Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Caractérisation des protéines thérapeutiques, transfert de méthodes sur des systèmes PAT

David LASCOUX,

Business Development Manager
Biopharmaceutical and Proteomic Market – Southern Europe, Waters

Waters
Business Overview

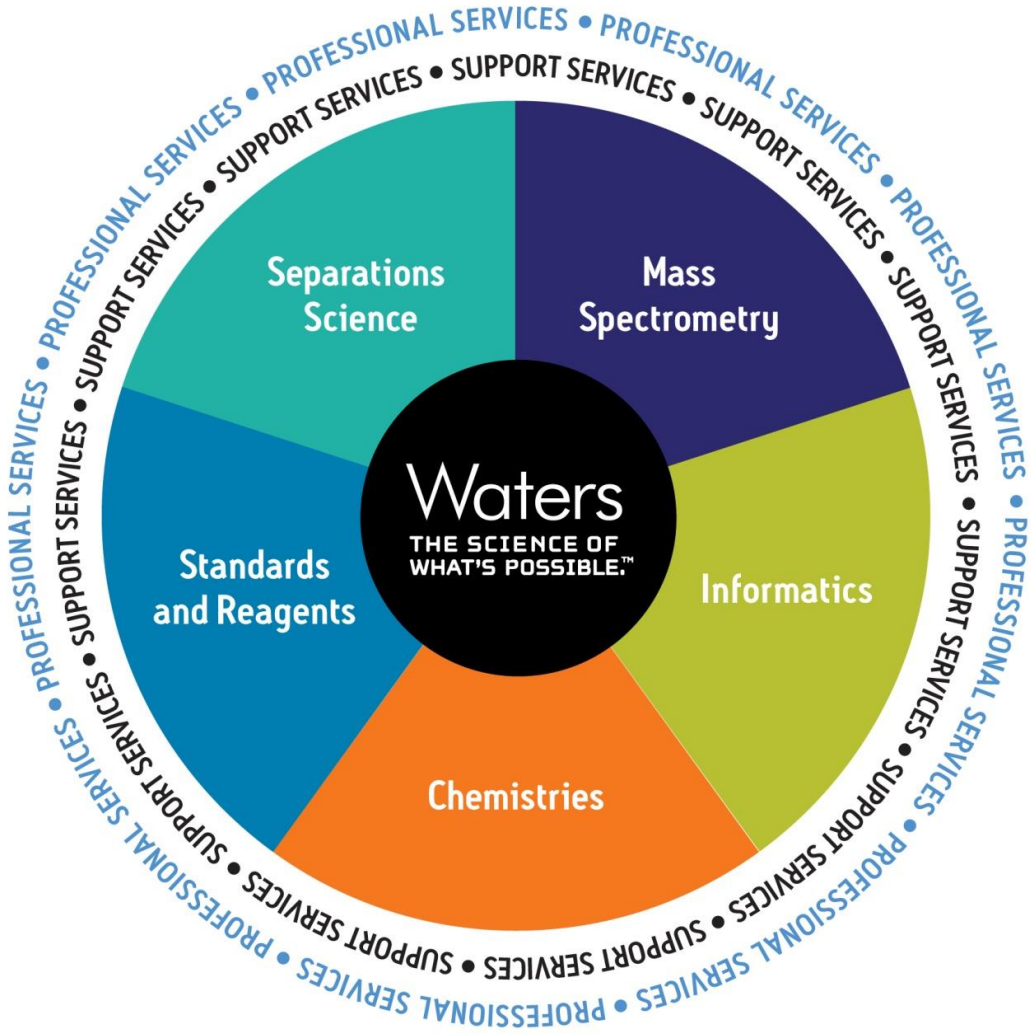
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

- Worldwide HQ
- Divisional HQ
- Sales HQ
- Manufacturing
- Sales Offices

- $1.85 billion in annual revenue in 2012
- ~6,000 employees with 10-year average length of service
- All facilities **cGMP**-compliant and ISO 9001, others include ISO 14385, ISO 17025, ISO Guide 34, ISO Guide 43…
- 53 years of manufacturing expertise, globally located
- Direct sales, **service and support** in 89 offices serving 54 countries worldwide

Waters
Technology Focus

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Préparation d'échantillon

↓

Séparation

↓

Détection

↓

Traitement de données

Service et Support

Application-Specific Solutions
Biopharmaceutical market

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

- UPLC
  - AAA
  - Peptide Mapping
  - Released Glycans
  - Intact RP
  - Intact SEC
  - Intact IEX
  - Oligonucleotides

