

6th YSS EBF

Determination of thoriumconjugated antibodies from plasma by different LC-MS technologies

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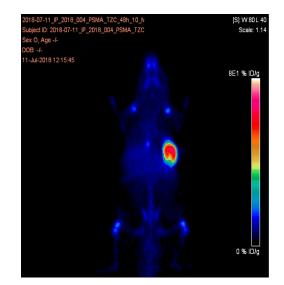
<u>Terence Hetzel</u>, Daniel Bochmann, Christoph Rolke, Mark Jean Gnoth

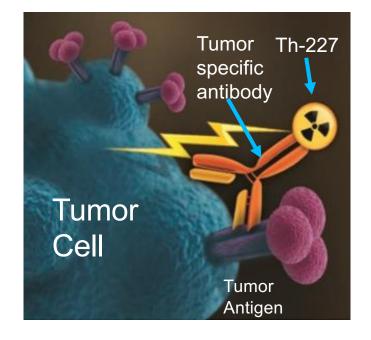


Introduction to thorium-conjugated antibody

Principle of Targeted Thorium-227 Conjugate (TTC's)

- // Combination of an antibody and warhead like Antibody Drug Conjugate (ADC)
- // TTC's: Antibody covalently linked to a chelator which contains an alpha emitting nuclide
- // The released alpha particle is believed to induce DNA breaks in cancer cells and may lead to cell death
- // New treatment option for cancer patients



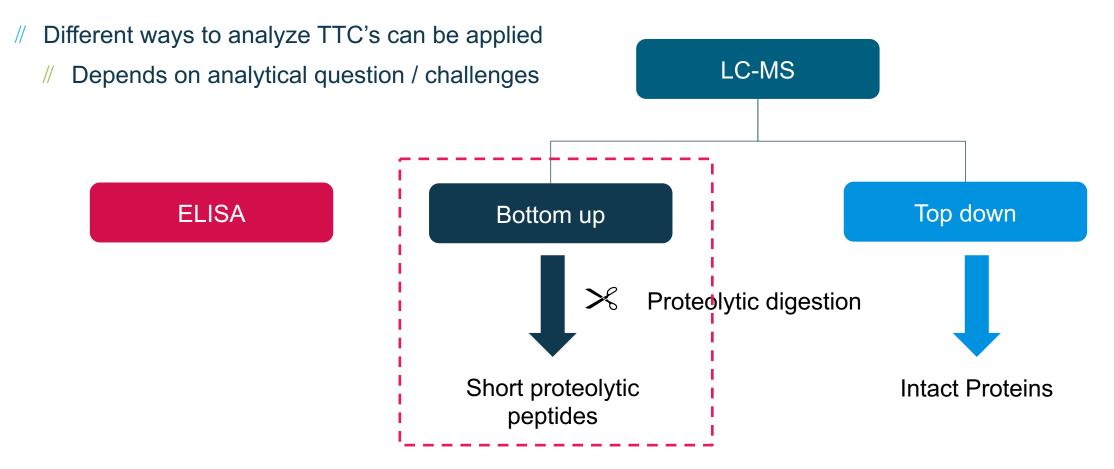


Which analytical methodologies can be applied for the analysis?

BAYER



Ways to analyze antibodies

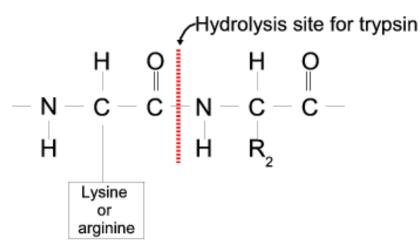


Different case studies: Comparison of ELISA and LC-MS results – gain of additional information by MS?



