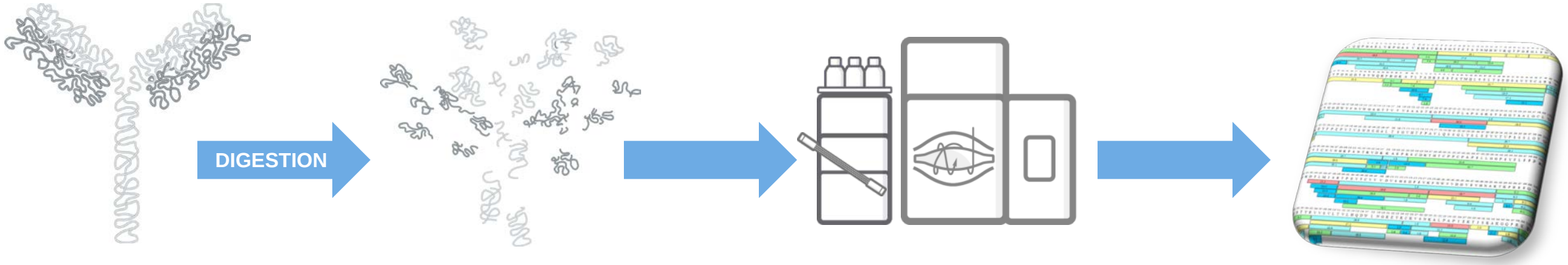
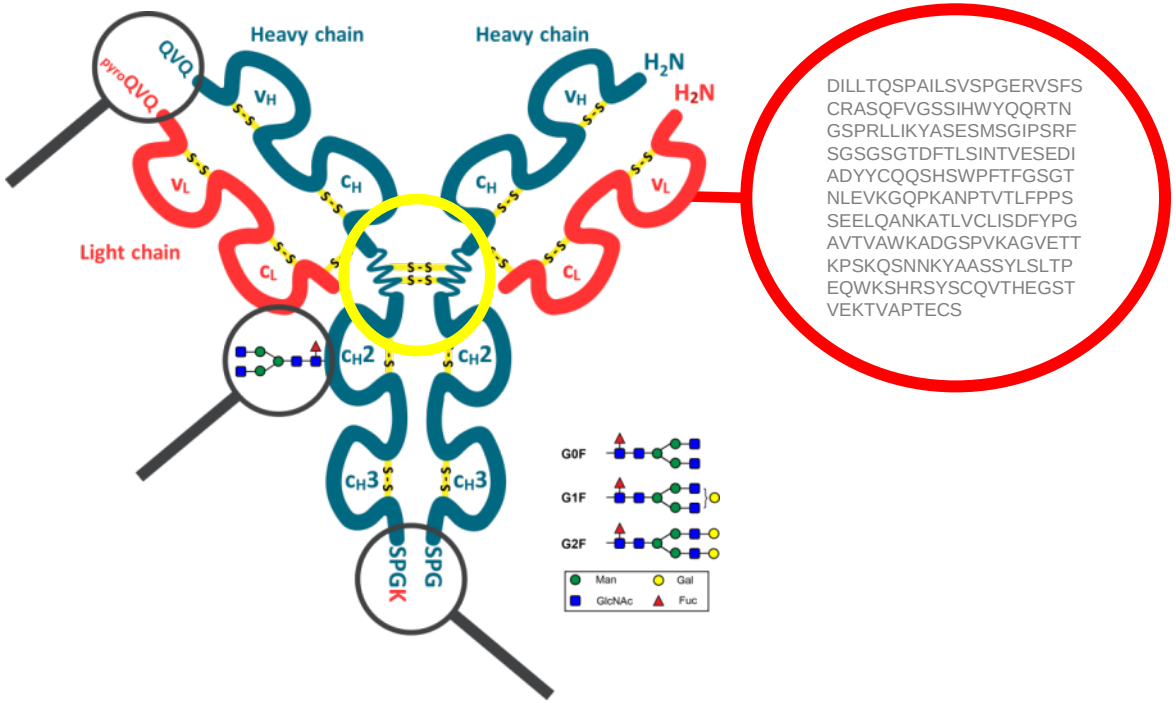
ThermoFisher SCIENTIFIC

Upgrade Your Maps:
New, rapid and reproducible peptide mapping workflows

Rowan Moore, PhD
Pharma & BioPharma Marketing Manager

Why Peptide Mapping?

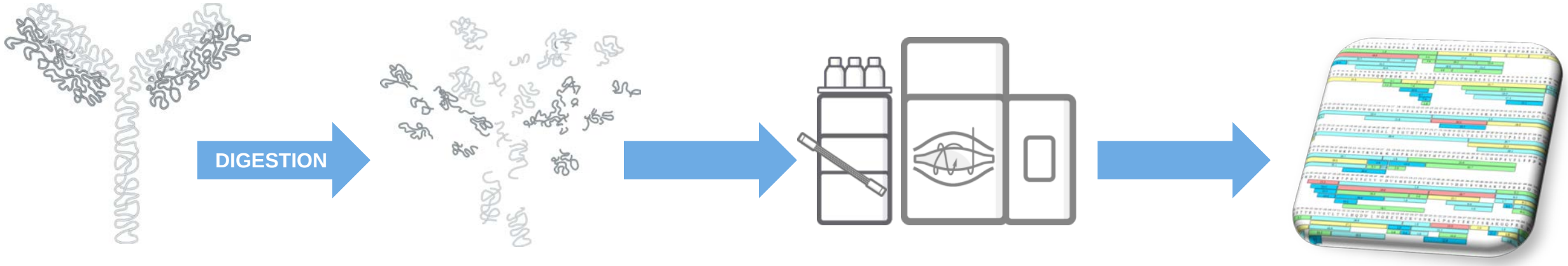




DILLTQSPAILSVSPGERVSFS
CRASQFVGSSIHWYQQRTN
GSPRLLIKYASESMSGIPSRF
SGSGSGTDFTLSINTVESEDI
ADYYCQQSHSWPFTFGSGT
NLEVKGQPKANPTVTLFPPS
SEELQANKATLVCLISDFYPG
AVTVAWKADGSPVKAGVETT
KPSKQSNNKYAASSYLSLTP
EQWKSHRSYSCQVTHEGST
VEKTVAPTECS

ThermoFisher SCIENTIFIC

Why Peptide Mapping?



Identity & Purity | Comparability | Quantitation | Lot Release | Regulatory

ThermoFisher SCIENTIFIC

Upgrade Your Maps with a Complete Peptide Mapping Solution

- **Full workflow solution**
- **Robust and reliable**
- **Fast and reproducible**
- **Easy and convenient**
- **Gives you:**
  - *Sequence verification*
  - *Modifications analysis*
  - *Sequence variants*
  - *Relative abundance quantification*

Why Upgrade Your Maps?

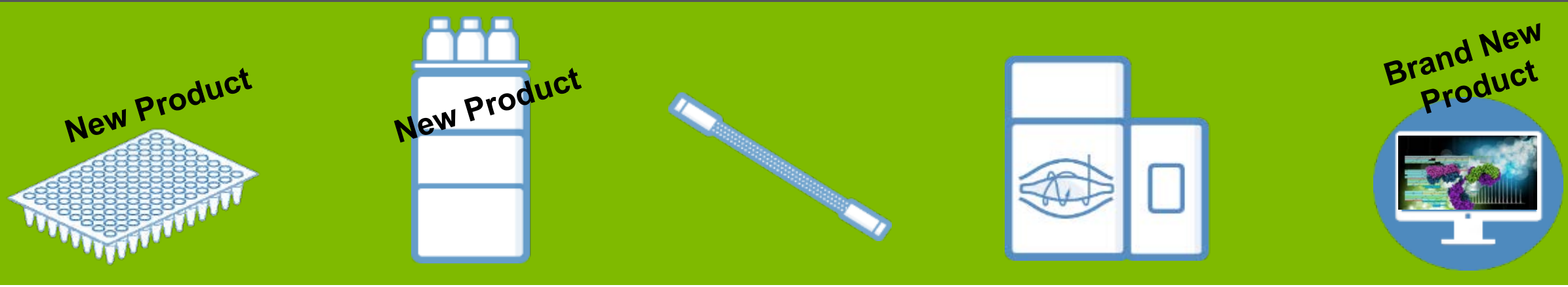
What will I gain if I upgrade my maps?

Sample preparation, separation, MS detection & data analysis of proteins.

Confirmed amino acid sequence with 100% coverage, identify and quantify modifications, identify variants.

Most Important: A simpler life! Less training required, results within a few hours.

Upgrade Your Maps: Our Workflow Solution



Thermo Scientific™ **SMART Digest™ Kits** offers extremely reproducible and rapid protein digestion

Thermo Scientific™ **Vanquish™ Flex UHPLC Systems** are engineered for high resolution, reproducible peptide separations

Thermo Scientific™ **Acclaim™ VANQUISH™ C18 column** is the perfect column choice to ensure sharp peaks during peptide mapping

Thermo Scientific™ **Q Exactive™ Hybrid Quadrupole-Orbitrap™ mass spectrometers** are the gold standard for accurate mass measurements

Thermo Scientific™ **BioPharma Finder™ mass informatics platform** is the perfect software tool for peptide identification and sequence mapping

Upgrade your Maps: Our Workflow Solution

SMART Digest Kits

Achieve reproducible protein digestion

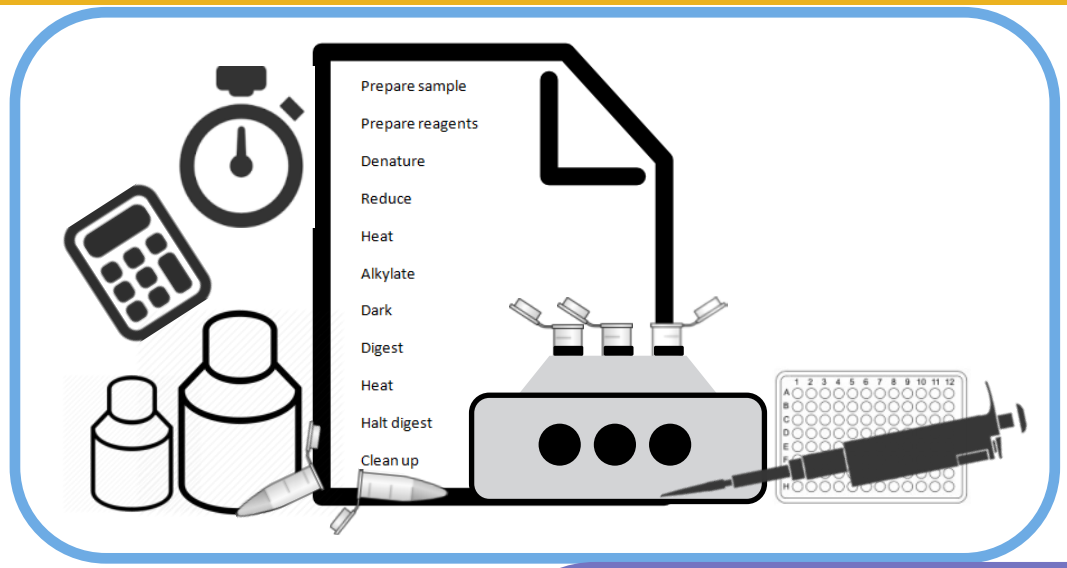
- within minutes

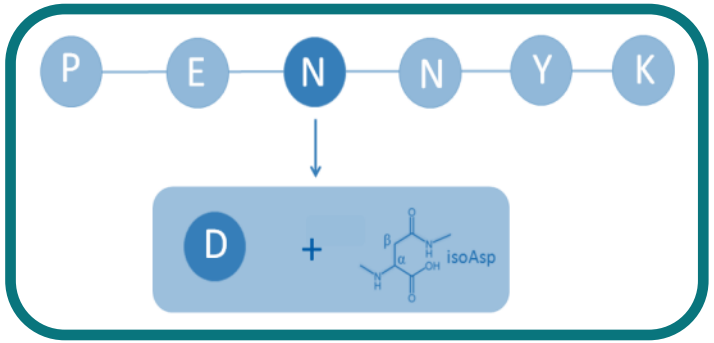
- with a simple 3-step protocol

ThermoFisher SCIENTIFIC

What is the Problem with Protein Digestion?

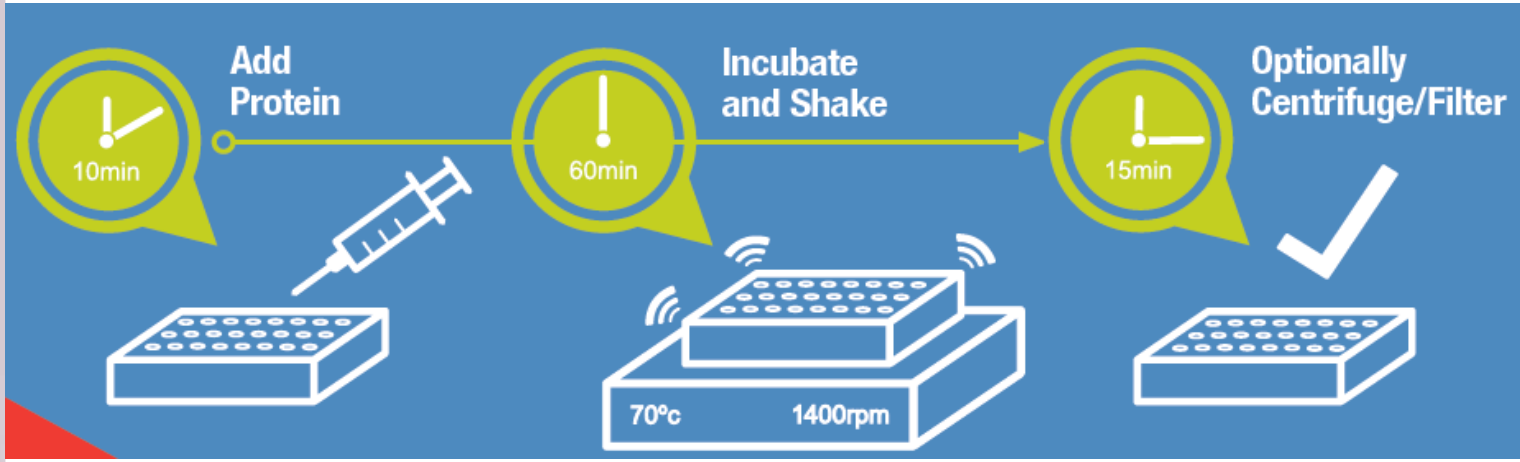
- Lengthy multi-step protocols
- Process-induced PTMs
- Reproducibility
- Throughput/speed
- Method development ease





ThermoFisher SCIENTIFIC

Thermo Scientific™ SMART Digest™ Kits



Denaturation

Digestion

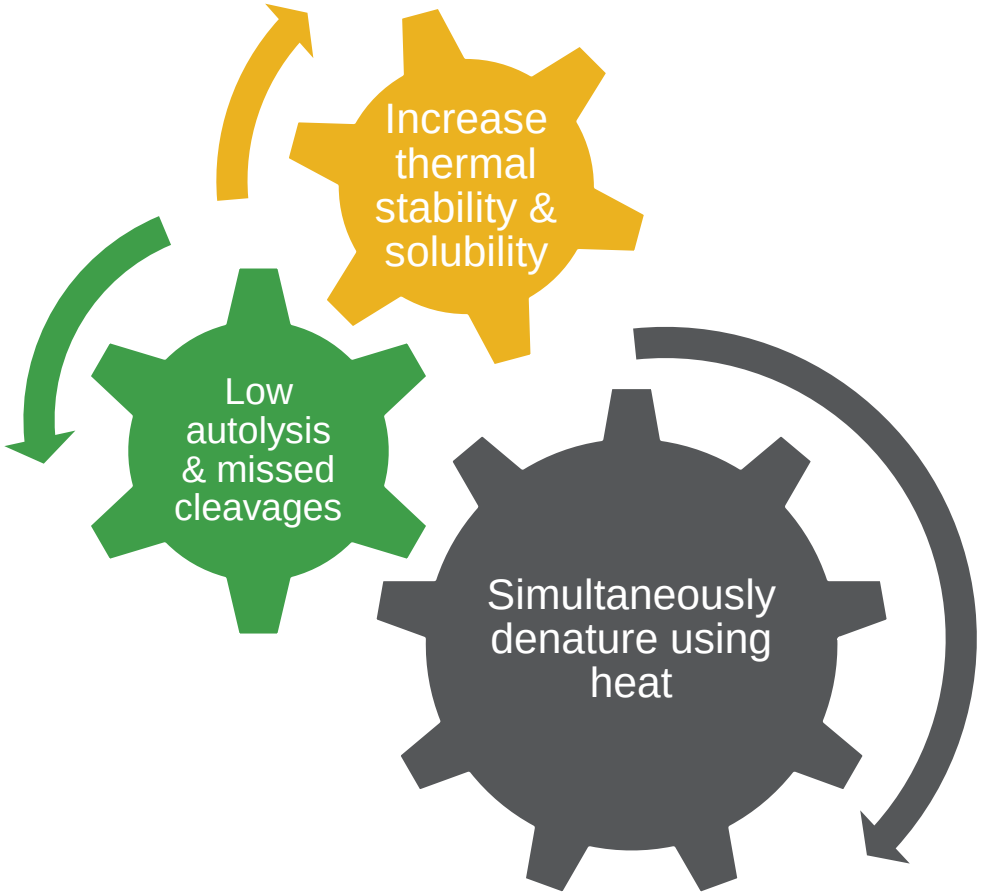
Clean up

ThermoFisher SCIENTIFIC

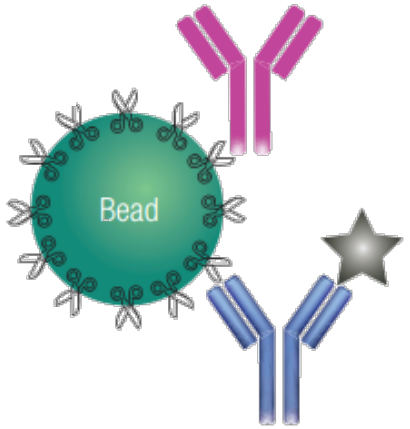
Let's Immobilize Trypsin…and Make it Heat Stable!