- UPLC/MS
  - Peptide Mapping
  - Released Glycans
  - Intact RP
  - HDX
  - HCPs

Application-Specific Solutions
Biopharmaceutical market

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

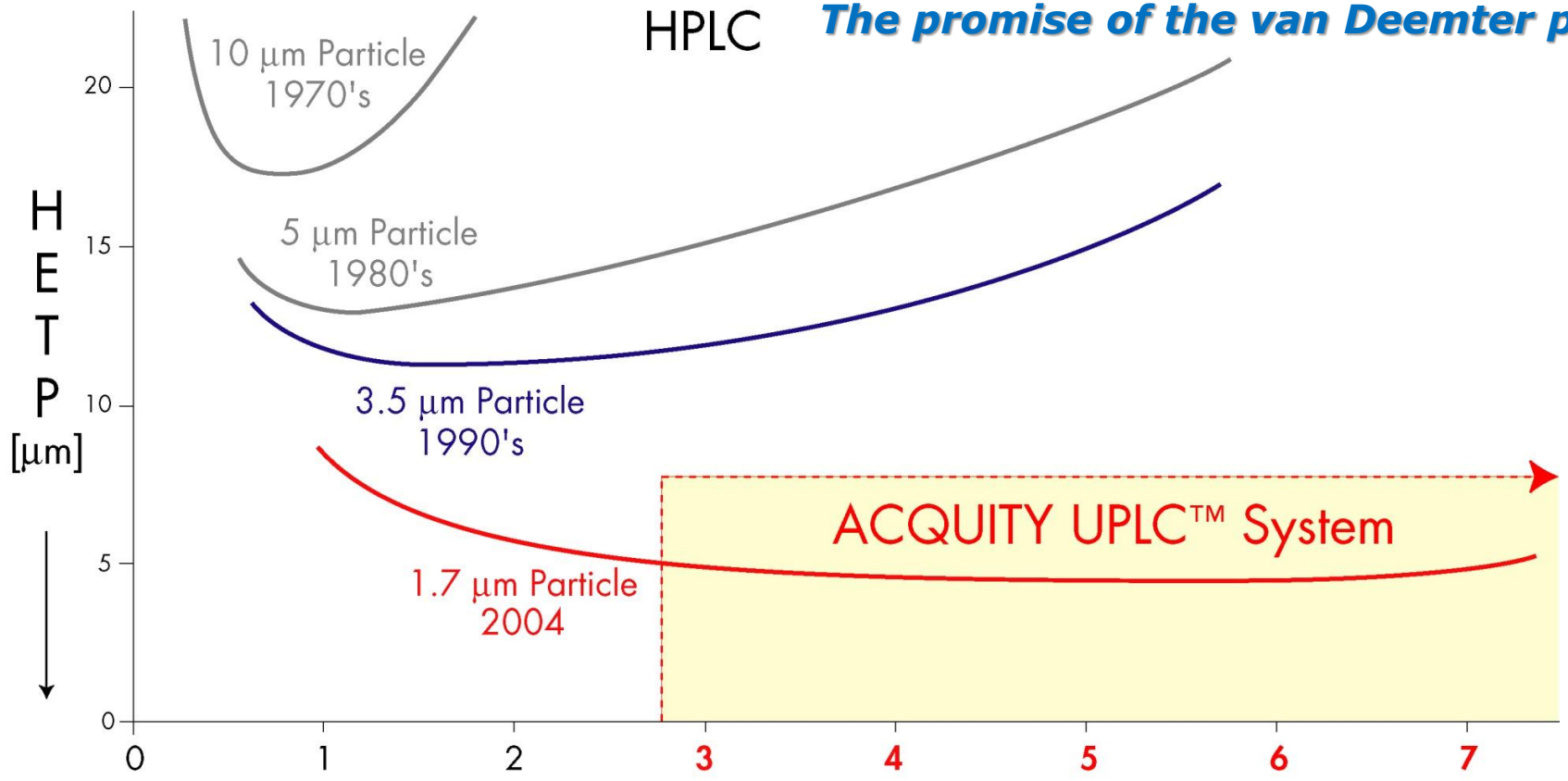
- UPLC
  - AAA
  - Peptide Mapping
  - Released Glycans
  - Intact RP
  - Intact SEC
  - Intact IEX
  - Oligonucleotides