Bottom-Up – proteolytic digestion

- // Trypsin is the most commonly used proteases
- // Cleaves at arginine (R) and lysine (K)
- // Example for one letter code peptide sequence

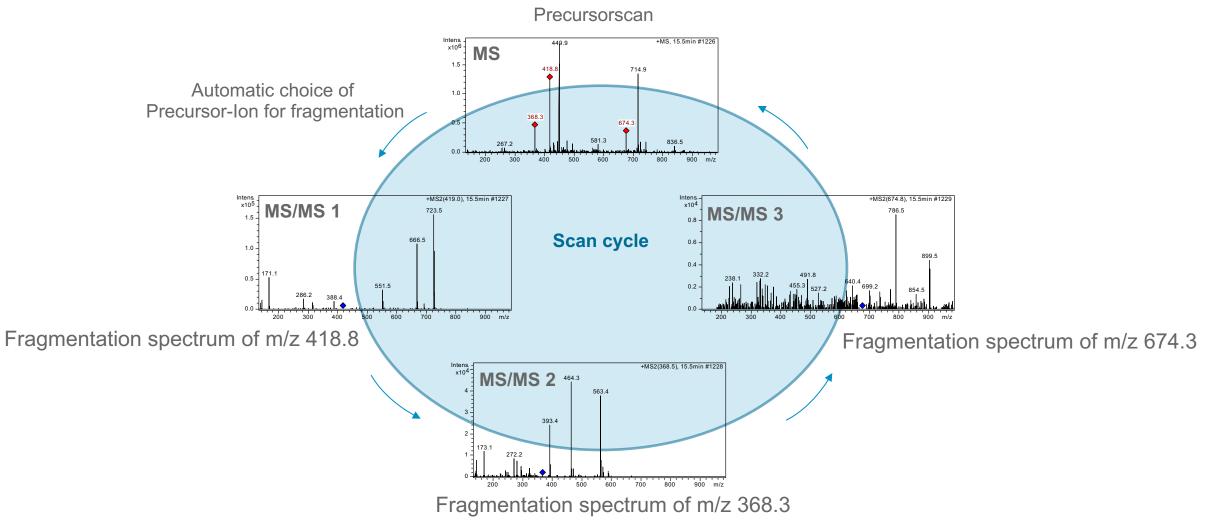


 $\label{eq:constraint} ... IYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSR ... \\ \begin{matrix} \chi & \chi & \chi \\ \end{matrix}$ IYPTNGYTR YADSVKGR FTISADTSK NTAYLQMNSLR AEDTAVYYCSR

- // When analyzing peptides by LC-MS
 - // In silico digestion via e.g. Skyline
 - // Information dependent acquisition (IDA)



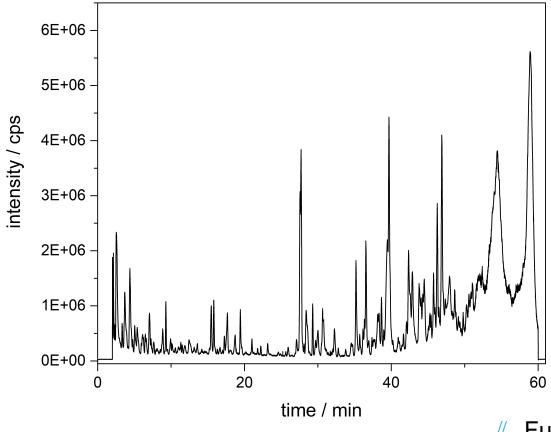
Principle of Information Dependant Acquisition (IDA)