Enzyme | Solubility

Denaturation | Diffusion



Yellowstone



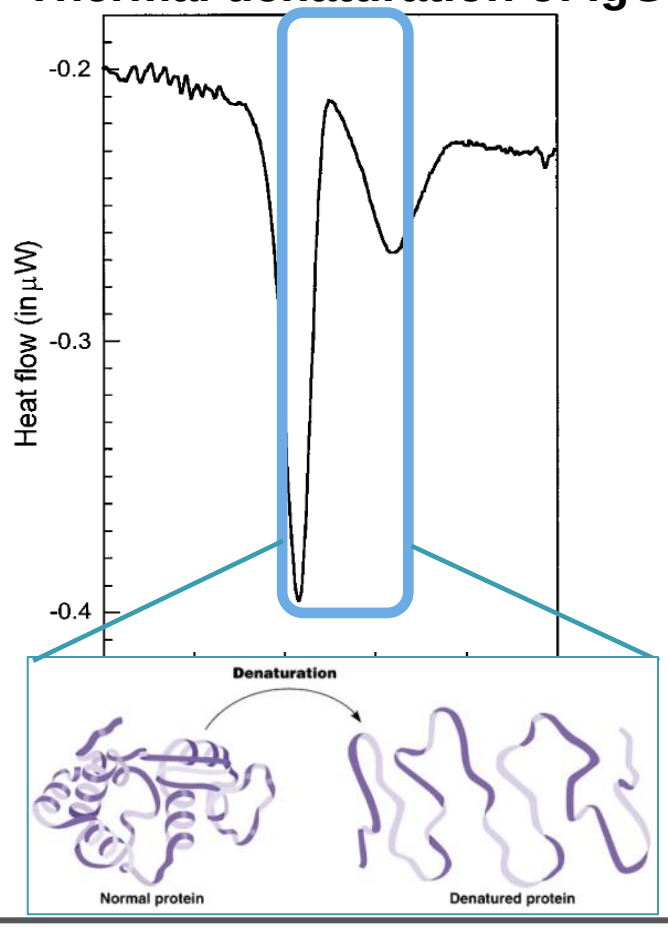
- **Save time**
  - Reagent prep/denaturation, reduction/alkylation
- **Simplify**
  - low autolysis
- **Increase sensitivity**
- **Increase robustness**
  - Stable, reproducible activity

Let's Optimize Heat Denaturation!

Enzyme | Solubility

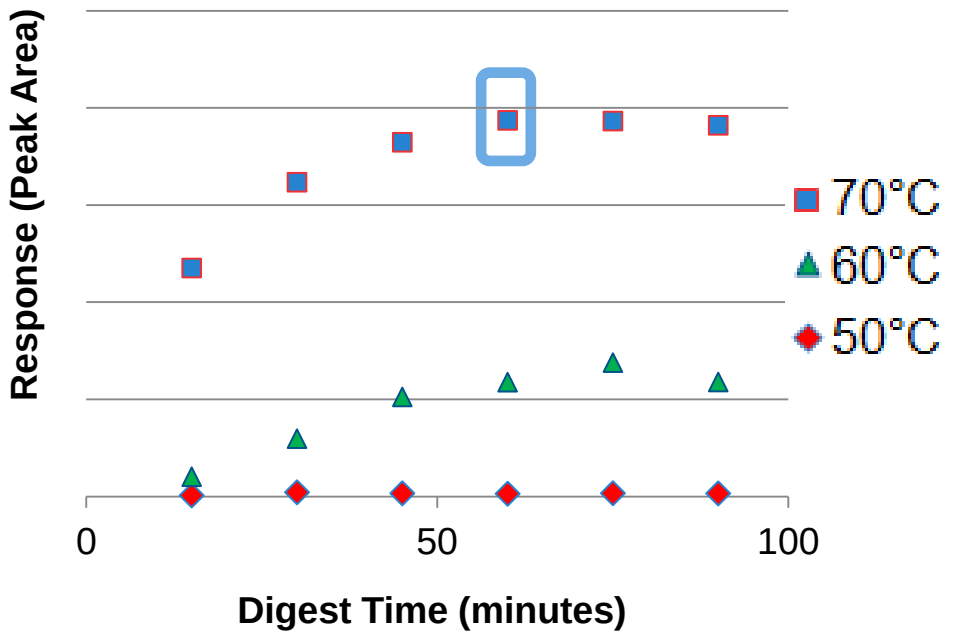
Denaturation | Diffusion

Thermal denaturation of IgG



Native IgG Digest Profile

monitoring VVSVLTVLHQDWLNGK



394 Biophysical Journal Volume 78 January 2000 394–404

The Thermal Stability of Immunoglobulin: Unfolding and Aggregation of a Multi-Domain Protein

Anal. Chem. **2000,** *72,* 2667–2670

Thermal Denaturation: A Useful Technique in Peptide Mass Mapping

ThermoFisher SCIENTIFIC

New Application Note on SMART Digest: No. 1159

thermoscientific

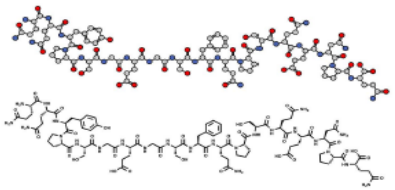
APPLICATION NOTE

No. 1159

SMART Digest compared to classic in-solution digestion of rituximab for in-depth peptide mapping characterization

Authors: Martin Samonig[1], Alexander Schwahn[2], Ken Cook[3], Mike Oliver[4], and Remco Swart[1]

[1]Thermo Fisher Scientific, Germering, Germany; [2]Thermo Fisher Scientific, Basel, Switzerland; [3]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [4]Thermo Fisher Scientific, Runcorn, United Kingdom



Key words
SMART Digest, tryptic digestion, in-solution protein digestion, monoclonal antibody, mAb, Vanquish, reversed phase, mass spectrometry, Q Exactive, Orbitrap, biopharmaceutical, biomolecules, peptide mapping

Goal
To compare the results achieved by using the newly developed Thermo Scientific™ SMART Digest™ kit to those obtained from classic in-solution protein digestion methods, focusing on protein sequence coverage and identified post-translational modifications (PTMs), including deamidation, oxidation, and glycosylation. A Thermo Scientific™ Acclaim™ VANQUISH™ C18 column with conventional water/acetonitrile-based gradients and the Thermo Scientific™ Vanquish™ Flex UHPLC system were used for separation in combination with the Thermo Scientific™ Q Exactive™ HF Hybrid Quadrupole-Orbitrap™ mass spectrometer.

Introduction
Peptide mapping is a common technique in the biopharmaceutical industry to characterize monoclonal antibodies (mAbs) for the determination of product identity and stability. Many conventional sample preparation methods are time consuming with digestion times of several hours and can introduce modifications such as deamidation, oxidation, and carbamylation.[1] In this study, two classic in-solution digestion approaches were compared to the recently developed SMART Digest kit method to quantify the extent of post-translational and chemical modifications of a therapeutic recombinant mAb. The critical requirements for each

ThermoFisher SCIENTIFIC

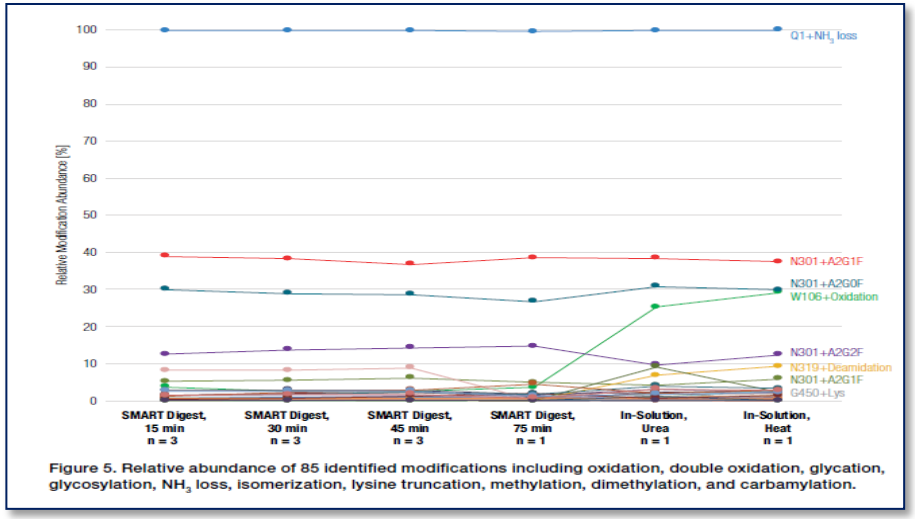


Figure 5. Relative abundance of 85 identified modifications including oxidation, double oxidation, glycation, glycosylation, NH_3 loss, isomerization, lysine truncation, methylation, dimethylation, and carbamylation.

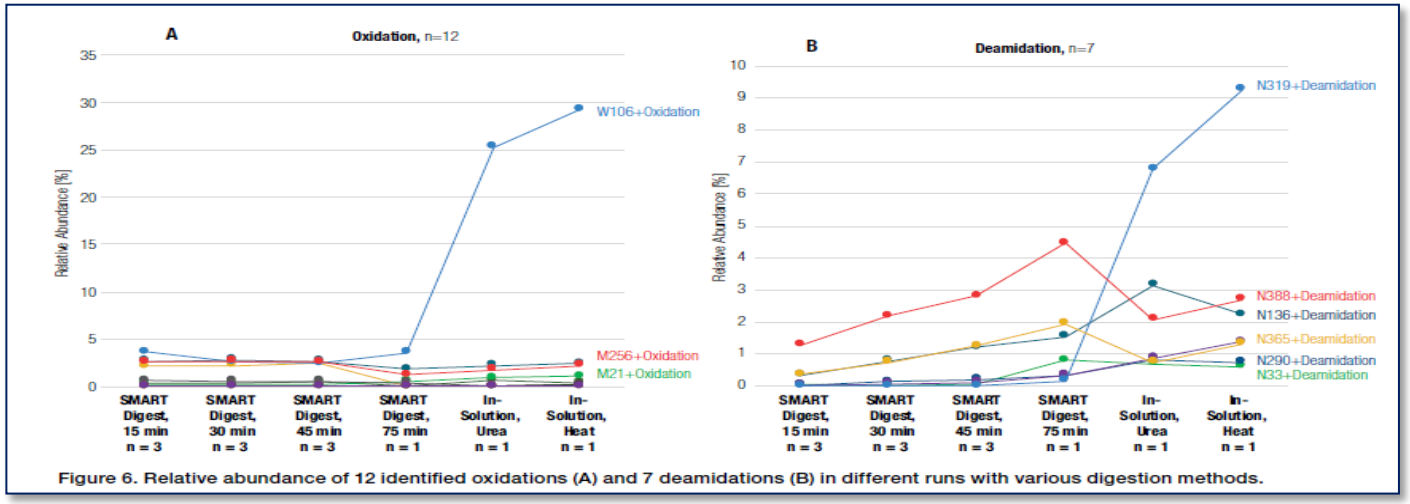


Figure 6. Relative abundance of 12 identified oxidations (A) and 7 deamidations (B) in different runs with various digestion methods.

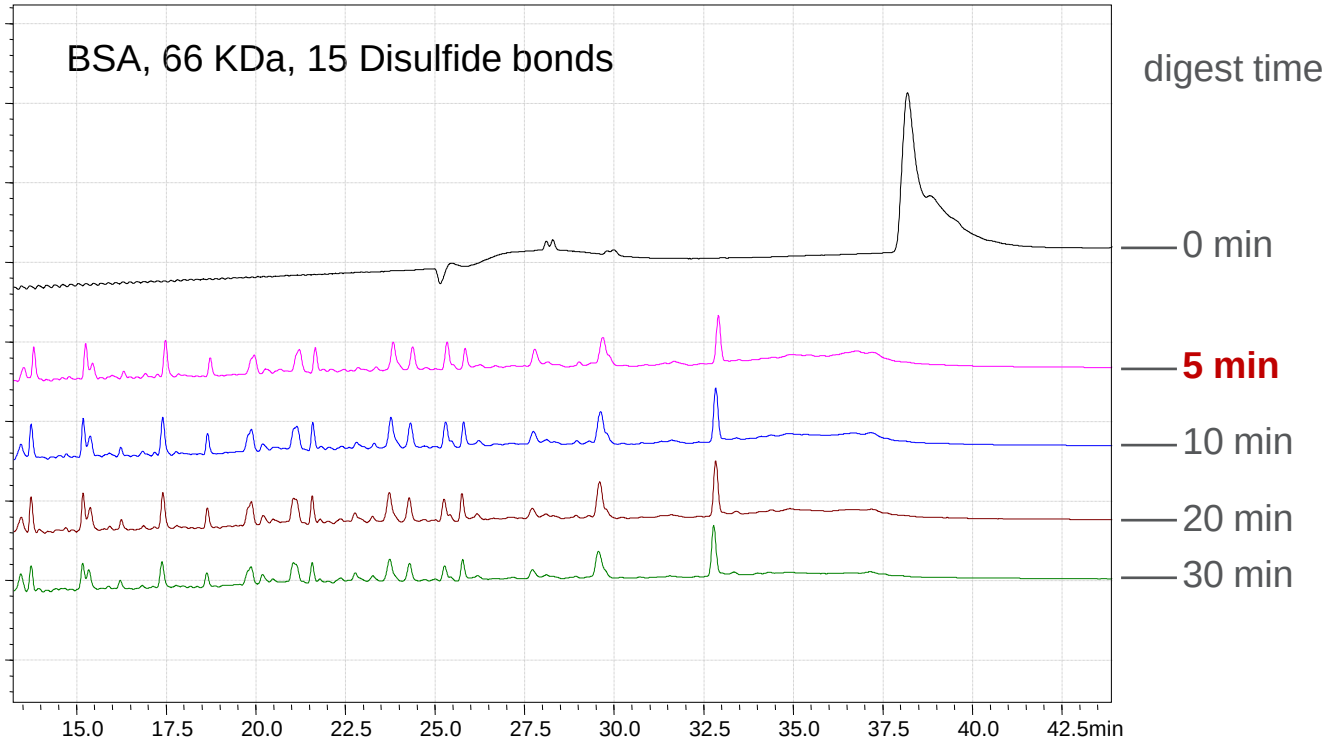
ThermoFisher SCIENTIFIC

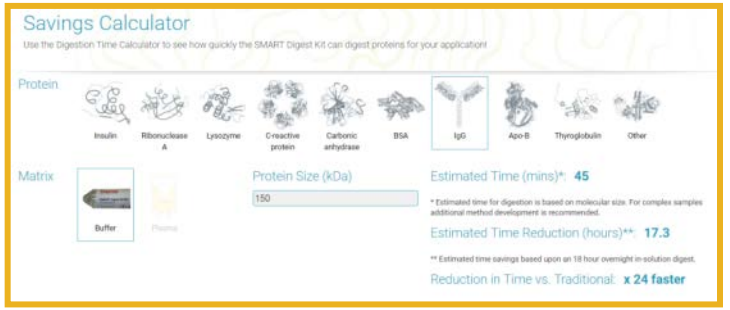
SMART Digest Kits: Complete Digestion in Minutes