Caractérisation des protéines thérapeutiques par UPLC

Smaller Particles
The Productivity Enabler

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

The promise of the van Deemter plot



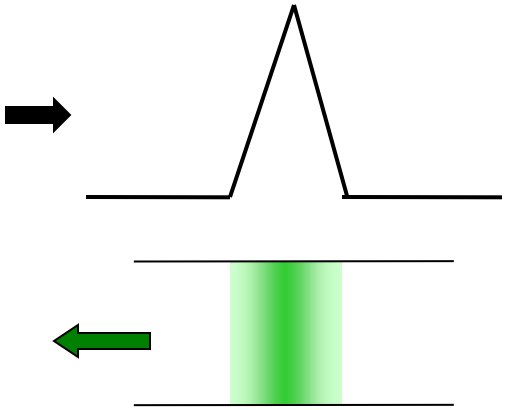
Flow Rate [mL/min]:							
ID = 1.0 mm	0.04	0.07	**0.10**	**0.13**	**0.17**	**0.20**	**0.24**
ID = 2.1 mm	0.15	0.3	**0.45**	**0.6**	**0.75**	**0.9**	**1.05**
ID = 4.6 mm	*0.7*	*1.4*	*2.1*	*2.8*	*3.5*	*4.2*	*4.9*

Impact of Band Spreading on Resolution

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

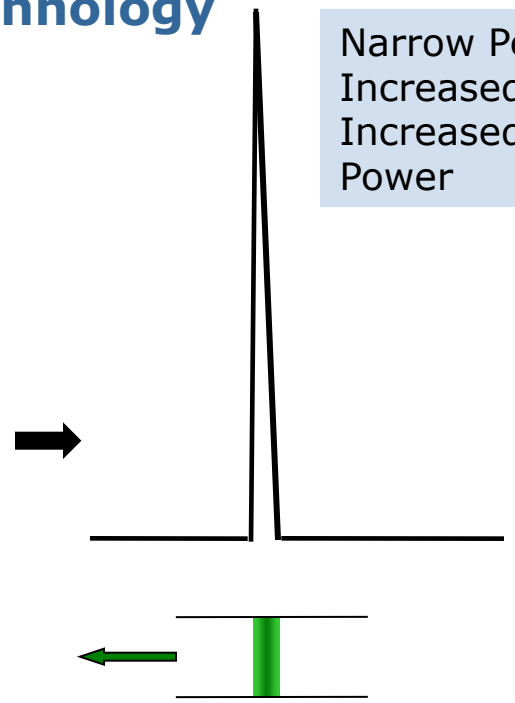
HPLC

Broad Band
Broad Peak
Less Sensitivity
Less Resolving Power



UPLC® Technology

Narrow Peak
Increased Sensitivity
Increased Resolving Power



Requires *Columns* and *Instrumentation* to Minimize Band Spreading

Acquity H-Class Bio

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Acquity H-Class

High pressure Quaternary pump

« Flow Through » Injector

Stainless Steel

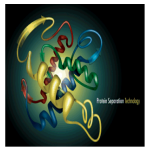
- ✓ Corrosion
- ✓ Unwanted adsorption

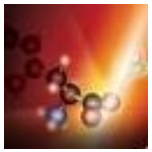
Alliage Titane et/ou NiCo

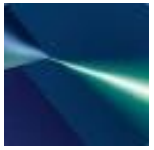
- ✓ Primary & accumulator pump heads
- ✓ Check-valves
- ✓ UPLC Valves (Vent, Injector, CM, etc..) & SSV
- ✓ Mixer housing, mixer manifold, sinkers
- ✓ SM Needle Assembly
- ✓ APH Assembly
- ✓ UPLC tubing assemblies
- ✓ PDA & TUV Flow Cells

- ➢UPLC performances
- ➢Biological solvent and buffer compatibility
- ➢Biological separation compatibility

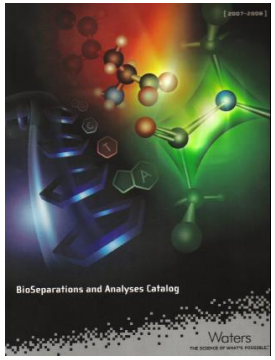
Overview of Waters solutions for Biomolecules