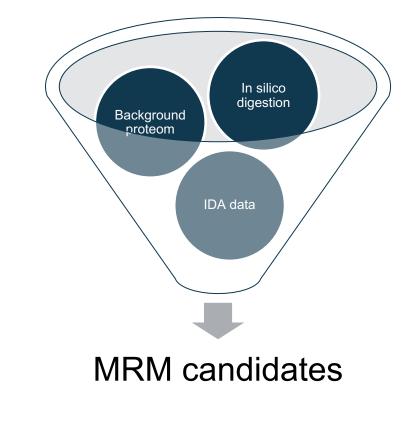




TIC from IDA run

// Tryptic digest from spiked monkey plasma

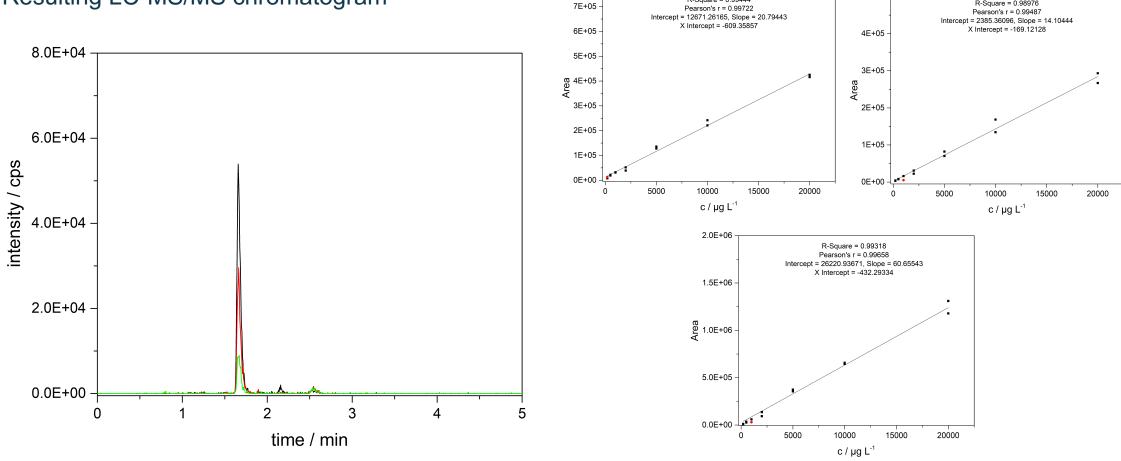




// Further selectivity increase by using immunoprecipitation



Resulting LC-MS/MS chromatogram



5E+05

R-Square = 0.98976

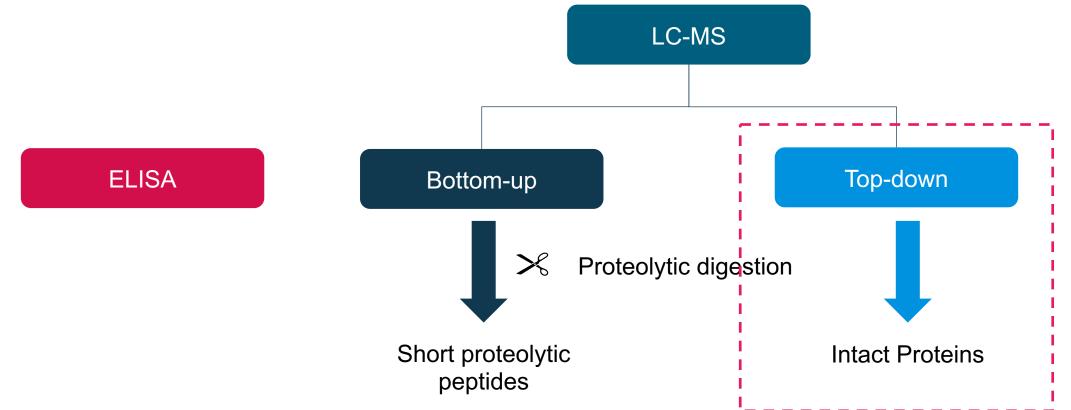
R-Square = 0.99444

- Calibration using a working range of 200 20000 µg/L
- At least 2 different peptides with \geq 2 mass transitions

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- // Different ways to analyze TTC's can be applied
 - // Depends on analytical question / challenges





