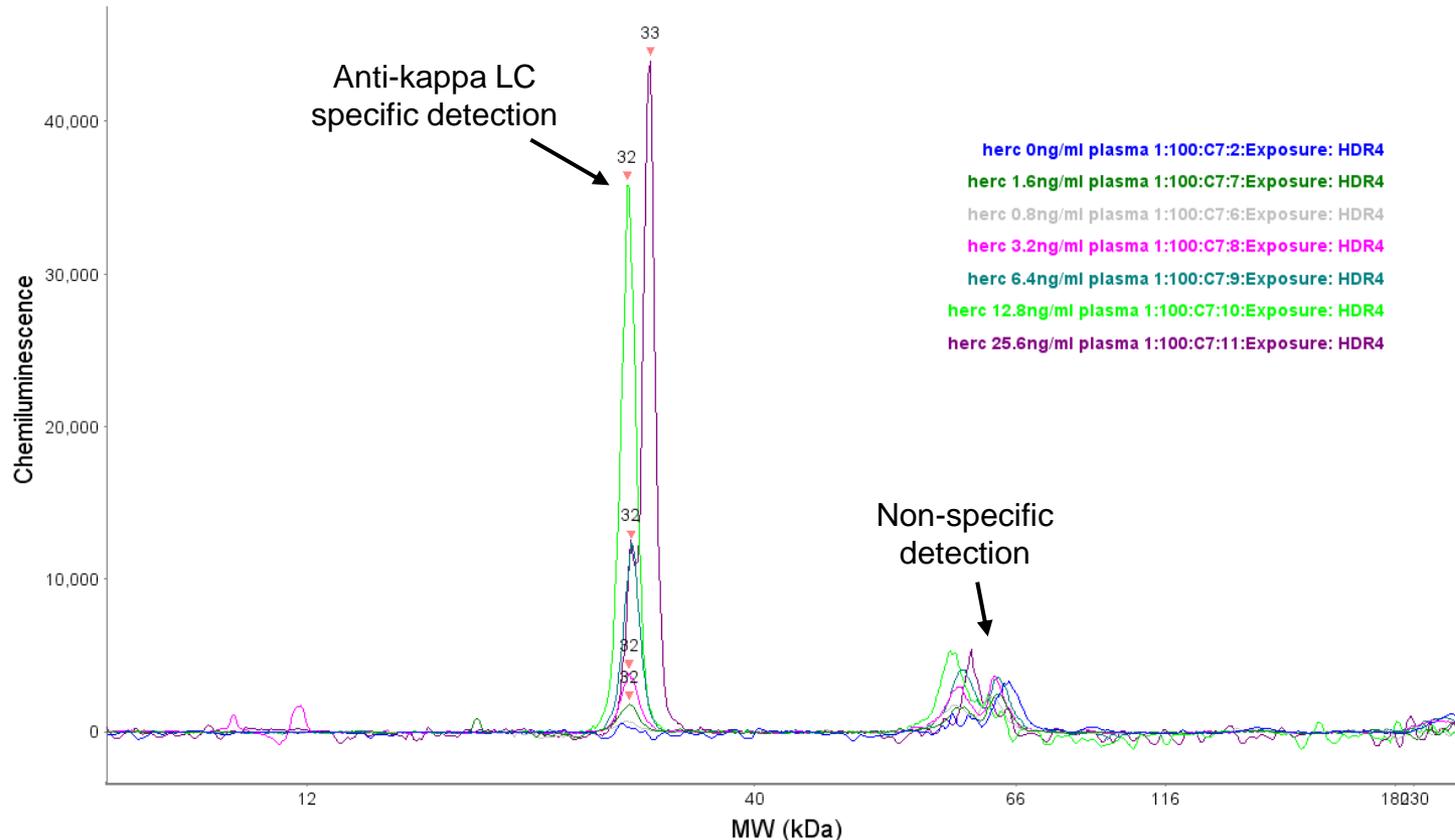
**Quantitate**

**PeggySue:**  
Automated Multiplex  
Western Blot System



# LC- or HC-specific primary antibodies allow highly specific and sensitive detection of clipping events

Herceptin spiked in diluted C57BL/6 plasma @ 0 – 25.6 ng/mL



- *In vivo* samples can be directly analyzed without affinity capture after dilution
- Although sensitive, the dynamic range of CE Western is narrow 1~2 orders of magnitude