Recommended digestion starting conditions for known proteins*	
Protein	**Digest Time (min)**
Insulin	4
BSA	< 5
Carbonic anhydrase	< 5
Lysozyme	< 5
Apo-B	30
IgG	45
IgG in 50 µL plasma	75
Ribonuclease A	150
Thyroglobulin	240
C-reactive protein	240

* 200 µL protein solution (100 µg/mL);
IgG in plasma: 17.5 µg/mL

Temperature: 70°C



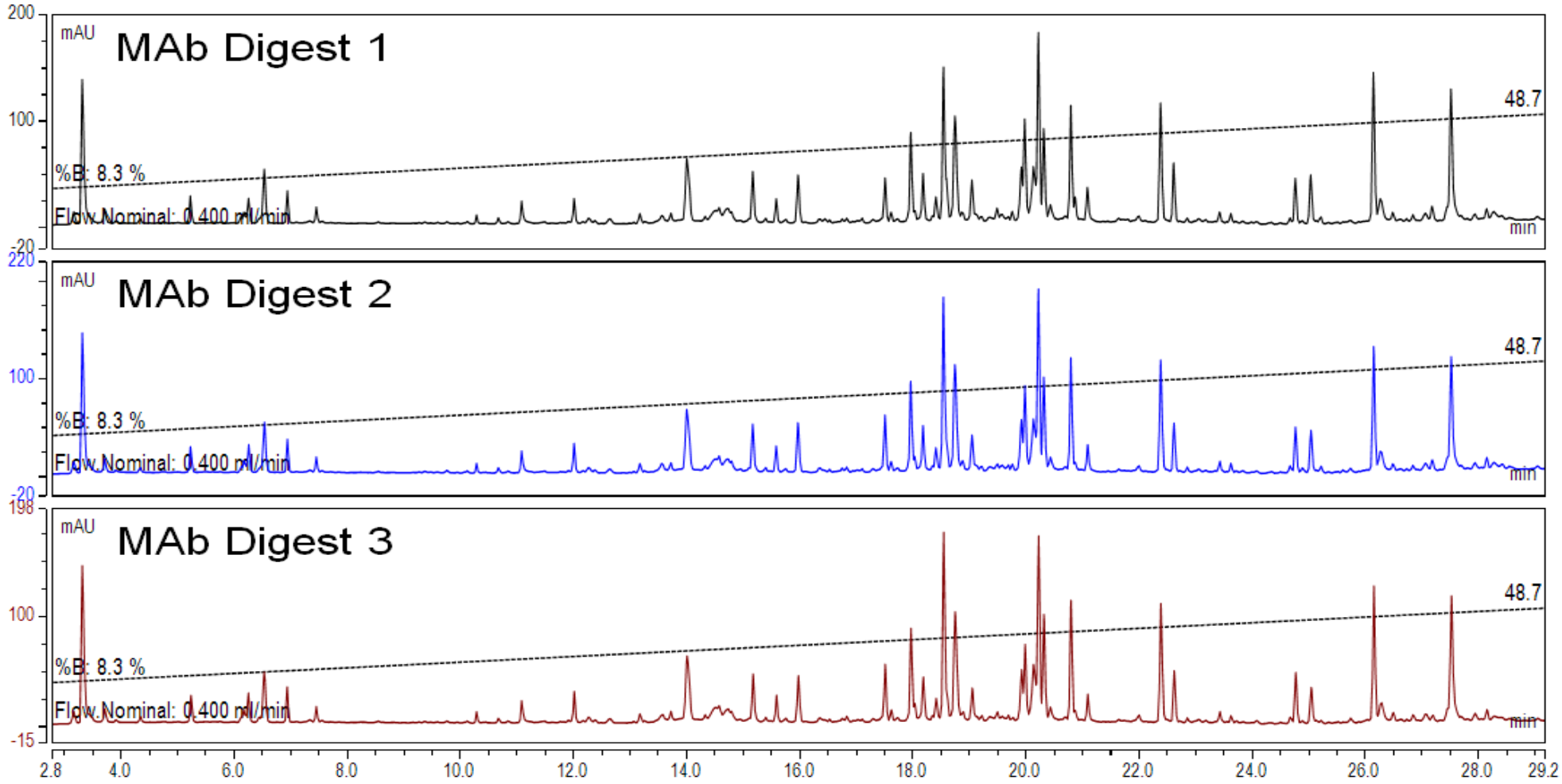


Discover the Savings Calculator:
www.thermofisher.com/upgradeyourmaps

ThermoFisher SCIENTIFIC

SMART Digest Kits: Outstanding Digestion Reproducibility

Repeatability of a monoclonal antibody SMART Digest Kits digestion



ThermoFisher SCIENTIFIC

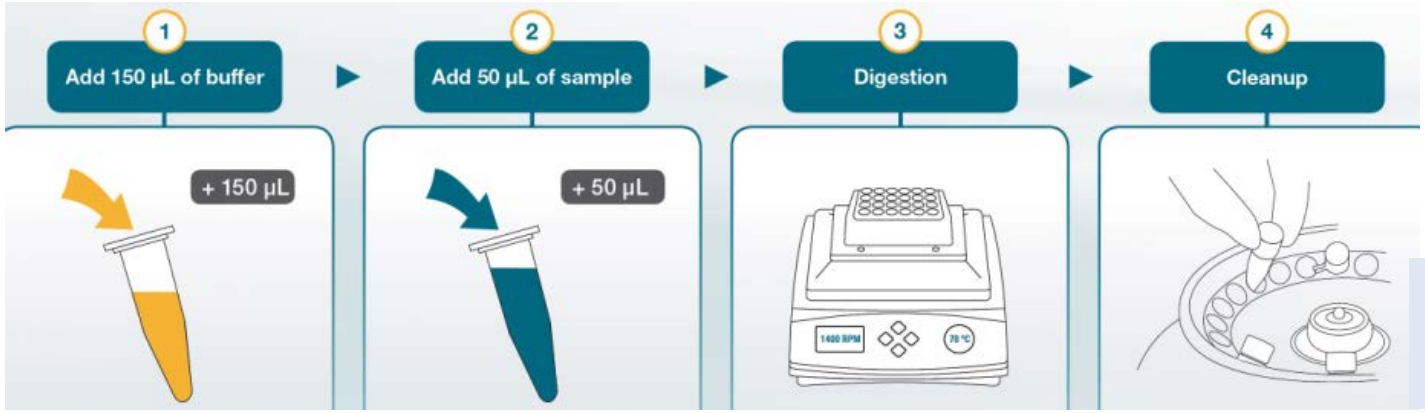
To Reduce, or Not to Reduce…and/or Alkylate

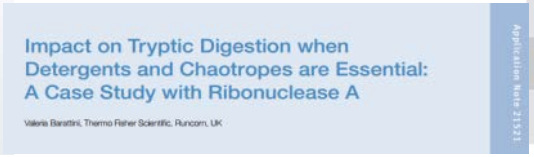
- I want 100 % sequence coverage - **maybe**
- I am quantifying my protein via surrogate peptide monitoring - **no**
- I am worried I may see scrambled disulphides/ my protein has free cysteines – **alkylate before**
- I want to know where my disulphides are! – **yes & no**
- My mass spectrometer won't acquire/is not optimized for higher mass peptides - **maybe**

Protein Digestion with SMART Digest Kits: Tips & Tricks

- How much protein to load? **200 pg - 3.5 mg**
- How long to digest my sample? **Start with the online calculator**
- What are the tubes and heater/shaker? **PCR tubes; heater/shaker *must* have a lid**
- I bet it won't be that simple. **It really is!**
- Will a quick spin will be enough to clean up? **Often, yes! Gel loader tips useful; filter/SPE for complex matrix; divert salts to waste**
- My protein is really difficult to denature- I always add detergents. **OGS has proved not to inhibit digest & led to improved digestion rate**

http://www.separatedbyexperience.com/smartdigest/





Recommended digestion starting conditions for known proteins*

Protein	Digest Time (min)
Insulin	4
BSA	< 5
Carbonic anhydrase	< 5
Lysozyme	< 5
Apo-B	30
IgG	45
IgG in 50 µL plasma	75
Ribonuclease A	150
Thyroglobulin	240
C-reactive protein	240

ThermoFisher SCIENTIFIC

Upgrade your Maps: Our Workflow Solution

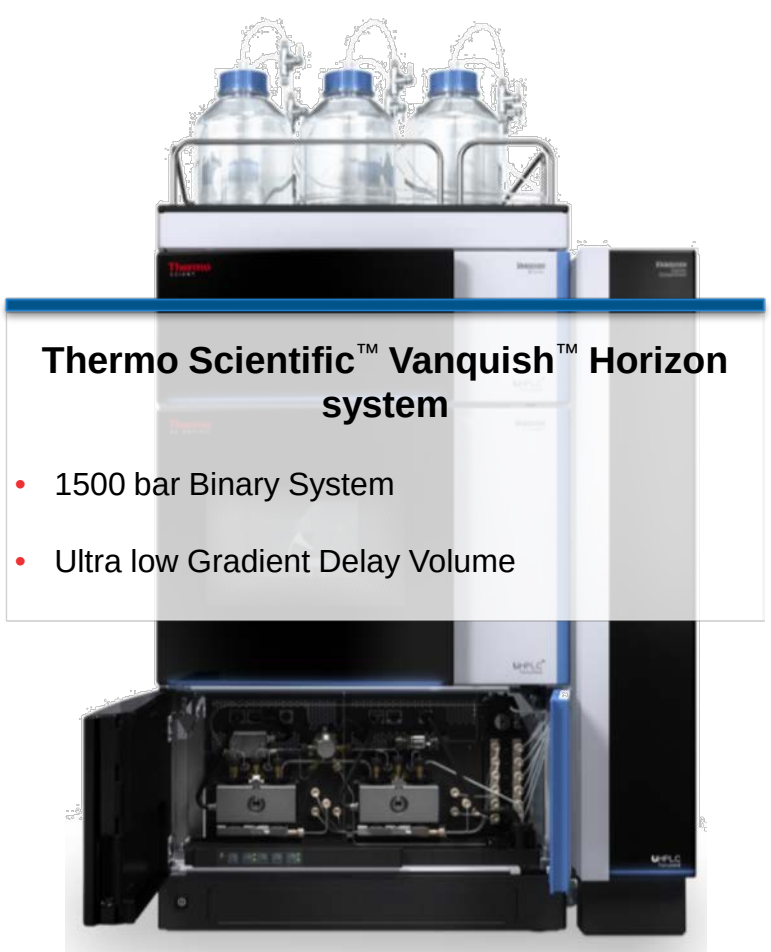
Vanquish UHPLC

Binary & Quaternary Biocompatible UHPLC Options

Acclaim Vanquish C18 Column

ThermoFisher SCIENTIFIC

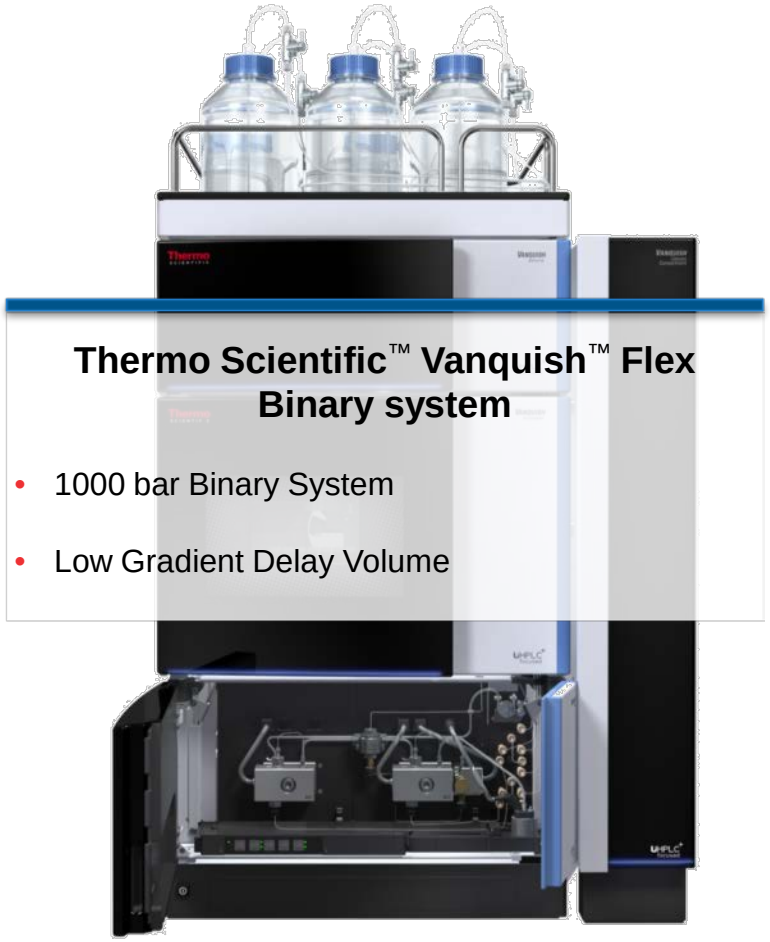
Vanquish Systems – Comparison



Thermo Scientific™ Vanquish™ Horizon system

- 1500 bar Binary System
- Ultra low Gradient Delay Volume

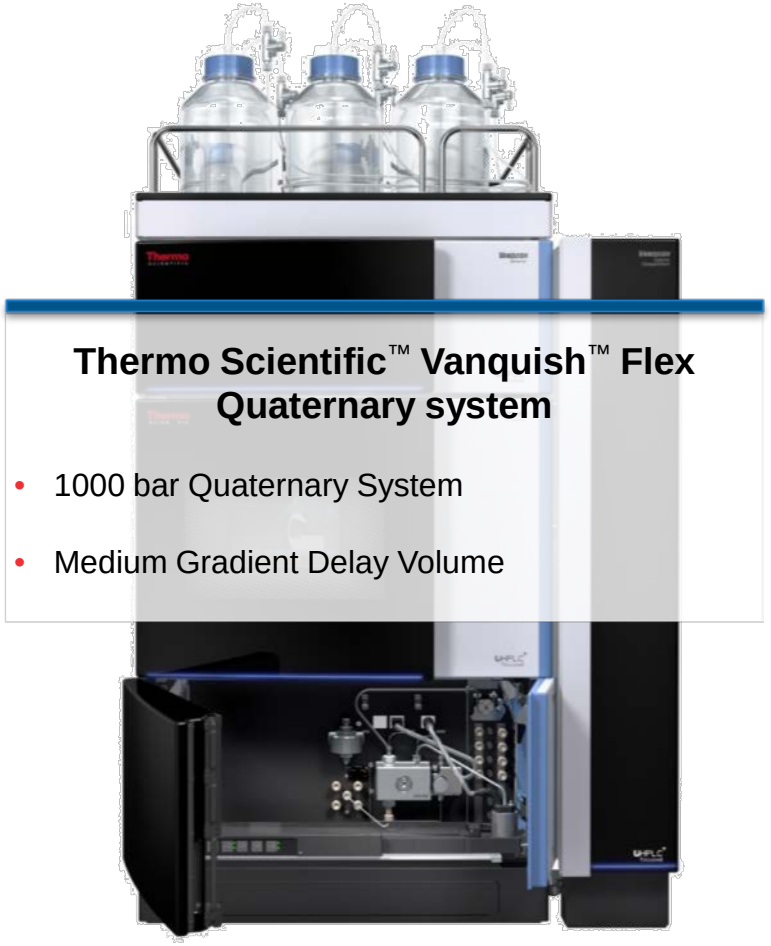
Highest performance for best separation or throughput