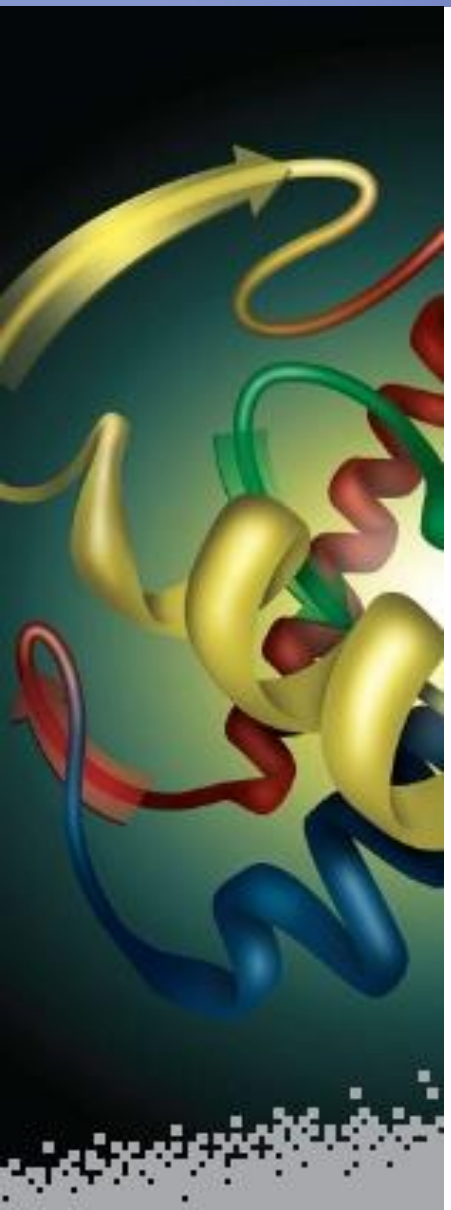



- Protein Characterization, Analysis and Purification (PrST)
  SEC, IEX, RP, HIC
- Peptide Separation Technology (PST)
  RP, HILIC
- Amino Acid Analysis (AAA)
  AccqTag Ultra
- Oligonucleotide Separation Technology (OST)
  IP-RP, IEX
- Glycan Separation Technology (GST)
  HILIC, RP
  Carbohydrates : SEC, IEX, HILIC, RP
- Sample preparation solutions and MS consumables
  - Phosphopeptide extraction
  - Digestion of proteins
  - Desalting devices
  - **Standards**



Chromatography of proteins

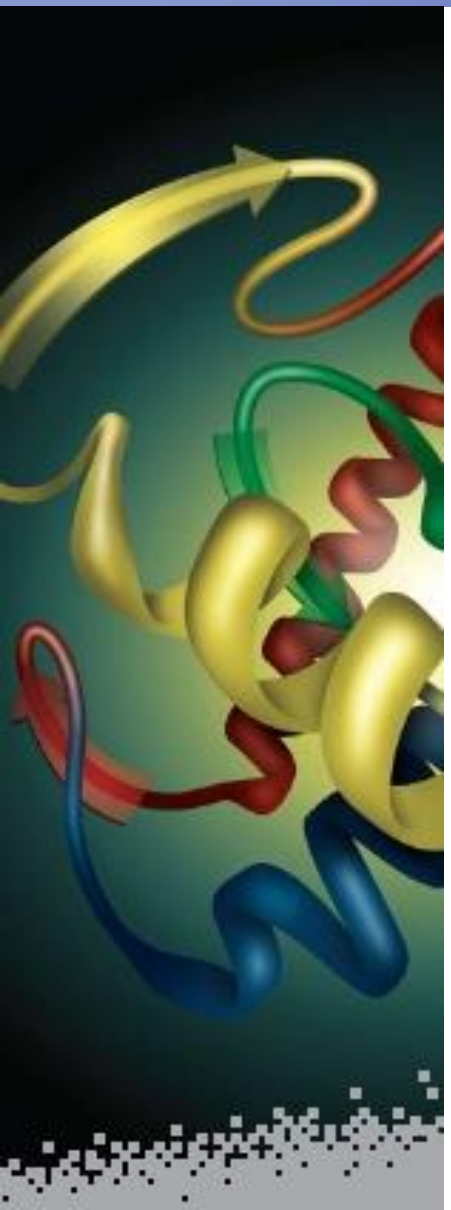
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



- Size Exclusion Chromatography :
  Aggregation, Fragmentation, Separation, Isolation, Quantification
- Ion Exchange Chromatography :
  Charge variants, fractionnation of complexe samples
- Reverse Phase Chromatography :
  Hydrophobicity separation, Intact Mass Analysis, Quantification