# Comparison of bioanalytical tools for *in vivo* clipping characterization and quantitation

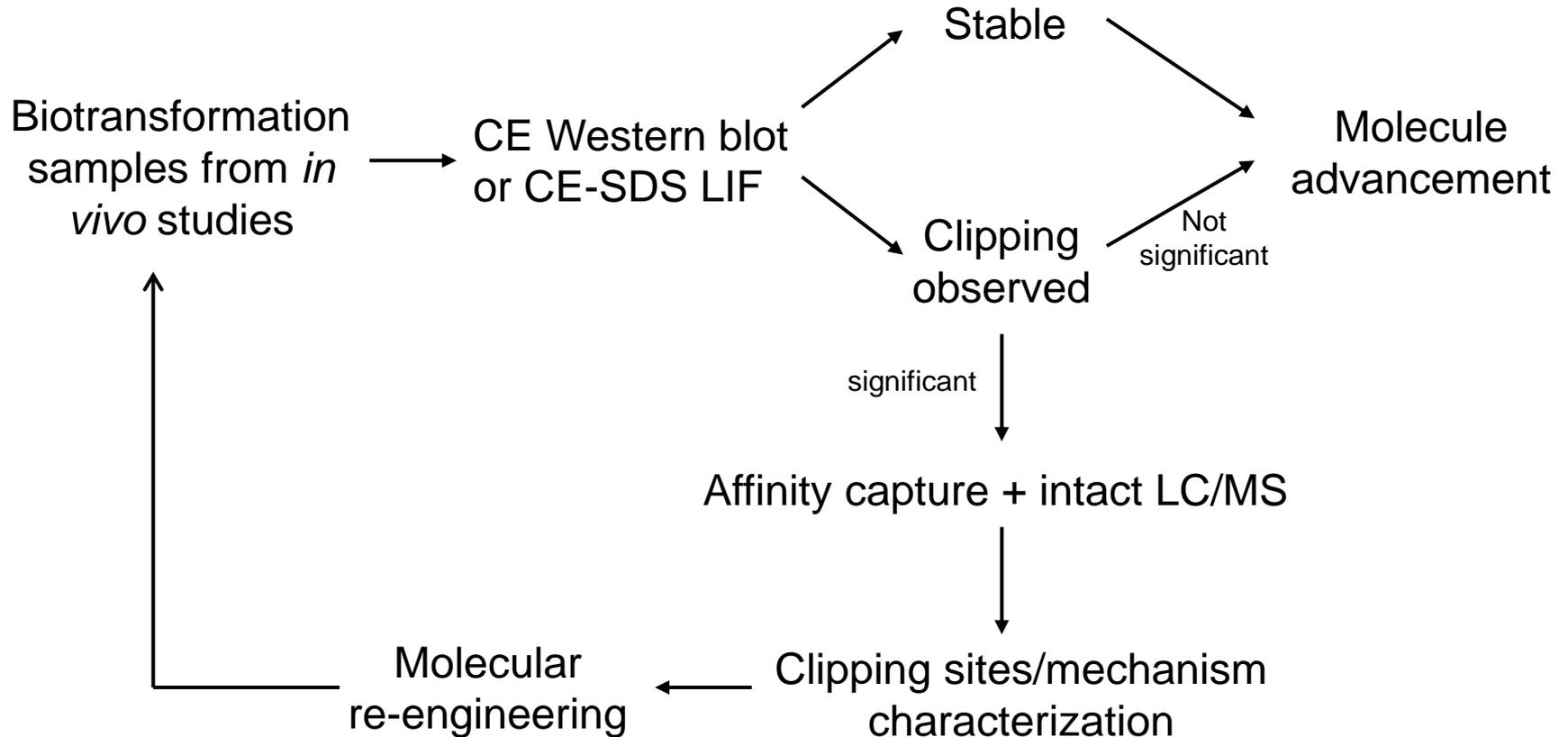


	LC-MS	CE-SDS LIF	CE-Western Blot
Specificity	High	Low	High
Sensitivity	Medium with MW bias	Medium non-biased	High non-biased
Relative quantitation ability	Standards and calibration curve required	LIF signal directly quantitative	Quantitative in a narrow dynamic range
Resolution	Single amino acid resolution	Chain level resolution	Chain level resolution
Robustness	Medium	High	Medium