Thermo Scientific™ Vanquish™ Flex Binary system

- 1000 bar Binary System
- Low Gradient Delay Volume

Throughput for targeted UHPLC separations



Thermo Scientific™ Vanquish™ Flex Quaternary system

- 1000 bar Quaternary System
- Medium Gradient Delay Volume

UHPLC for resolution or method development

Vanquish Systems – Comparison

Vanquish Platform

- Improved retention time precision
- Biocompatible by default
- Increased sample capacity
- SmartInject sample pre-compression
- Improved sample cooling
- Multiple heating modes
- Active and passive pre-heating
- 4 detection options
- Platform-inherent robustness & maintenance features

Thermo Scientific™ Vanquish™ Horizon system

- 1500 bar Binary System
- Ultra low Gradient Delay Volume

Highest performance for best separation or throughput

Thermo Scientific™ Vanquish™ Flex Binary system

- 1000 bar Binary System
- Low Gradient Delay Volume

Throughput for targeted UHPLC separations

Thermo Scientific™ Vanquish™ Flex Quaternary system

- 1000 bar Quaternary System
- Medium Gradient Delay Volume

UHPLC for resolution or method development

Acclaim VANQUISH C18 Column, 2.1 x 250 mm

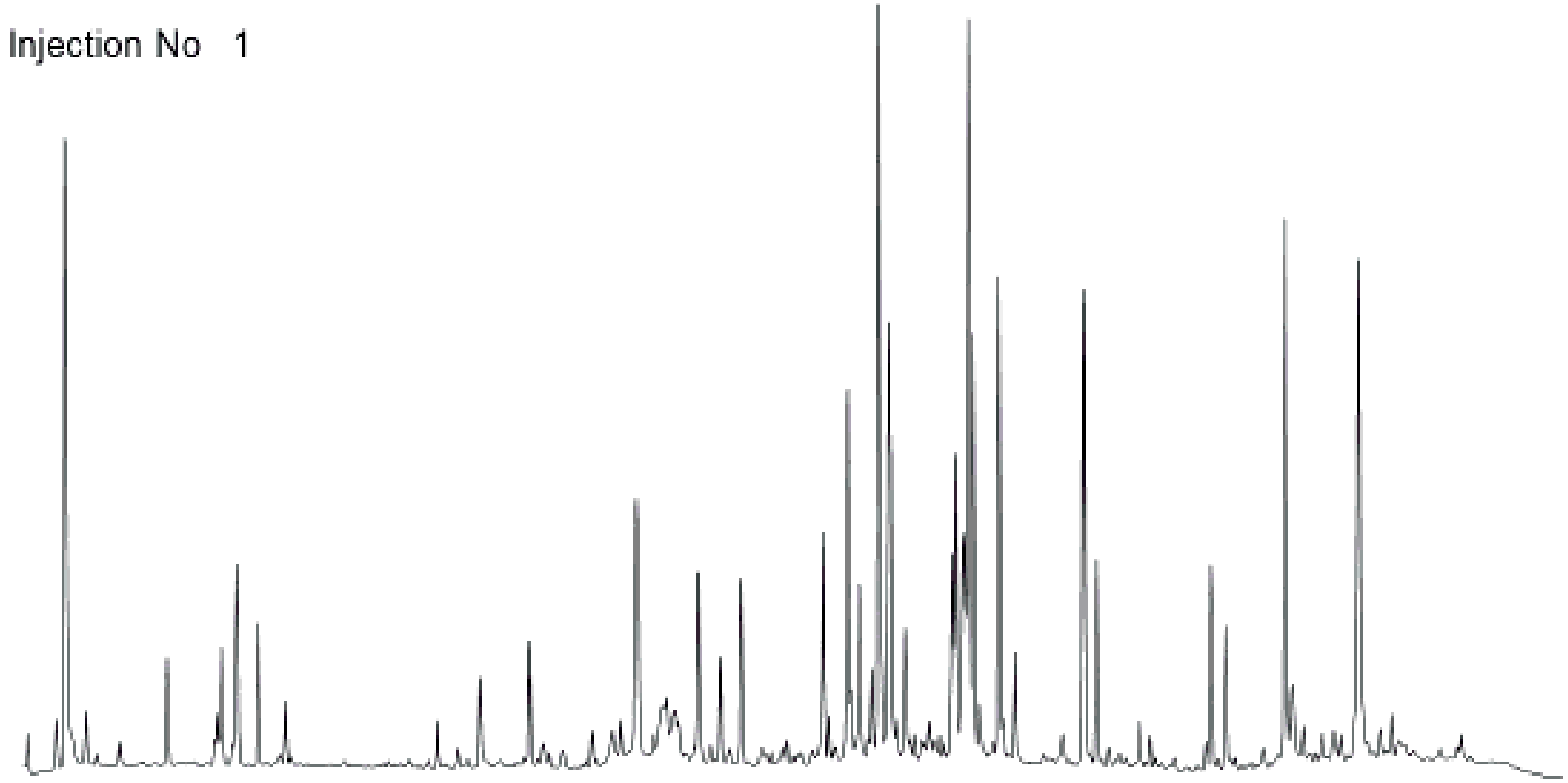
- High resolution peptide separations for increased protein identification
- High loadability for high sensitivity LC/MS
- Designed for TFA-free LC-MS, minimizing ion-suppression effects
- High column-to-column reproducibility
- 1500 bar Vanquish-compatible
- Robust design easy installation using Thermo Scientific™ Viper™ fingertight fittings

Viper™ fingertight fitting

ThermoFisher SCIENTIFIC

Vanquish UHPLC System: Retention Time Reproducibility

Retention time reproducibility of a peptide separation



Retention time Repeatability

peak #	RT (min)	RSD (%)
3	3.315	0.082
9	5.231	0.065
14	6.532	0.017
15	6.937	0.023
19	10.290	0.021
23	12.013	0.012
31	14.011	0.013
39	15.177	0.012
42	15.589	0.010
51	17.511	**0.007**
55	17.969	0.011
61	18.546	0.010
83	20.798	0.010
85	21.095	0.012
87	22.386	**0.009**
96	24.774	0.012
103	26.155	**0.009**
106	26.155	**0.009**
109	27.529	0.010

Overlay of 13 consecutive chromatographic runs of a peptide sample separated on an analytical Acclaim™ 120 C18 column and prepared from a mAb digested with the SMART™ Digest Kit.

Upgrade your Maps: Our Workflow Solution

BioPharma Finder

A single software platform for

- Top-Down & Bottom-Up analysis

- Dedicated to biotherapeutics

BioPharma Finder: Protein Deconvolution and Peptide Mapping

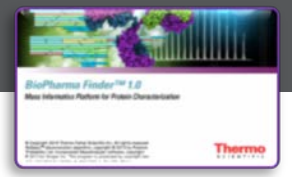
BioPharma Finder

- Intact protein analysis and peptide mapping in one package
- Peptide mapping of biotherapeutics and other recombinant proteins
- Supports all Orbitrap™ & ion-trap-based instruments

More confidence, more modifications, less time

ThermoFisher SCIENTIFIC

Data Analysis With BioPharma Finder – Peptide Mapping



Thermo BioPharma Finder 1.0

Thermo SCIENTIFIC BioPharma Finder

Help

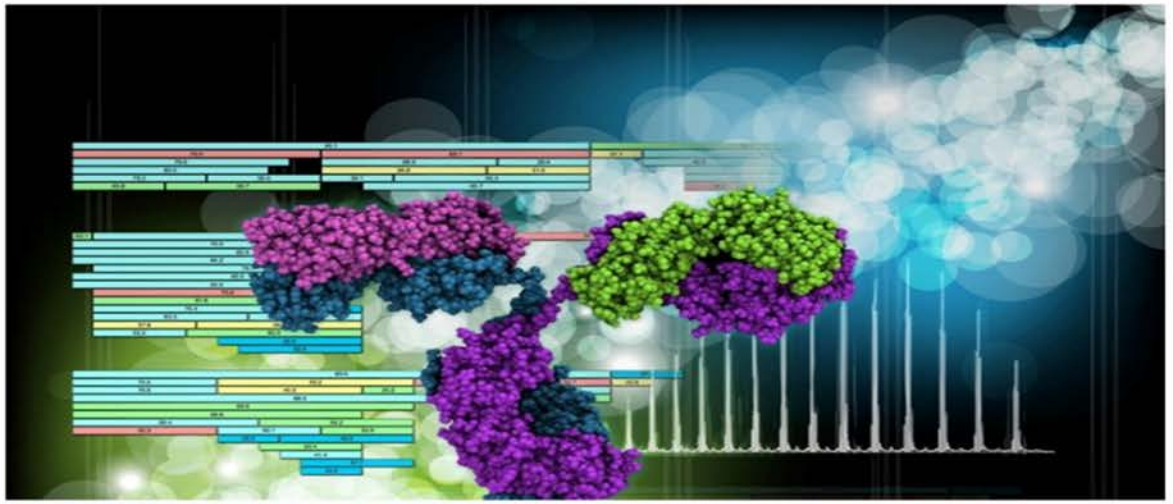
Home

Select an experiment type.

Experiment Types

- Protein Sequence Manager
- Peptide Mapping Analysis
- Intact Protein Analysis

A powerful integrated software solution for in-depth characterization of proteins. Thermo Fisher's BioPharma Finder™ software automates the analysis of LC-MS data for intact mass analysis and LC-MS/MS data for peptide mapping which includes identification and relative quantitation of Disulfide bonds, post-translational Modifications and Sequence Variants. Using the industry-leading, high-resolution, accurate-mass Thermo Scientific™ Orbitrap™ technology with BioPharma Finder software, the most accurate and confident PTM profiles and identifications can be achieved more quickly than ever before.

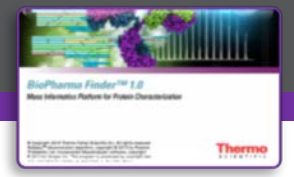


Peptide Mapping Analysis

Intact Protein Analysis

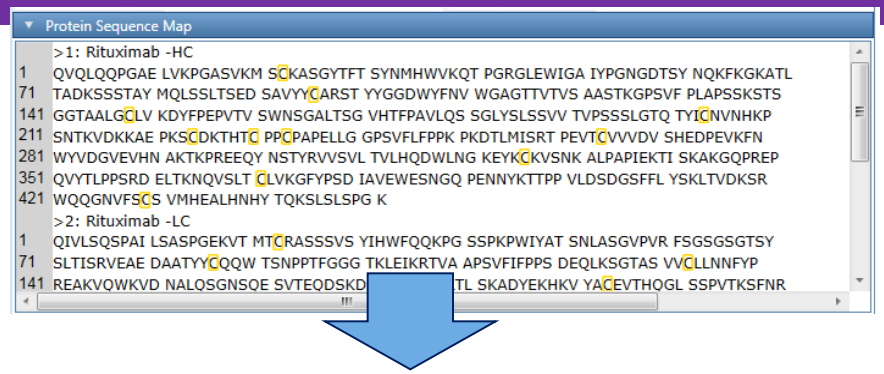
ThermoFisher SCIENTIFIC

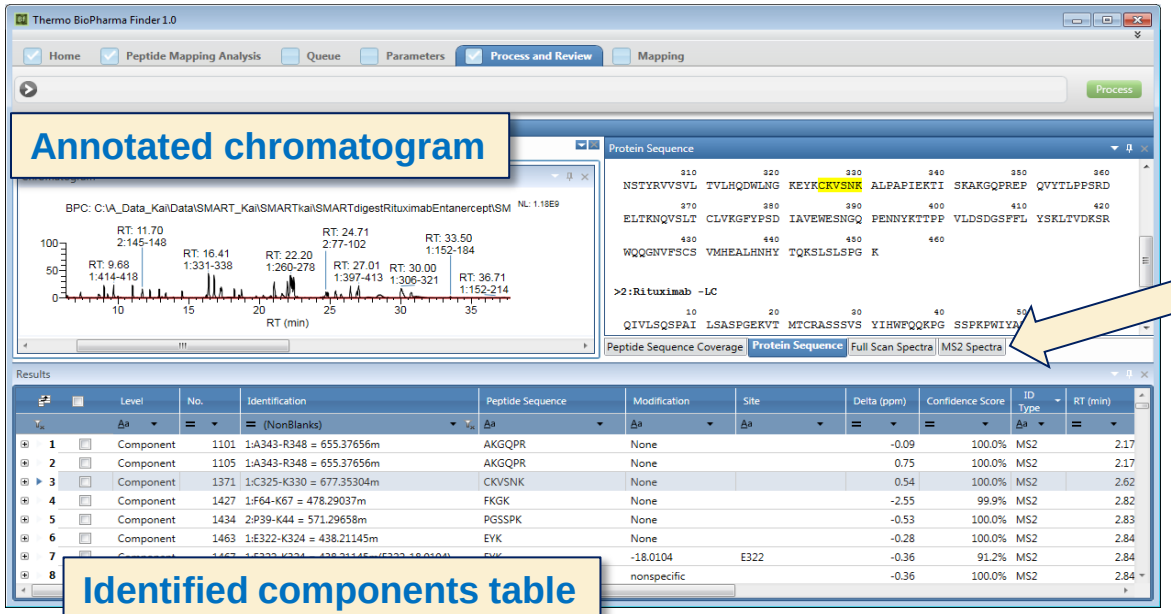
Data Analysis With BioPharma Finder – Peptide Mapping

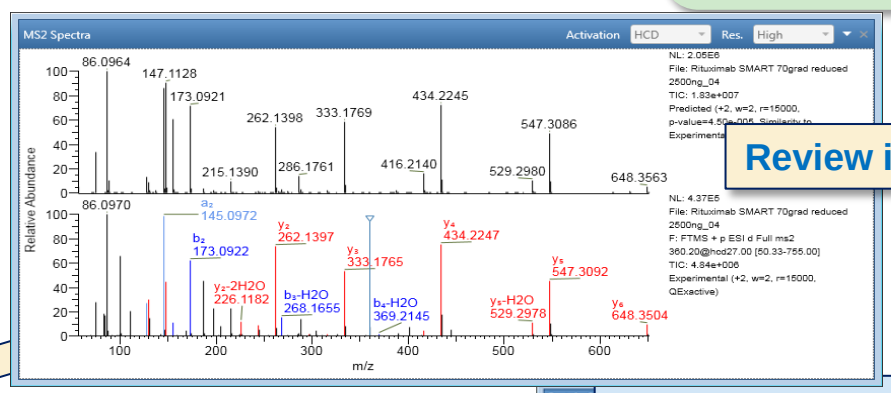


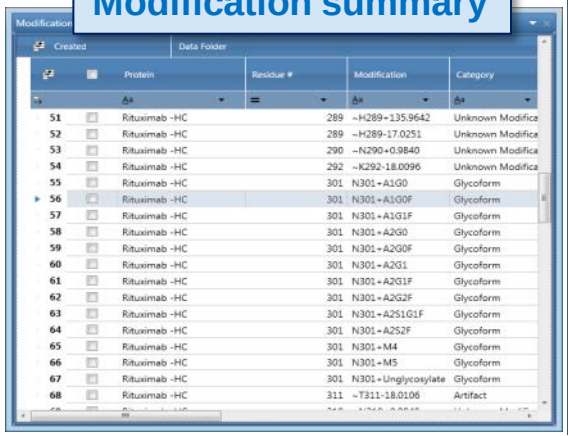
1) Provide protein sequence(s) in the Protein Sequence Manager, define modifications, protease & all search parameters