Analysis of intact biomolecules

Challenges

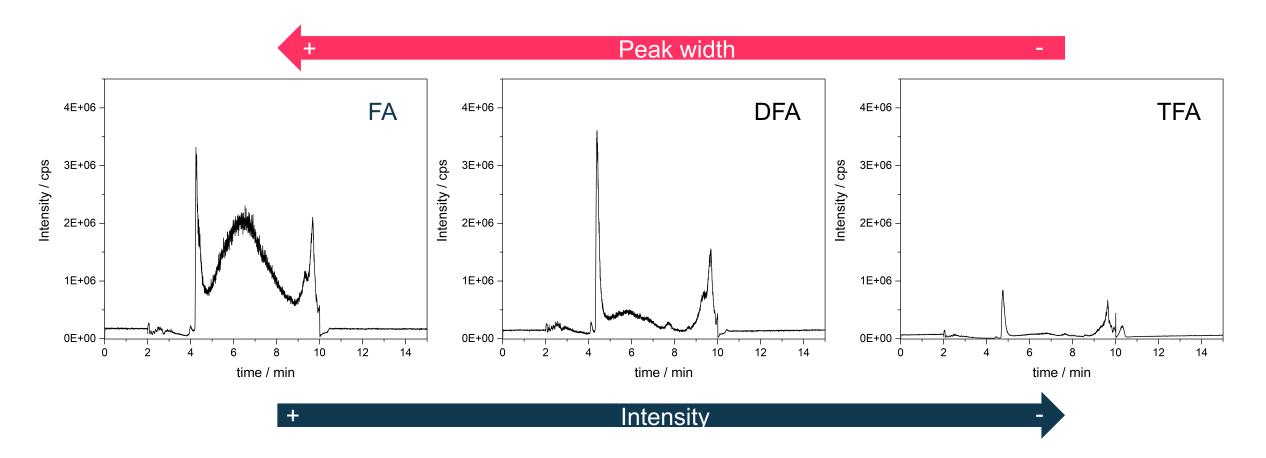
- // Secondary interactions between the analyte and stationary phase when using conventional phase material
- // Broad charge state distribution (up to more than 50 charges)

Possible solutions

- // State-of-the-art biocompatible chromatographic columns
- // Use of trifluoroacetic acid (TFA)
- // Elevated column temperatures up to 90°C