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# *In vivo* intact stability triaging strategy for novel modalities



# Future directions



- **Evaluate the connection and difference between**
  - In circulation vs at site of action
  - healthy vs disease tissues
- **Characterize the mechanisms of *in vivo* clipping**
  - Enzymatic proteolysis
  - Chemical hydrolysis
  - *In vitro* system to recapitulate clipping *in vivo*
- **Explore charge-based CE Western for other types of biotransformation**
  - Deamidation
  - Glycosylation
  - Other charge-altering modifications



# Acknowledgment

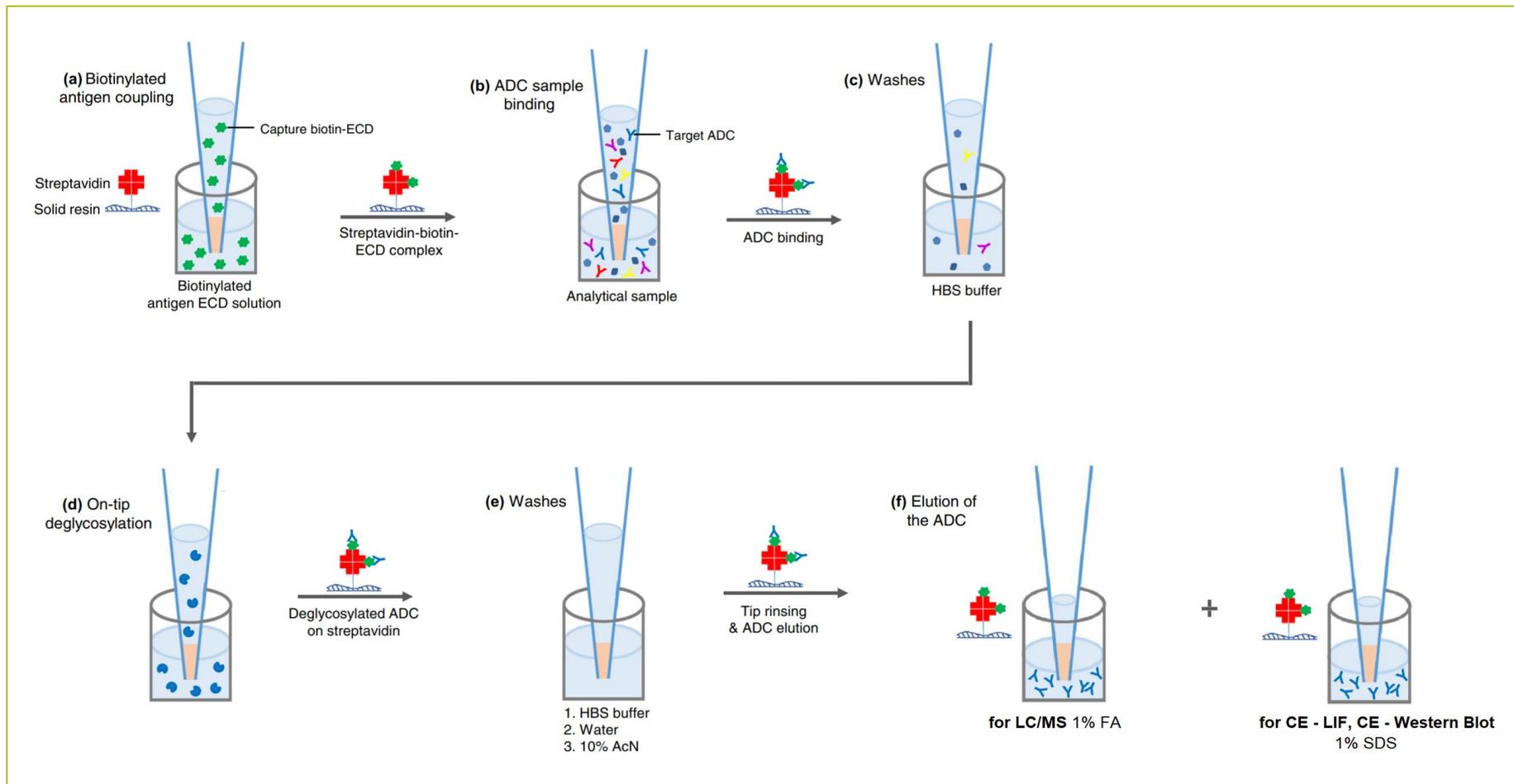
- **Biochemical and Cellular Pharmacology**
  - John Tran
  - Hilda Hernandez-Barry
  - Hannah Chi
  - Gawon Shin
  - Phillip Chu
  - Neha Srikumar
  - William Sawyer
  - Aarushi Grover
  - Siao Ping Tsai
  - Kelly Loyet
  - Gloria Meng
  - Ryan Cook
  - Zhengmao Ye
  - Jerry Wang
  - Yichin Liu
  - Mercedesz Balazs
  - Margaret Porter-Scott
- **Antibody Engineering**
  - Nick Agard
  - Greg Lazar
- **Protein Chemistry**
  - Diego Ellerman
  - Rachana Ohri
  - Richard Vandlen
  - Adel ElSohly
  - Breanna Vollmar
- **Protein Analytical Chemistry**
  - Brian Roper
  - Thomas Niedringhaus
  - David Michels
- **PTPK**
  - Vittal Shivva
- **Molecular Oncology**
  - Minhong Yan
- **Translational Immunology**
  - Kristin Kallapur
- **AB Sciex**
  - Julia Sergunova
  - John Mazzanti
  - Dennis Price
  - Robert Swart
- **Protein Simple**
  - Adrian Papas
  - David Voehringer
  - Steven Le
  - Ed Chase
- **Agilent**
  - Dan Fedyk
  - Randy Bolger
  - Rachel Loui
  - Jose Meza
  - Stephanie Diamond
  - Brinker Gildersleeve