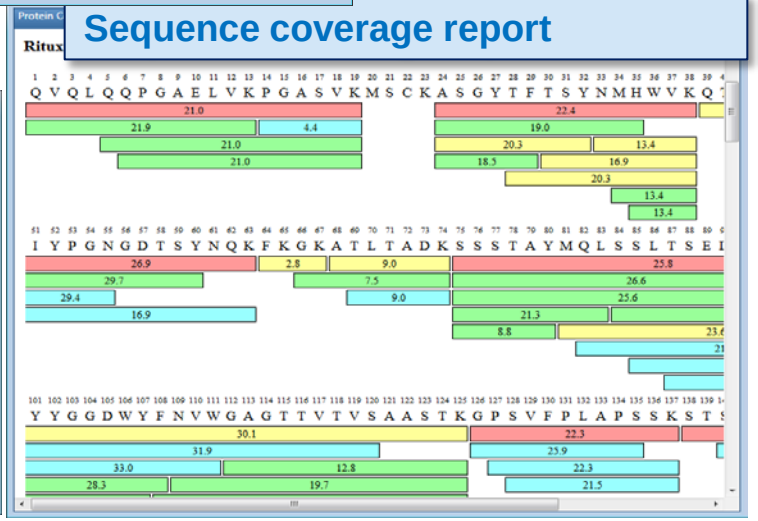
2) Data Analysis in 3 steps:
- **a) Component Detection**
- **b) Peptide Identification**
- **c) Quantification**







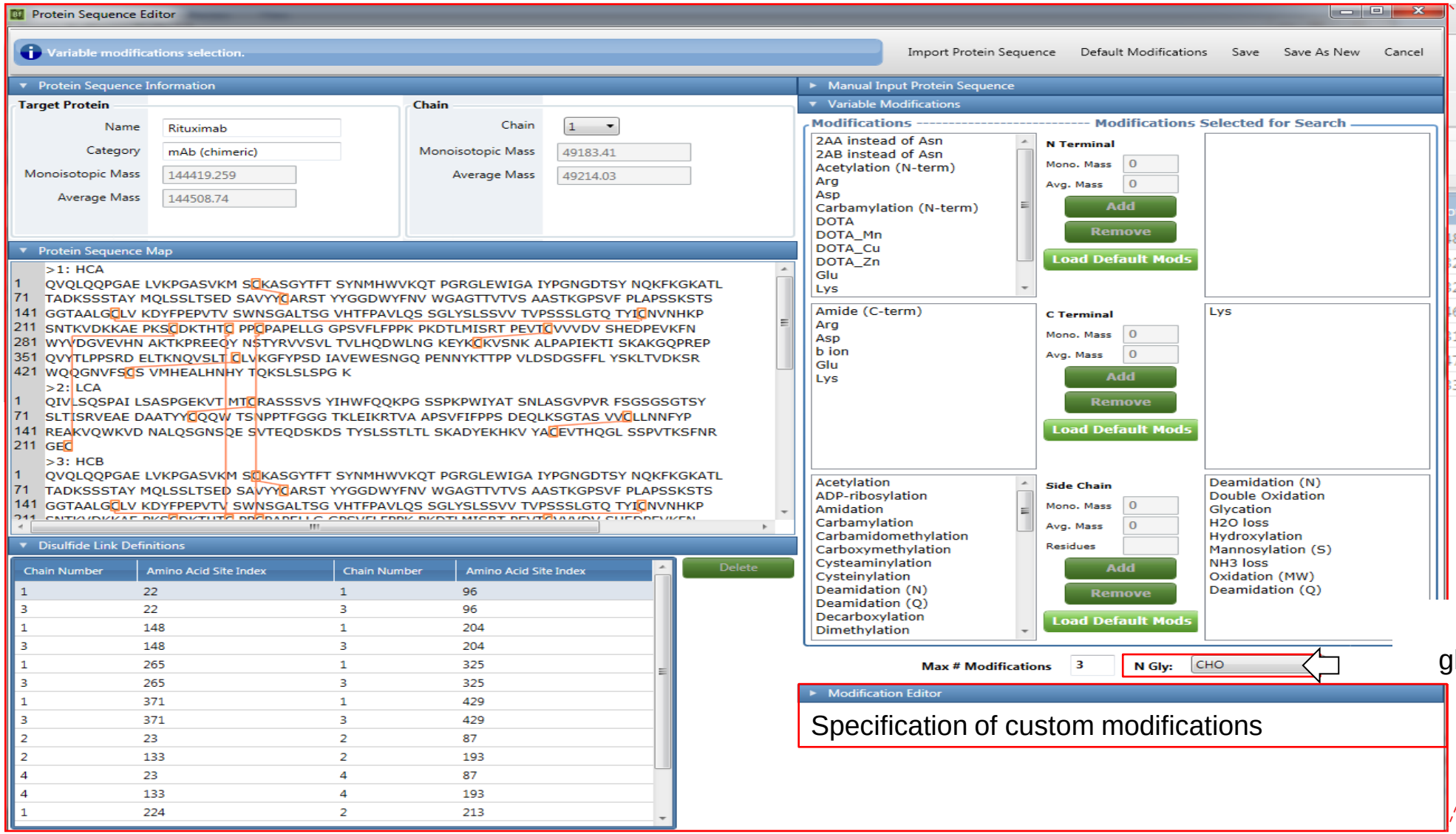




Reference: *Zhongqi Zhang. Large-Scale Identification and Quantification of Covalent Modifications in Therapeutic Proteins. Anal. Chem. 2009, 81, 8354-8364*

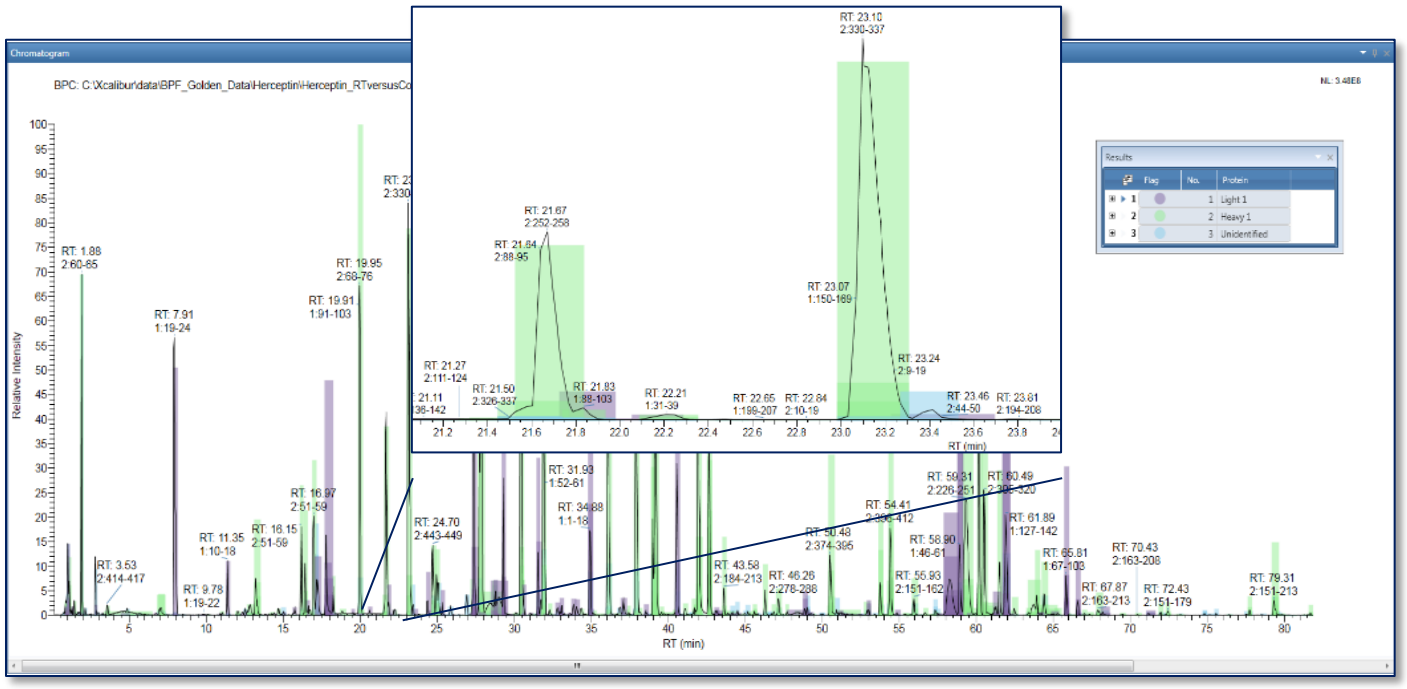
ThermoFisher SCIENTIFIC

BioPharma Finder Software: Protein Sequence Information



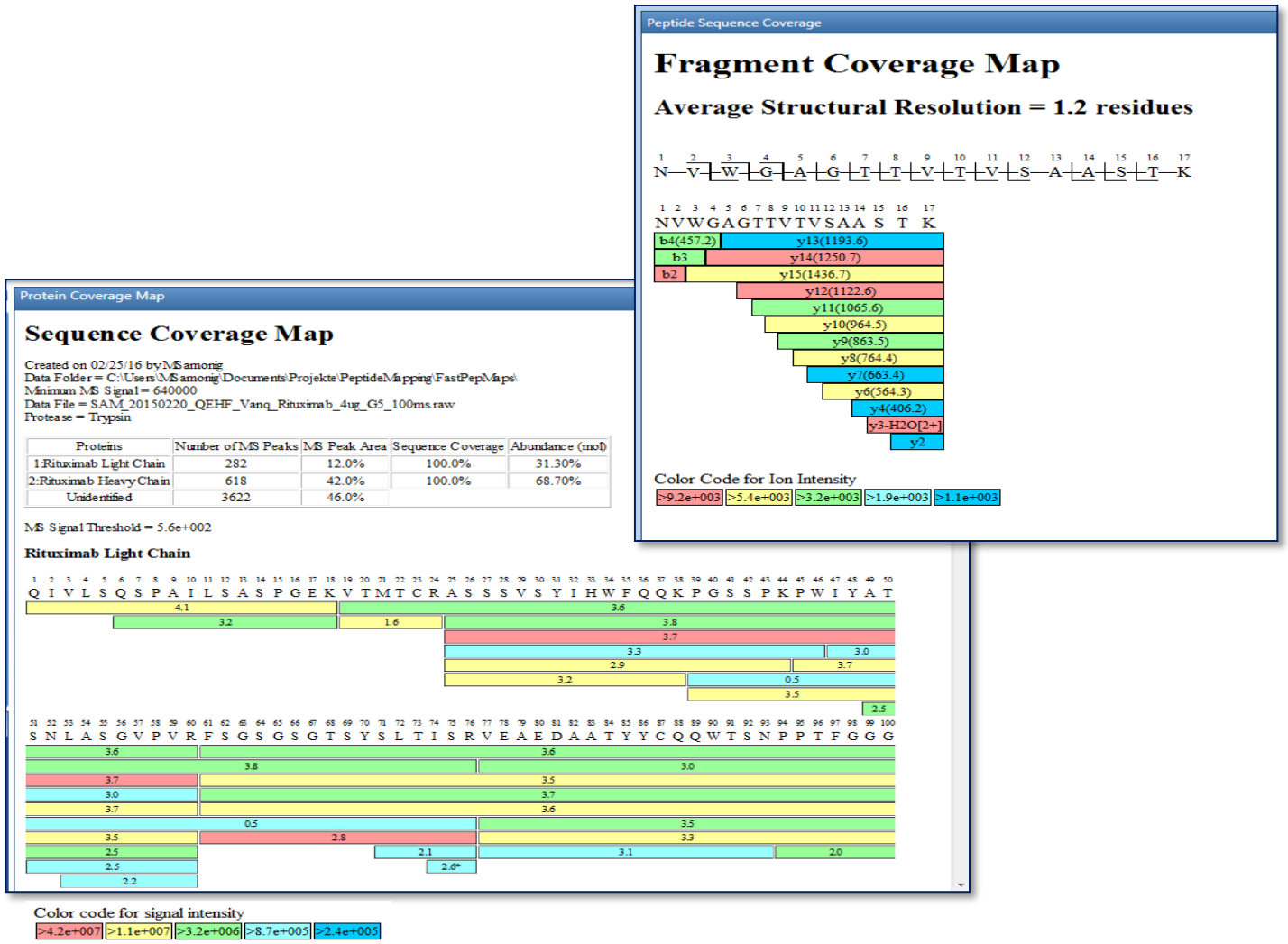
pre-defined set of glycosylation profiles: *human CHO*

Data Analysis With BioPharma Finder: Chromatographic Peak Shading



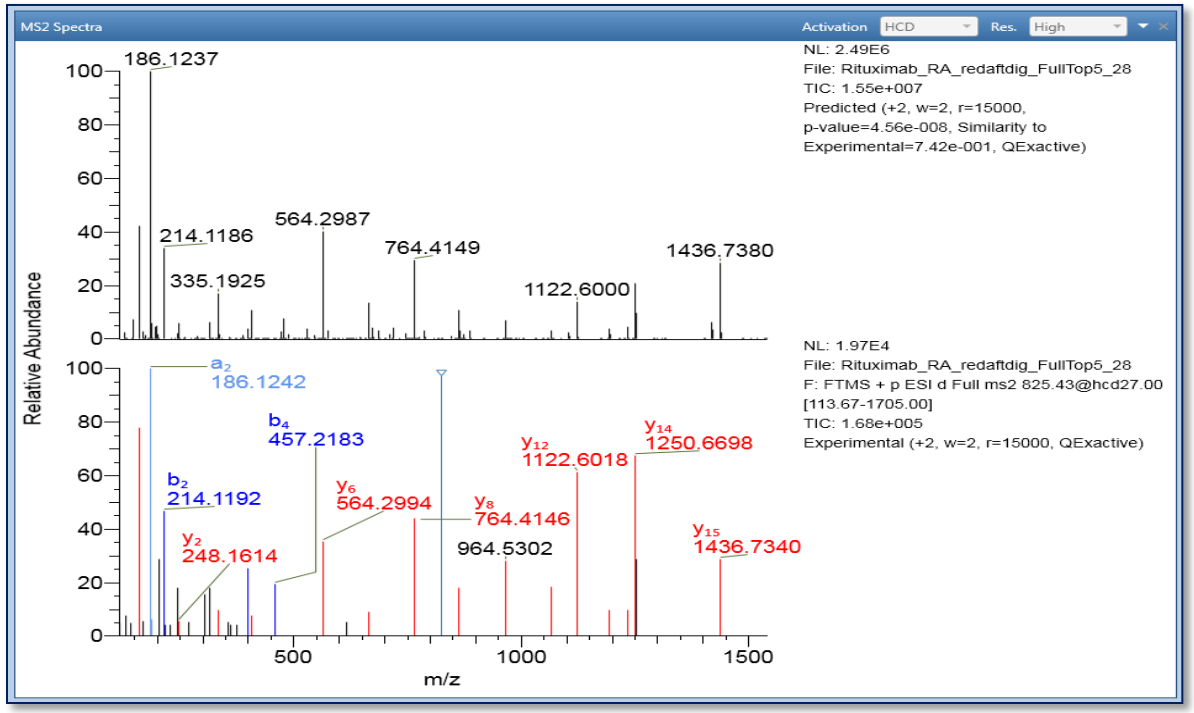
- Protein sequence manager stores sequence information for quick use
- Maximum throughput through simple method editor, allowing batch analyses
- Interactive results display allows you to review data how you want
  - Sequence/fragment coverage maps
  - Chromatographic shading – never miss a thing
  - Compare real and predicted spectra
  - Powerful modification and results summary