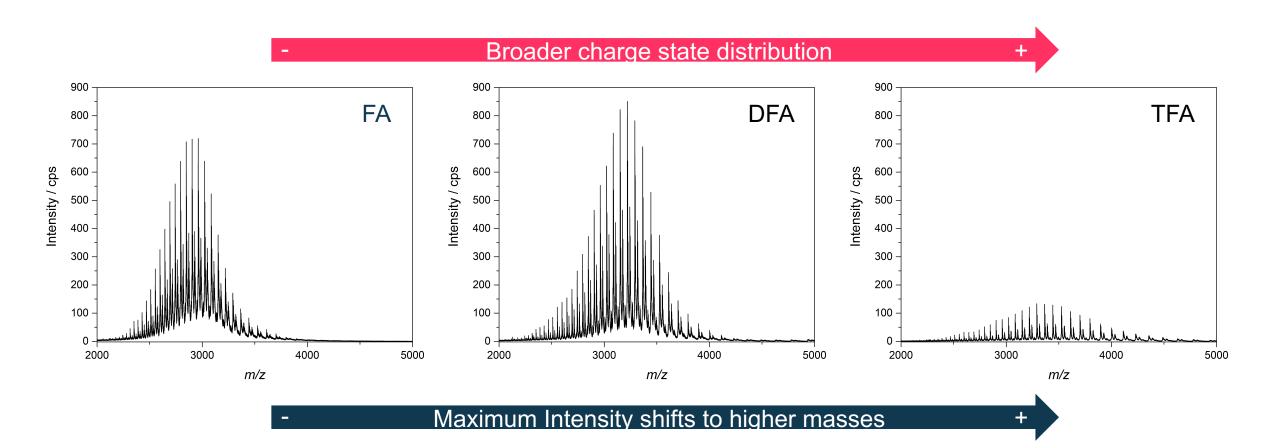
Separation on a C4 column



DFA = difluoroacetic acid

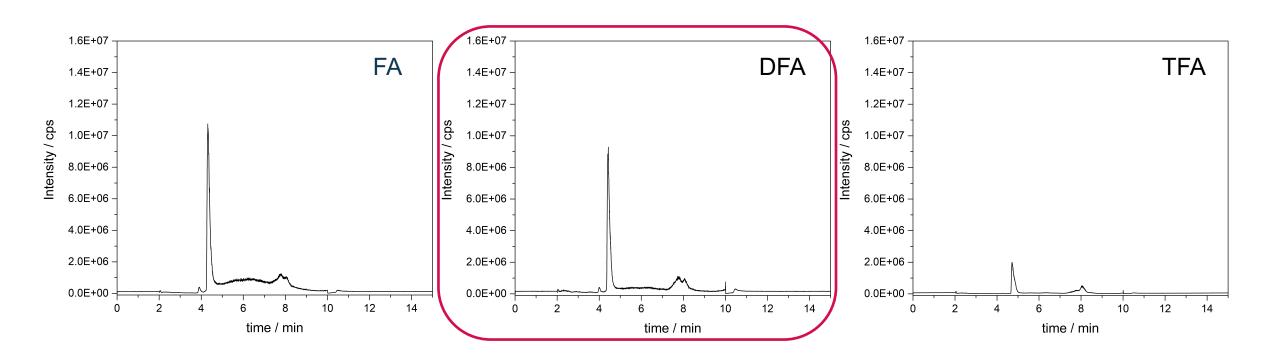


Influence on charge state distribution



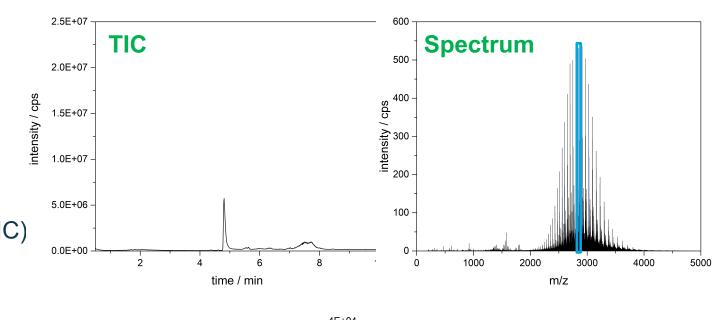


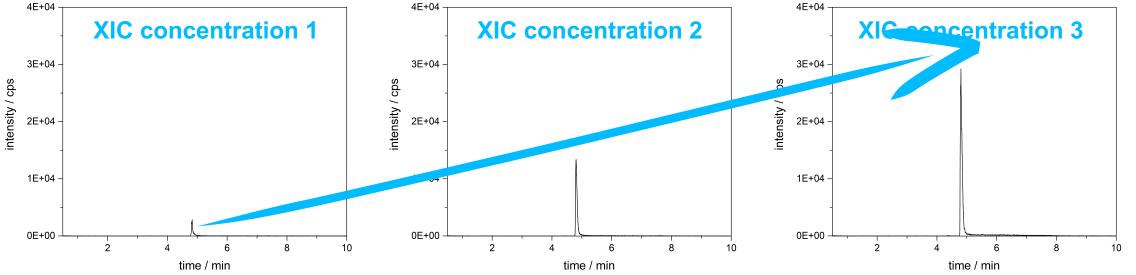
Separation on a Polyphenyl column



Top Down

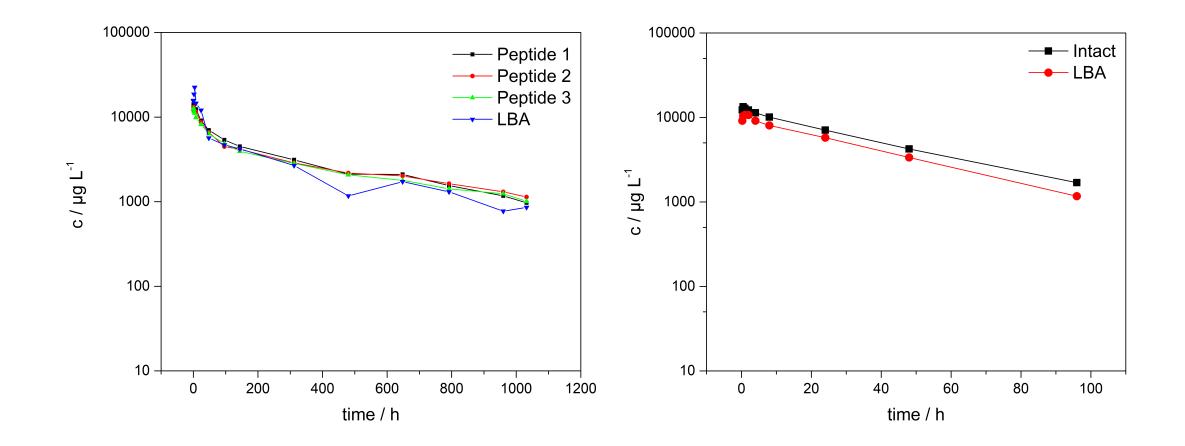
- // Top-down quantification
- // Check spectrum for a suitable mass
- // Use of extracted ion chromatogram (XIC)