# Genentech

*A Member of the Roche Group*

# AFFINITY CAPTURE ON ASSAYMAP



# Comparison of various affinity capture approaches

		Pros	Cons
Bead based		<ul style="list-style-type: none"> <li>Compatible with dirty matrix; not prone to clogging</li> <li>Compatible with various elution methods</li> <li>Semi-automated</li> </ul>	<ul style="list-style-type: none"> <li>Bead pellets to bottom of well; incomplete bead removal</li> <li>Consumes more starting materials, reagents and labware</li> <li>Time-consuming</li> </ul>
Plate based		<ul style="list-style-type: none"> <li>Amenable to automation</li> <li>High throughput (&gt;&gt;1 plate)</li> <li>Fast</li> </ul>	<ul style="list-style-type: none"> <li>Well-to-well variability</li> <li>Method dev needed for on-plate degly and/or digestion</li> <li>Dead volume</li> </ul>
Tip based	MISA tip*	<ul style="list-style-type: none"> <li>Amenable to automation</li> <li>Fast</li> <li>Ease of use</li> </ul>	<ul style="list-style-type: none"> <li>Tip binding capacity</li> <li>Prone to introducing bubbles</li> <li>Requires custom automation</li> <li>Not compatible with on-tip digestion</li> </ul>
	AssayMap	<ul style="list-style-type: none"> <li>Automated</li> <li>Fast (1-2 plates)</li> <li>Ease of use</li> <li>Highly veritable utilities</li> </ul>	<ul style="list-style-type: none"> <li>Temperature control (&gt;37°C)</li> <li>Tips are expensive consumables (reusable after testing)</li> <li>Integrability with custom automation</li> </ul>