Data Analysis With BioPharma Finder: Coverage Mapping



- Protein sequence manager stores sequence information for quick use
- Maximum throughput through simple method editor, allowing batch analyses
- Interactive results display allows you to review data how you want
  - Sequence/fragment coverage maps
  - Chromatographic shading – never miss a thing
  - Compare real and predicted spectra
  - Powerful modification and results summary

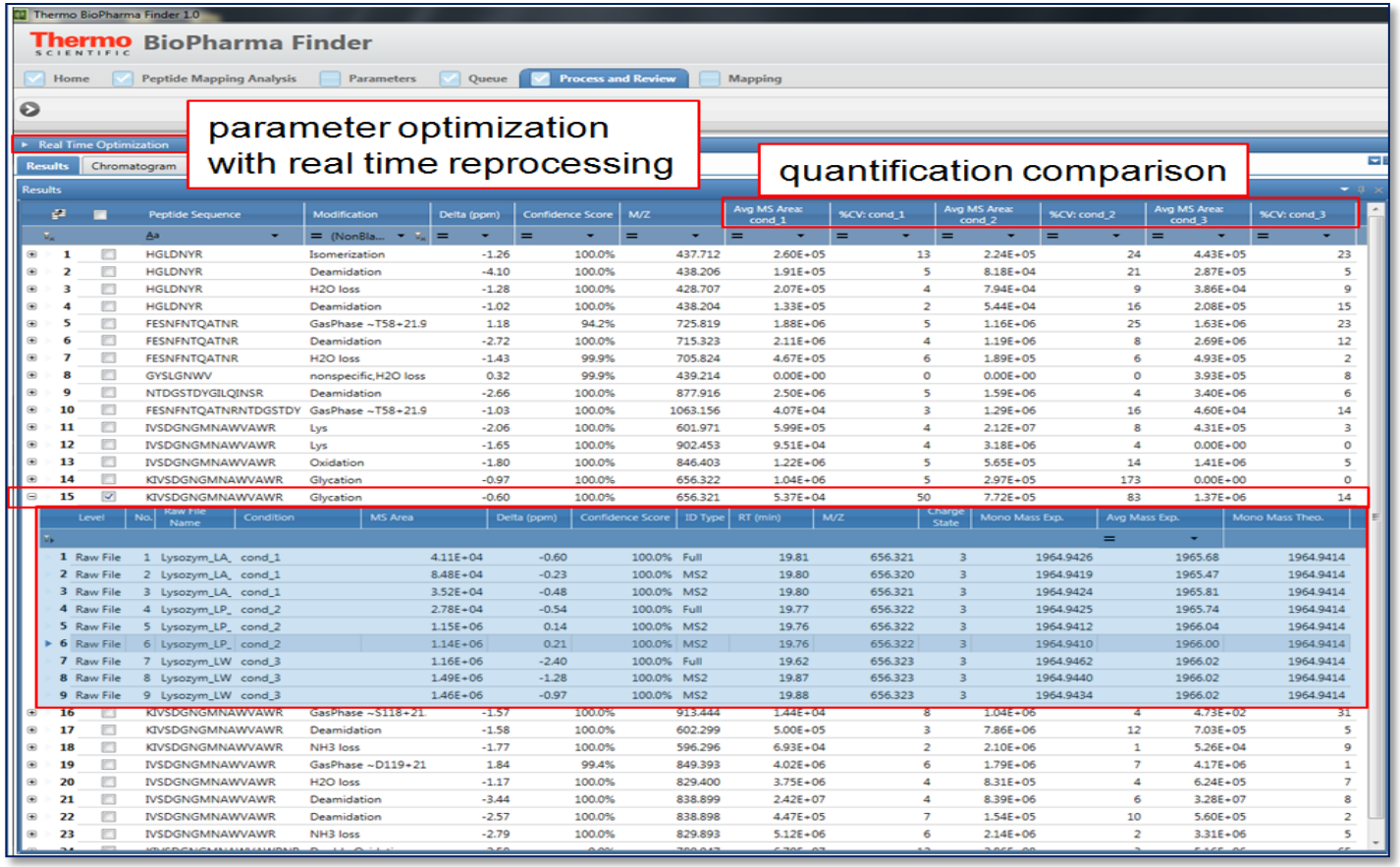
Data Analysis With BioPharma Finder: Spectral Confidence



Theoretically predicted fragment ion and their relative intensities are calculated for all peptide candidates and compared to the measured MS/MS spectrum

- Protein sequence manager stores sequence information for quick use
- Maximum throughput through simple method editor, allowing batch analyses
- Interactive results display allows you to review data how you want
  - Sequence/fragment coverage maps
  - Chromatographic shading – never miss a thing
  - Compare real and predicted spectra
  - Powerful modification and results summary

Data Analysis With BioPharma Finder: Modification Quantification



- Protein sequence manager stores sequence information for quick use
- Maximum throughput through simple method editor, allowing batch analyses
- Interactive results display allows you to review data how you want
  - Sequence/fragment coverage maps
  - Chromatographic shading – never miss a thing
  - Compare real and predicted spectra
  - Powerful modification and results summary

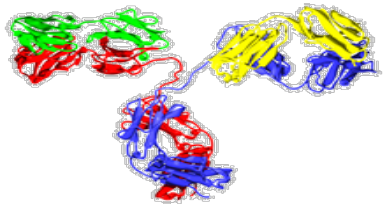
Upgrade your Maps: Our Workflow Solution

Application examples

Transfer your Maps:
Sensitive LC-MS to Routine LC-UV

Speed up your Maps:
UHPLC peptide mapping

Transfer your Maps: Sensitive LC-MS to Routine LC-UV



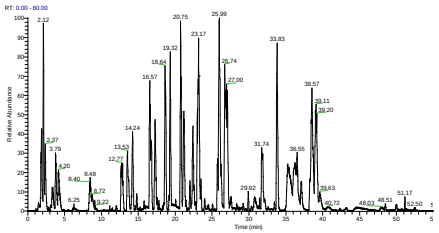
Intact Ab

SMART Digest

followed by optional reduction

Peptides

Bottom up



- **Peptide Map**
- **PTMs**
- **Impurities**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHW
VRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISA
DTSKNTAYLQMNSGTQTYICNVNHKPSNTKVDKKVE
PPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Sequence/PTMs unknown or need to be confirmed

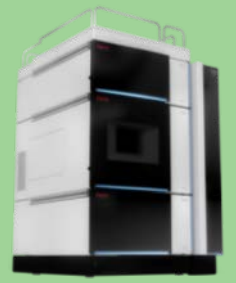
Peptide identification by MS and MS/MS

Fast analysis

Method Transfer to LC-UV

Result Transfer

- Sequence and PTMs known.
- No further information required
- Stability studies, QA/QC
- Batch release

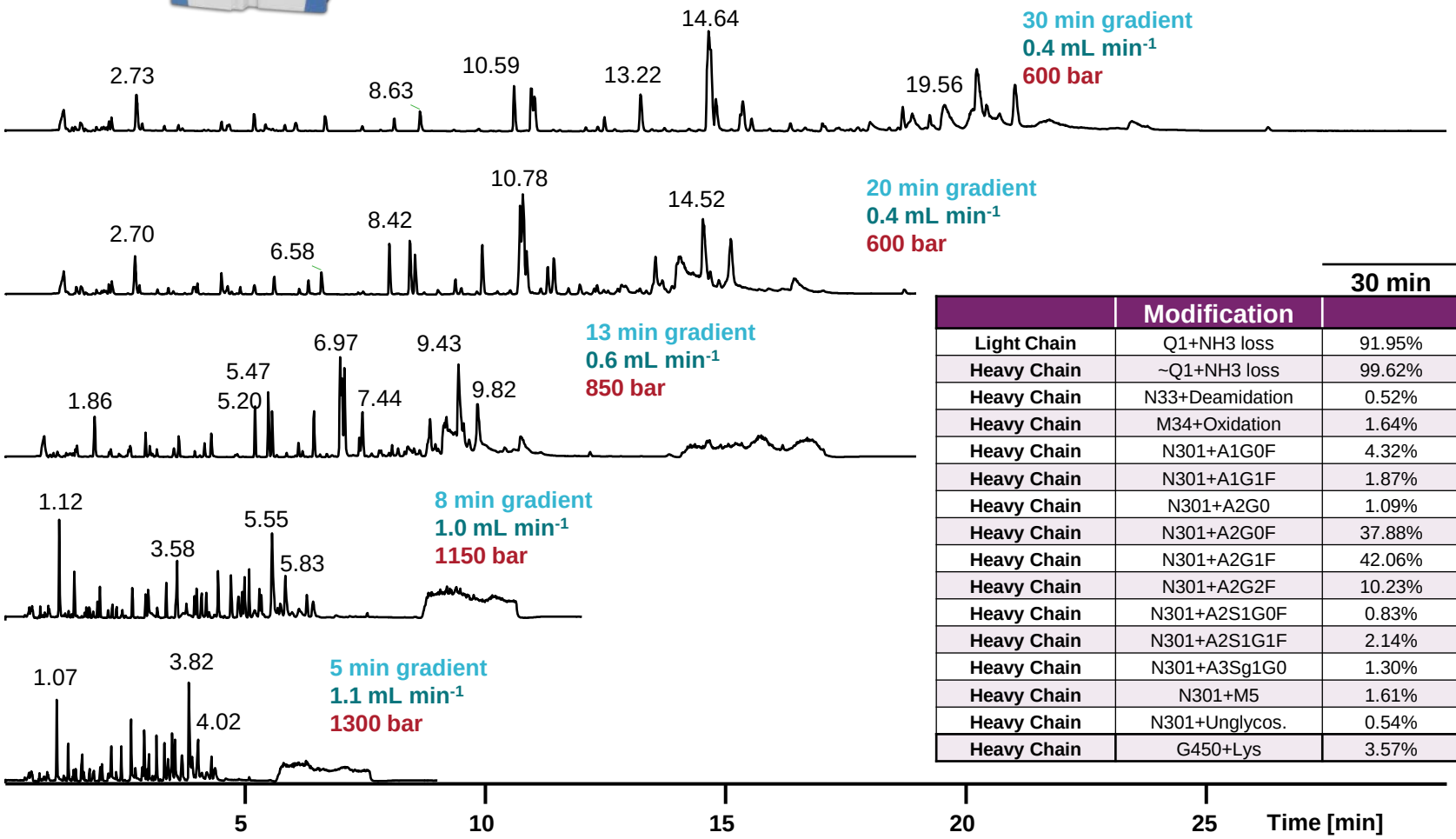


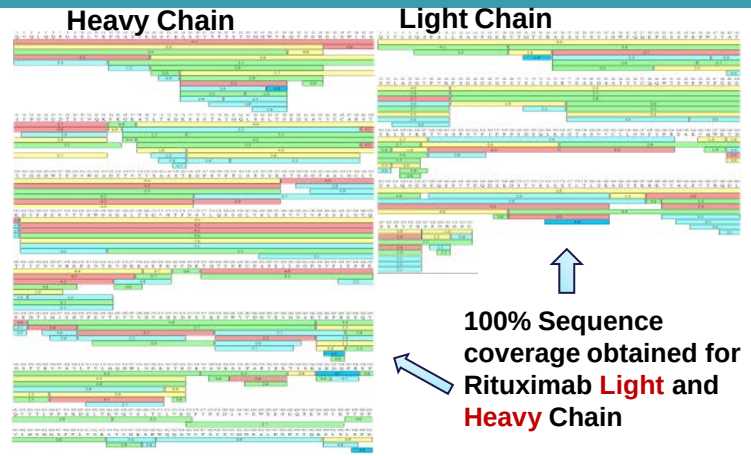
Peptide identification by unknown and reference sample chromatogram comparison (retention time comparison)

High degree of confidence on retention time determination is required!

Speed up your Maps: Short and Long UHPLC Methods for Peptide Mapping

Thermo Scientific™ Vanquish™ UHPLC coupled to a Thermo Scientific™ Q Exactive™ HF MS



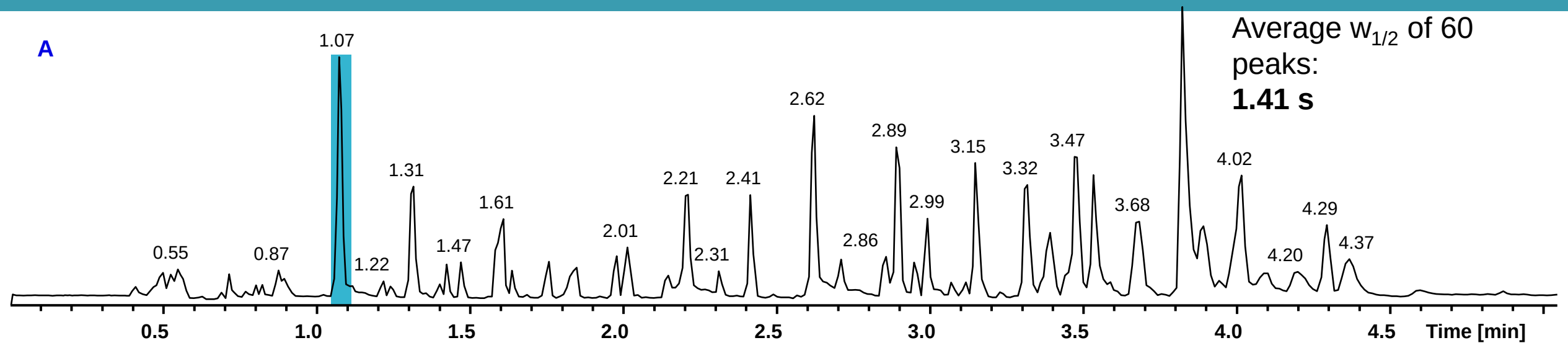


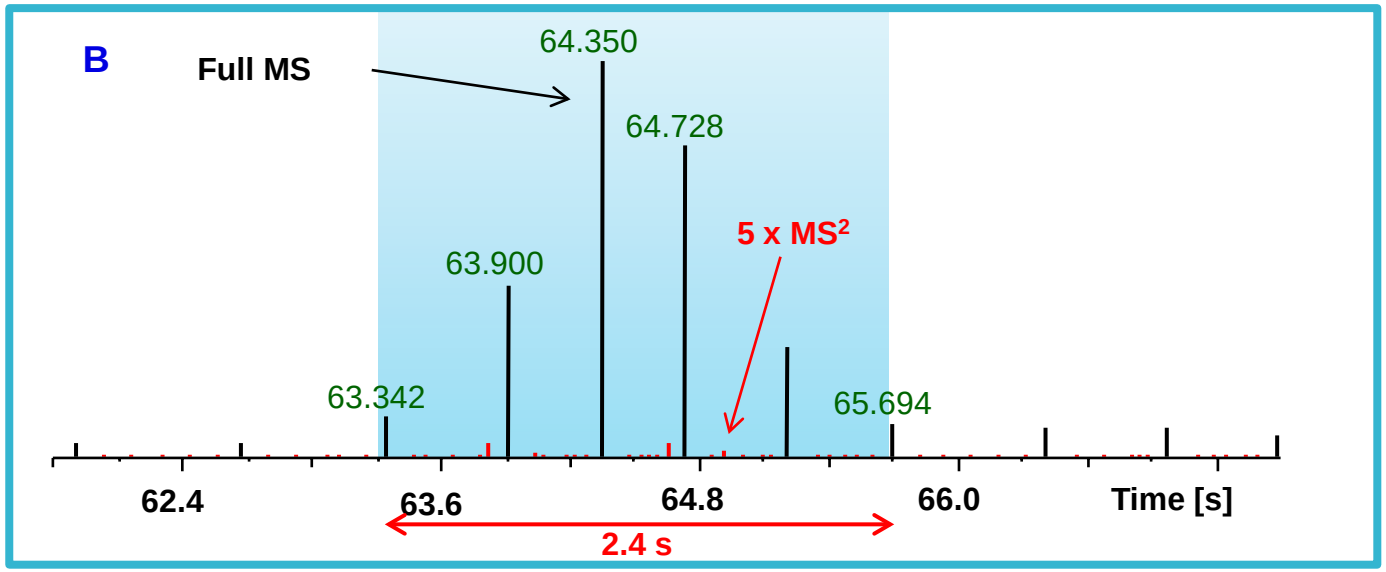
100% Sequence coverage obtained for Rituximab Light and Heavy Chain