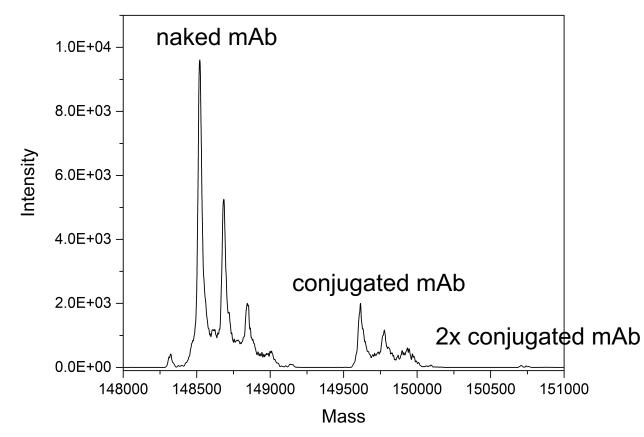
Comparison ELISA, Bottom-Up and Top-Down approach





Benefits of Top-down approach – Why using HRMS?

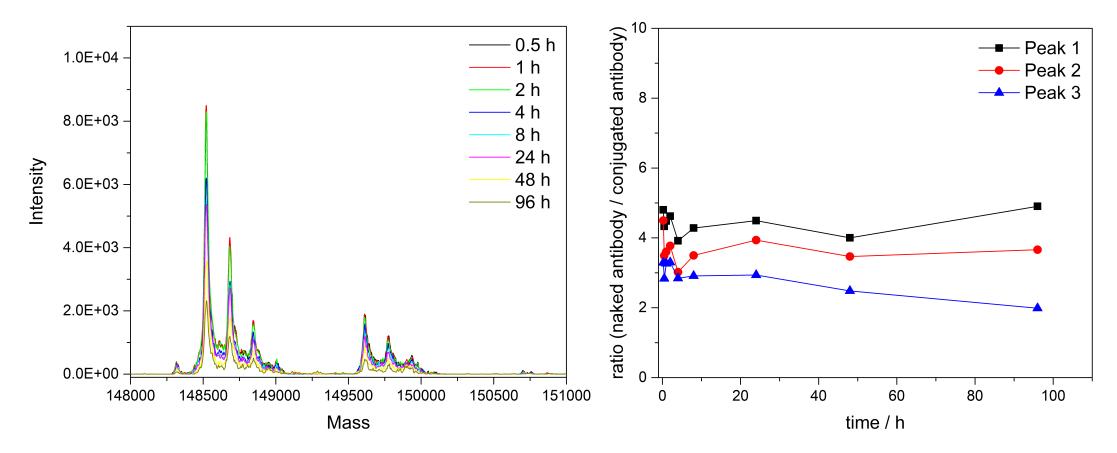
- // Deconvoluted mass of ",naked" and ",conjugated" antibody
- // Selectivity advantages





Benefits of Top-down approach – Why using HRMS?

// Deconvoluted mass of naked and conjugated antibody over time (0.5h – 96h after dosing)





Conclusion

Results and future steps

// Comparable results using all techniques!

- // Each technique has its advantages
- // Depends on analytical question / strategy which technique should be used
- // General advantages of mass spectrometry compared to LBA
 - // Selectivity!
 - // Mass information is available at any time
- // Possible future optimization for Top-Down approach
 - // Use of deconvoluted signals for data analysis instead of using extracted ion chromatogram (XIC)
 - // Use of miniaturized separation technology like nano- and/or micro-LC
 - // In-house evaluation is ongoing



Thank you!