		Gradient Time					
		30 min	20 min	13 min	8 min	5 min	
	Modification	Abundance					σ
Light Chain	Q1+NH3 loss	91.95%	91.17%	89.69%	90.93%	26.57%	28.80%
Heavy Chain	~Q1+NH3 loss	99.62%	99.67%	99.61%	99.68%	99.69%	0.04%
Heavy Chain	N33+Deamidation	0.52%	0.51%	0.58%	-	0.51%	0.03%
Heavy Chain	M34+Oxidation	1.64%	1.54%	1.73%	1.42%	1.45%	0.13%
Heavy Chain	N301+A1G0F	4.32%	4.42%	3.83%	3.52%	3.38%	0.46%
Heavy Chain	N301+A1G1F	1.87%	1.91%	1.72%	3.32%	1.46%	0.73%
Heavy Chain	N301+A2G0	1.09%	1.02%	1.02%	-	0.98%	0.05%
Heavy Chain	N301+A2G0F	37.88%	37.11%	38.59%	40.48%	43.12%	2.41%
Heavy Chain	N301+A2G1F	42.06%	41.89%	43.42%	43.20%	43.35%	0.75%
Heavy Chain	N301+A2G2F	10.23%	10.17%	9.81%	10.36%	10.05%	0.21%
Heavy Chain	N301+A2S1G0F	0.83%	0.86%	-	-	-	0.02%
Heavy Chain	N301+A2S1G1F	2.14%	-	-	-	-	-
Heavy Chain	N301+A3Sg1G0	1.30%	-	-	-	-	-
Heavy Chain	N301+M5	1.61%	1.59%	1.66%	1.87%	1.86%	0.14%
Heavy Chain	N301+Unglycos.	0.54%	0.90%	0.76%	0.83%	0.97%	0.16%
Heavy Chain	G450+Lys	3.57%	3.56%	3.92%	3.40%	3.15%	0.28%
						median	0.19%

More Details in Application Note 21465:1135: High-Throughput Peptide Mapping with the Vanquish UHPLC System and the Q Exactive HF Mass Spectrometer

Speed up your Maps: Fast UHPLC Peptide Mapping





6 Full MS scans
5 x Top5 MS^2 scans
Σ=31 scans over a chromatographic peak of 2.4 s width ($w_{1/2}$ = 0.9 s)

A) Total ion chromatogram of a five minute gradient separation of Denosumab.
B) Data point distribution for a Full MS / $ddMS^2$ Top5 method during a representative chromatographic peak.

More Details in Application Note 21465:1135: High-Throughput Peptide Mapping with the Vanquish UHPLC System and the Q Exactive HF Mass Spectrometer

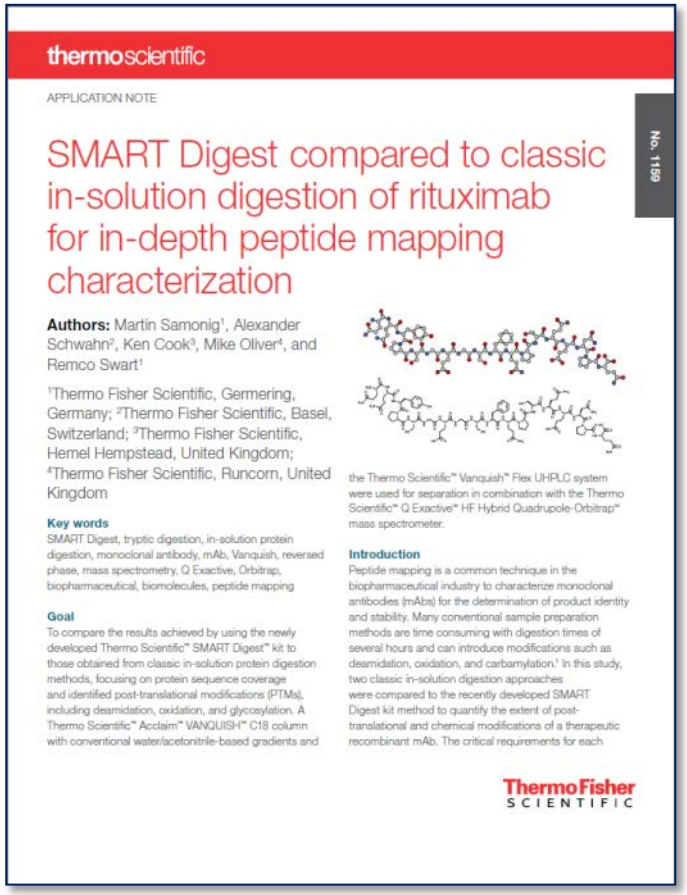
Peptide Mapping Workflow: Time Saving

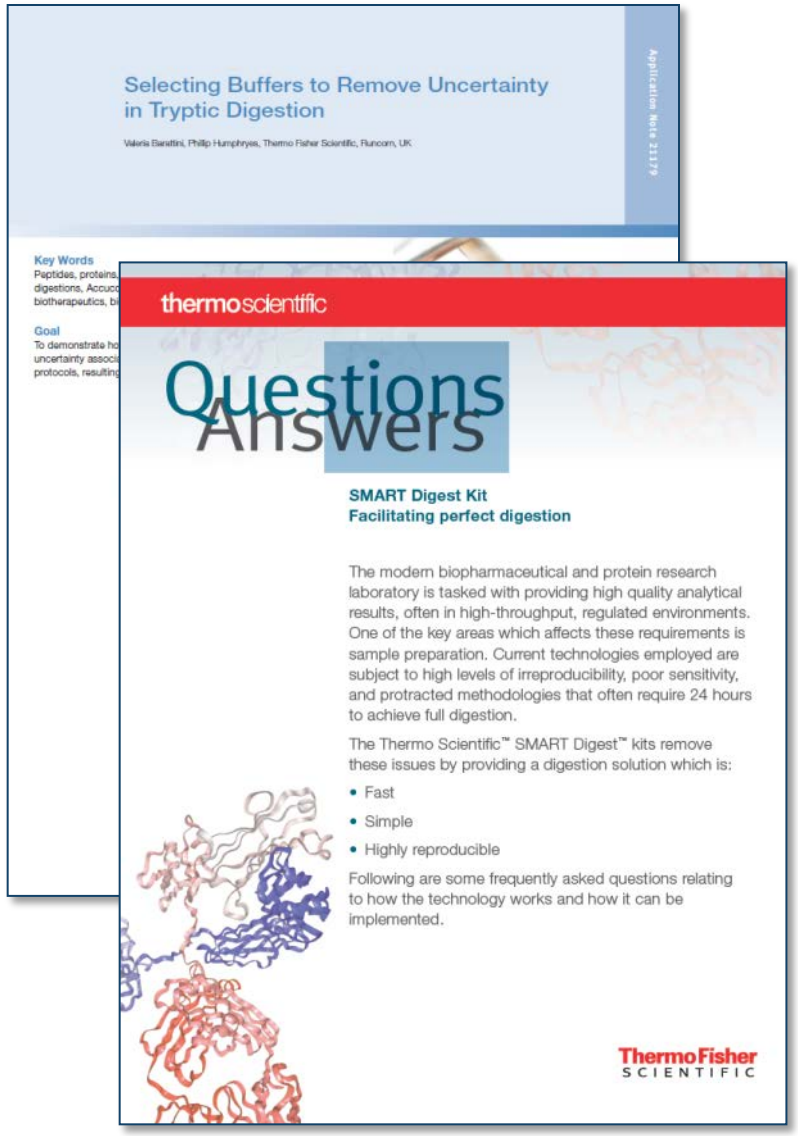
60 min **20 min** **10 min**

- **Complete workflow can be completed in less than 90 minutes**
- **MS analysis is rapid, stand-alone LC-UV even quicker**
- **Even inexperienced analysts can obtain highly reproducible results**

ThermoFisher SCIENTIFIC

Selected Application Notes on Peptide Mapping

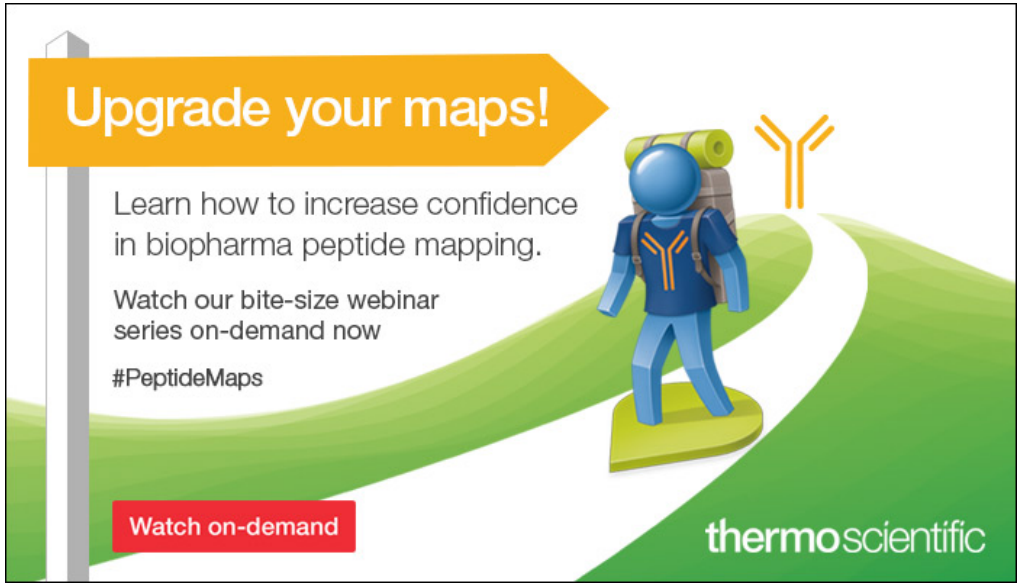




ThermoFisher SCIENTIFIC

On-Demand Webinar Series on Peptide Mapping

- **TAKE THE SMART ROUTE TO PROTEIN DIGESTION - How to increase reproducibility whilst reducing preparation time.**
  Wednesday, September 28, 2016, 03:00 PM BST
- **PEPTIDE SEPARATIONS WITH PINPOINT PRECISION - How to achieve ultimate retention time reproducibility & high resolution separation of peptides.**
  Wednesday, October 12, 2016, 03:00 PM BST
- **DON'T MISS A THING ON YOUR PEPTIDE MAPPING JOURNEY - How to get full coverage peptide maps using high resolution accurate mass spectrometry.**
  Wednesday, October 26, 2016, 03:00 PM BST
- **EASILY NAVIGATE ALL BIOTHERAPEUTIC MODIFICATIONS - How to confidently compare and interpret your peptide maps with powerful, yet intuitive software.**
  Wednesday, November 09, 2016, 03:00 PM GMT



bit.ly/UYPepMaps

ThermoFisher SCIENTIFIC

Questions?

Acknowlegements

- Kai Scheffler
- Alexander Schwahn
- Ken Cook
- Martin Samonig
- Mike Oliver
- Valeria Barattini
- Mauro De Pra
- Jennifer Sutton

bit.ly/BPM_4

BioPharMoore

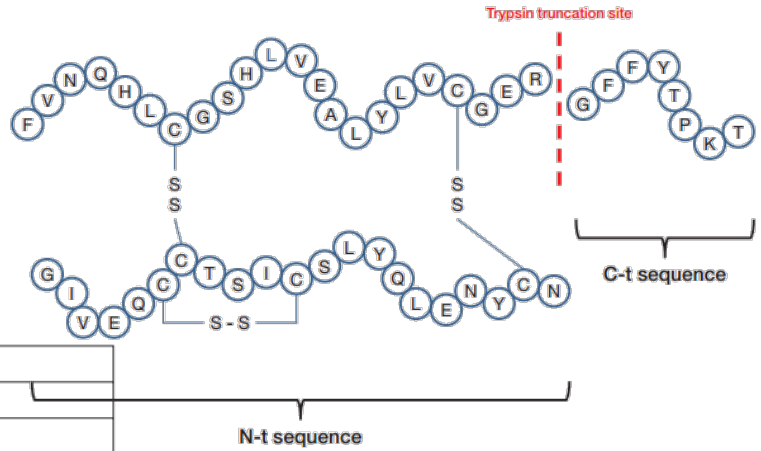
Your guide to the evolving bio/pharma universe.

ThermoFisher SCIENTIFIC

Backup slides

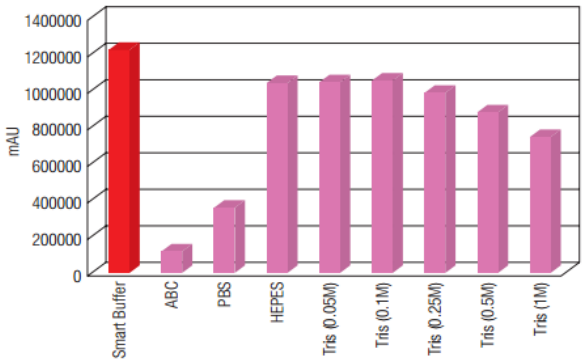
Let's Optimize the Digestion Buffer!

- Enzyme
- Solubility
- Denaturation
- Diffusion

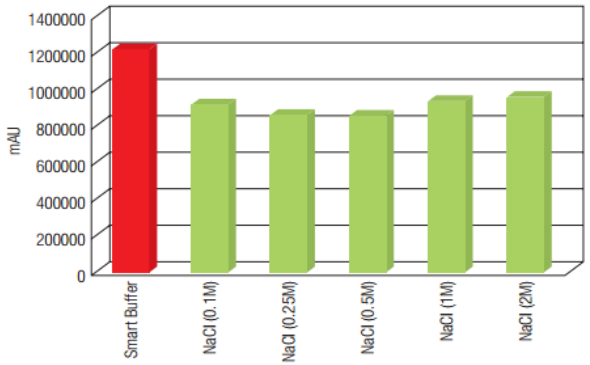


Insulin amino acid sequence, C-t peptide was monitored

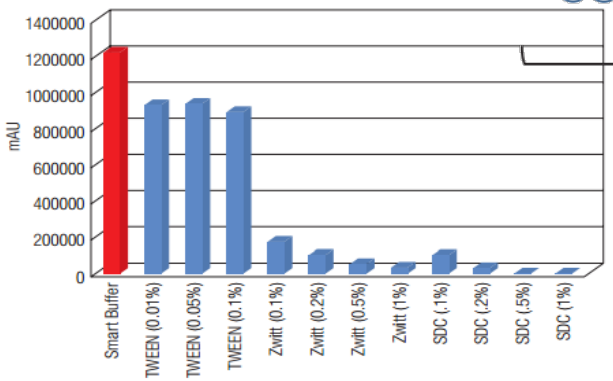
A Effect of buffering ion



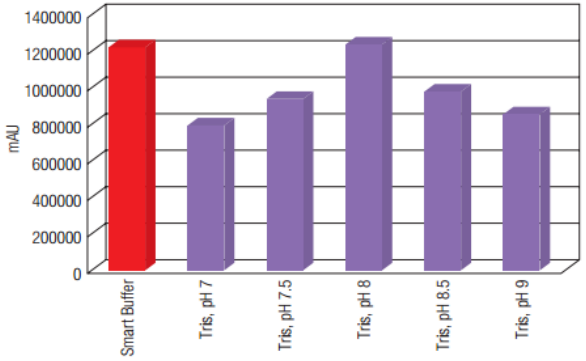
B Effect of salt concentration



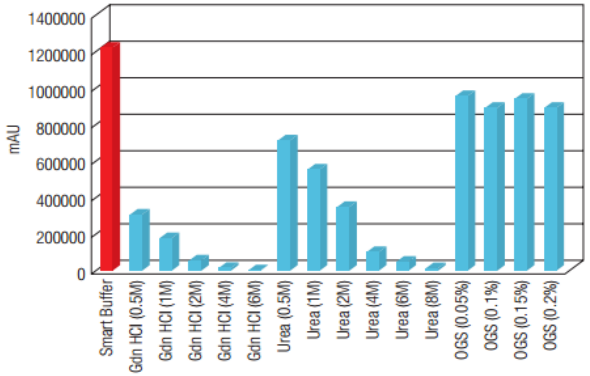
E Effect of detergents



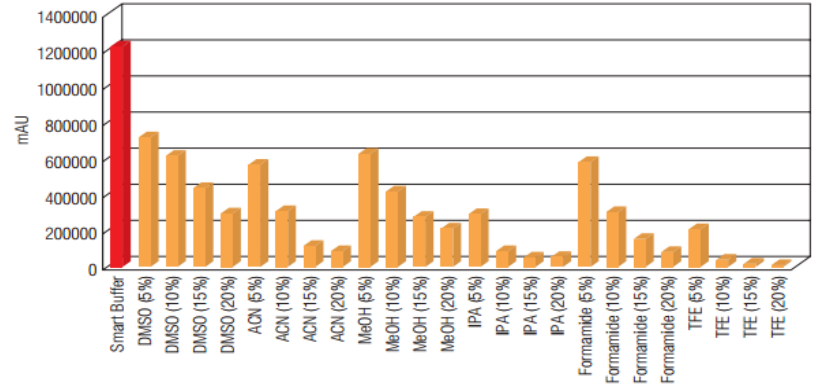
C Effect pf pH



D Effect of chaotropes



F Effect of co-solvents



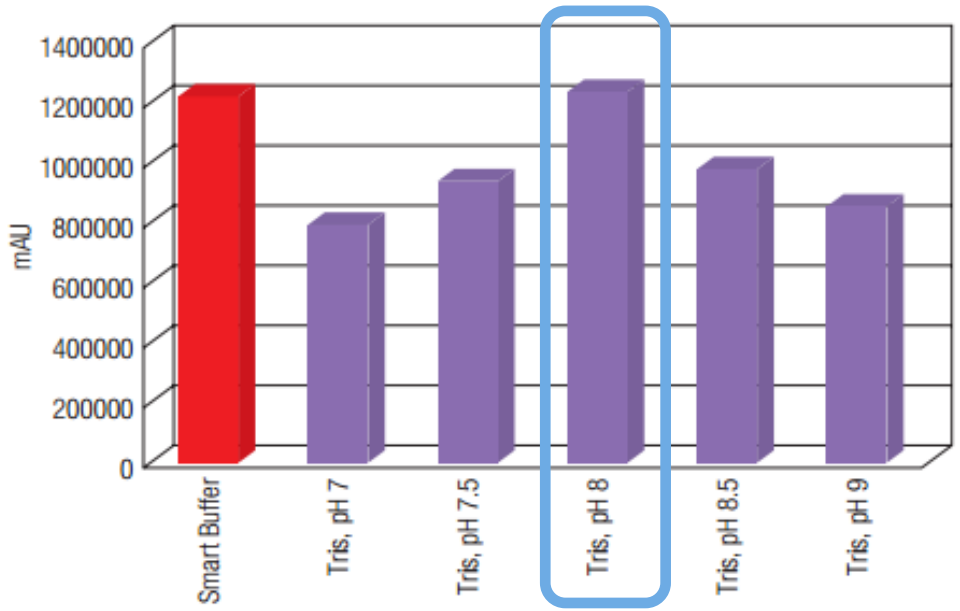
ThermoFisher SCIENTIFIC

Let's Optimize the Digestion Buffer!

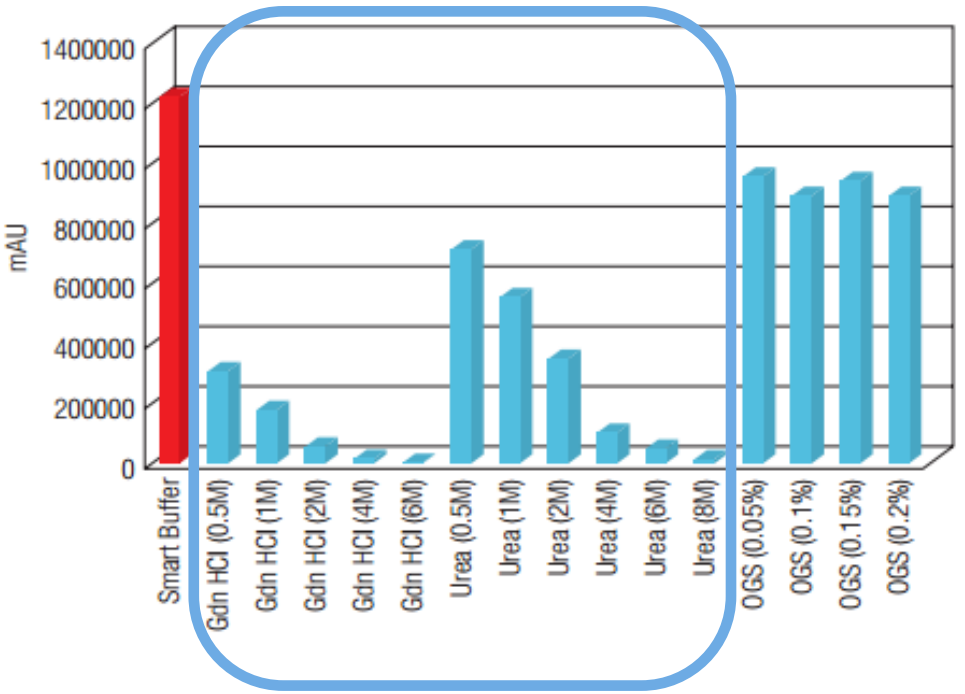
- Enzyme
- Solubility
- Denaturation
- Diffusion

Chemical Name	CAS No.	EINECS No.	Kit Component	Weight %
Water	7732-18-5	231-791-2	2	50-95%
Glycerol	56-81-5	200-289-5	2	< 20%
Tris Base	77-86-1	201-064-4	2	< 10%
Tris-HCl	1185-53-1	214-684-5	2	< 10%
Calcium Chloride	10043-52-4	233-140-8	2	< 10%
Sodium Azide	26628-22-8	247-852-1	2	< 0.1%

C Effect pf pH



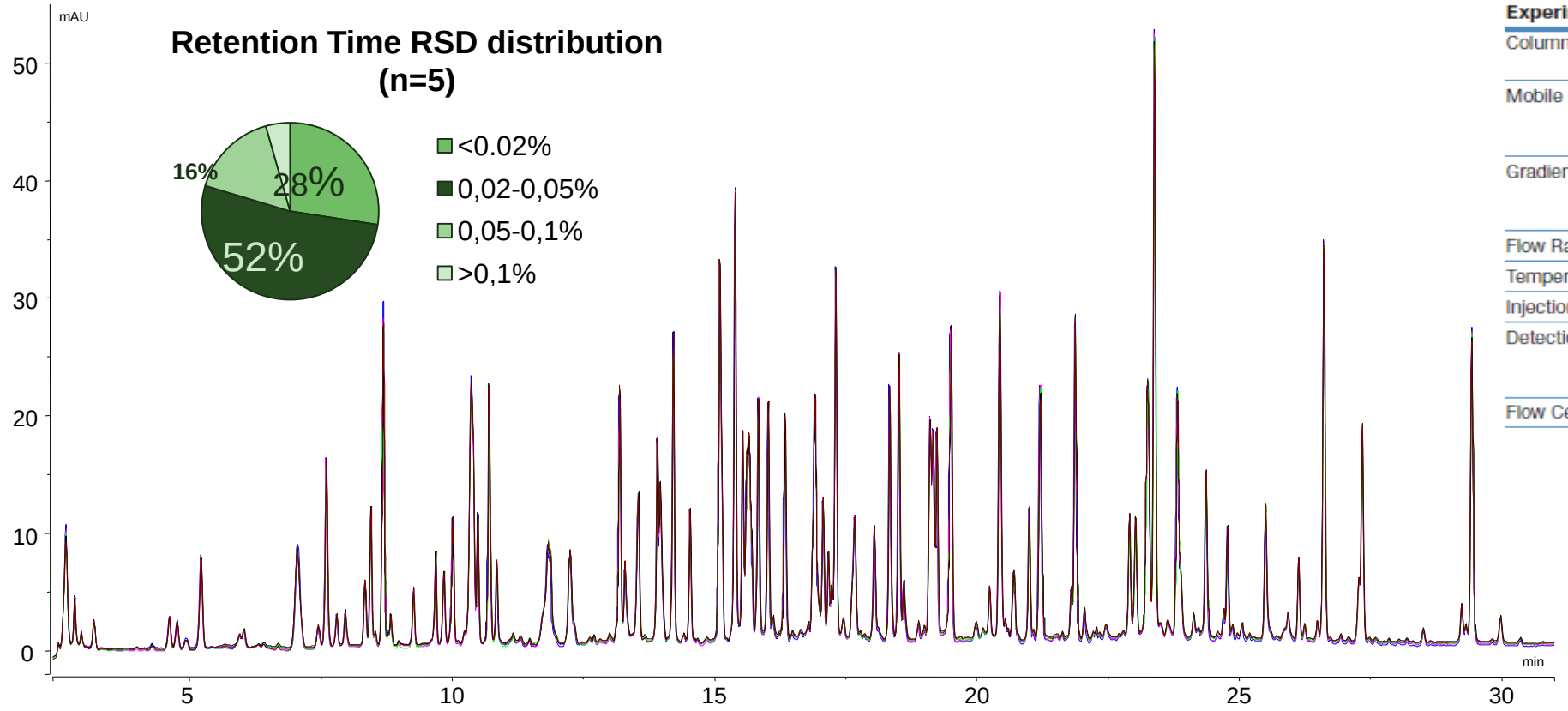
D Effect of chaotropes



ThermoFisher SCIENTIFIC

Vanquish Flex UHPLC System: Retention Time Reproducibility

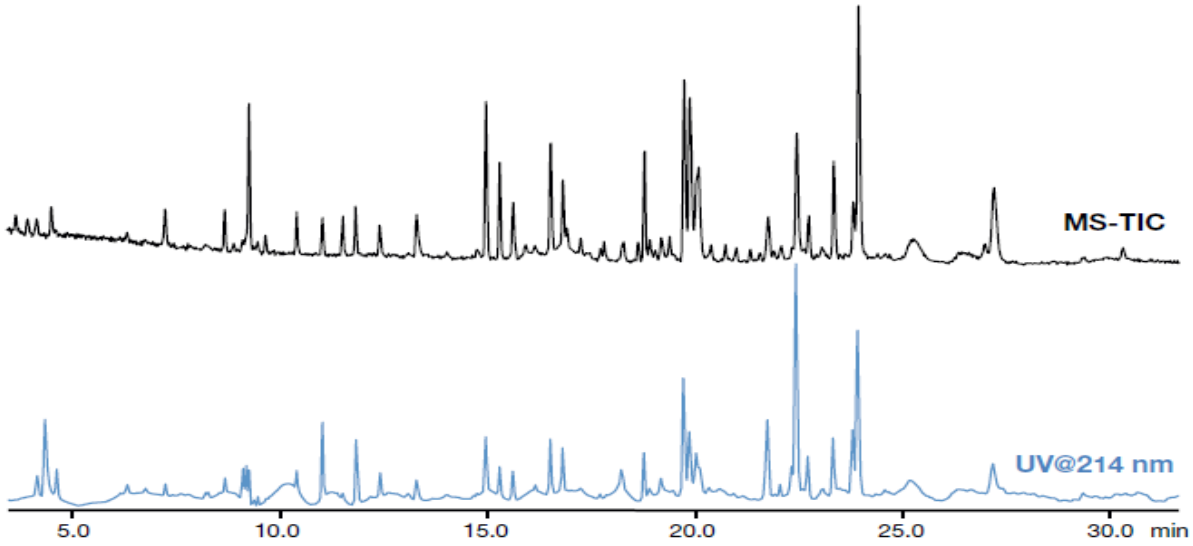
Outstanding retention time reproducibility for confident peptide annotation



Experimental Conditions	
Column:	Acclaim RSLC 120, C18, 2.2 µm Analytical (2.1 x 250 mm, P/N 074812)
Mobile Phase:	A: 0.05% TFA in water (P/N TFA 85183) B: 0.04% TFA in 8/2 acetonitrile/water (v/v), (P/N acetonitrile TS-51101)
Gradient:	0–30 min: 4%-55% B, 30–31 min: 55%–100% B, 31–35 min: 100% B, 35–36 min: 100%–4% B, 36–56 min: 4% B
Flow Rate:	0.3 mL/min
Temperature:	50°C still air
Injection Volume:	2 µL
Detection:	214 nm Data collection rate: 10 Hz Response time: 0.4 s
Flow Cell:	10 mm LightPipe

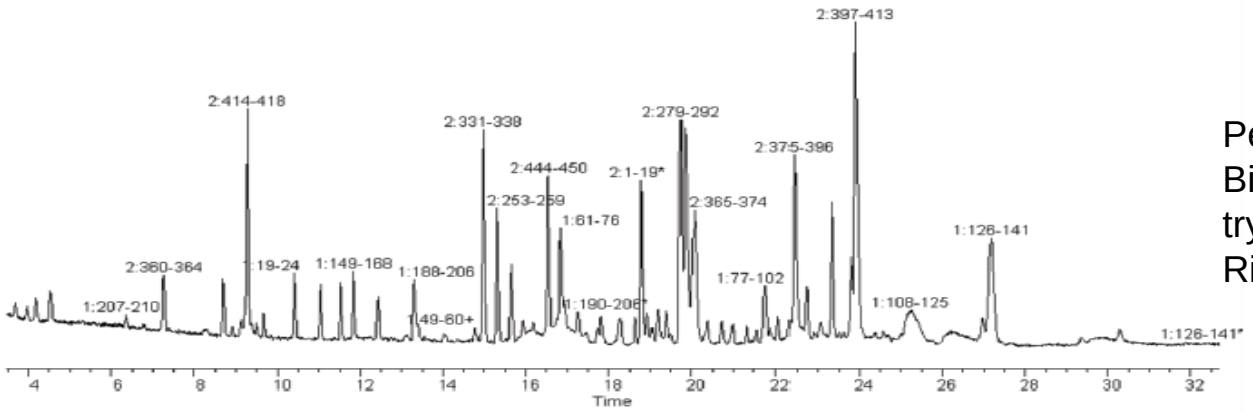
ThermoFisher SCIENTIFIC

Transfer your Maps: Sensitive LC-MS to Routine LC-UV



Total Ion Current (TIC) of a SMART digested Rituximab sample, measured by Q Exactive MS

Vanquish Flex: UV detection SMART digested Rituximab sample.



Peak assignment with Biopharma Finder of the tryptic peptides from Rituximab.

ThermoFisher SCIENTIFIC

Why Peptide Mapping?

- It’s an absolute essential step in biotherapeutic characterization
- It’s used at every stage, from discovery to QC
- It’s routine… but slow and painstaking

⇨ **we can make it easier!**

What Are The Peptide Mapping Pain Points?

- **Effort and Time consuming**
  - labour intensive, multi-step sample preparation, with little standardization
  - overnight digestion causes delay of results
- **Variability in digestion**
  different protocols and operators produce different results
- **Lack of reproducibility** – leading to a lack of data confidence
- **Difficult** – from digestion to data interpretation multiple skills are required.