Chromatography of proteins

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

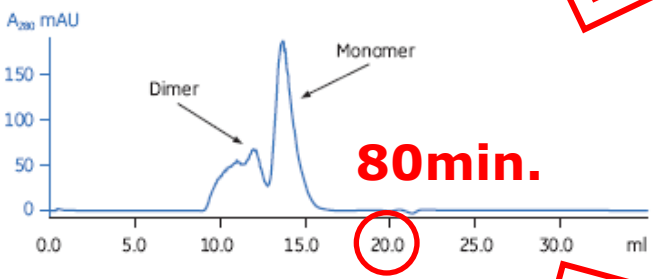


- Size Exclusion Chromatography :
  Aggregation, Fragmentation, Separation, Isolation, Quantification
- Ion Exchange Chromatography :
  Charge variants, fractionnation of complexe samples
- Reverse Phase Chromatography :
  Hydrophobicity separation, Intact Mass Analysis, Quantification

FPLC vs UPLC Performance for IgG aggregation

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

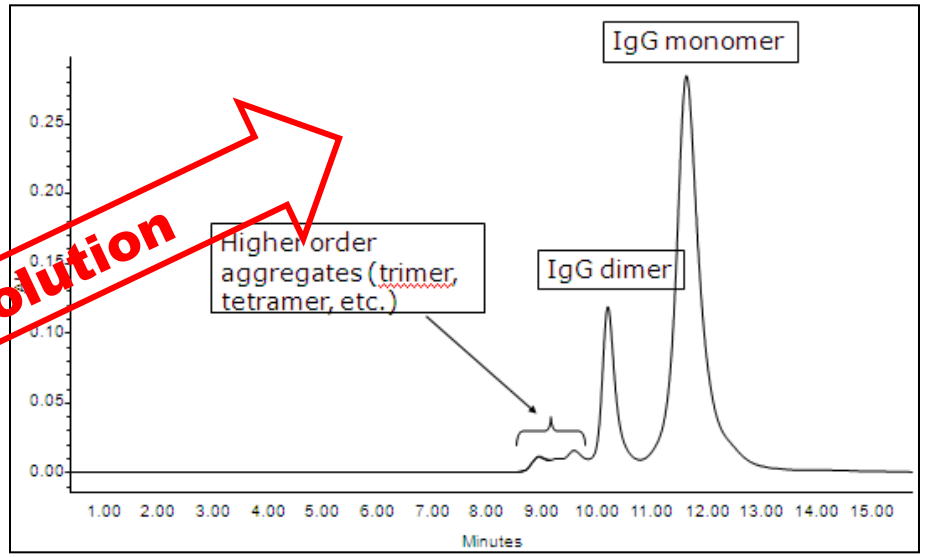
Column:	Superdex 200 10/300 GL
Sample:	Monoclonal antibody
Sample volume (load):	100 µl
Elution buffer:	0.02 M Tris™ HCl, pH 7.5, 0.15 M NaCl
Flow rate:	0.25 ml/min
System:	ÄKTAexplorer 100



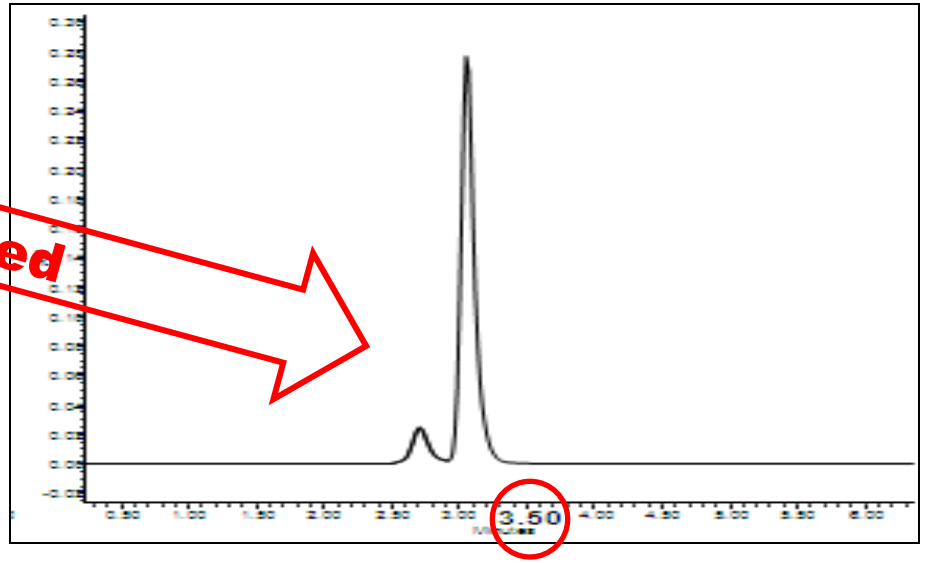
80min.

Fig 7. Separation of the monomer and dimer of a monoclonal antibody on Superdex 200 10/300 GL.

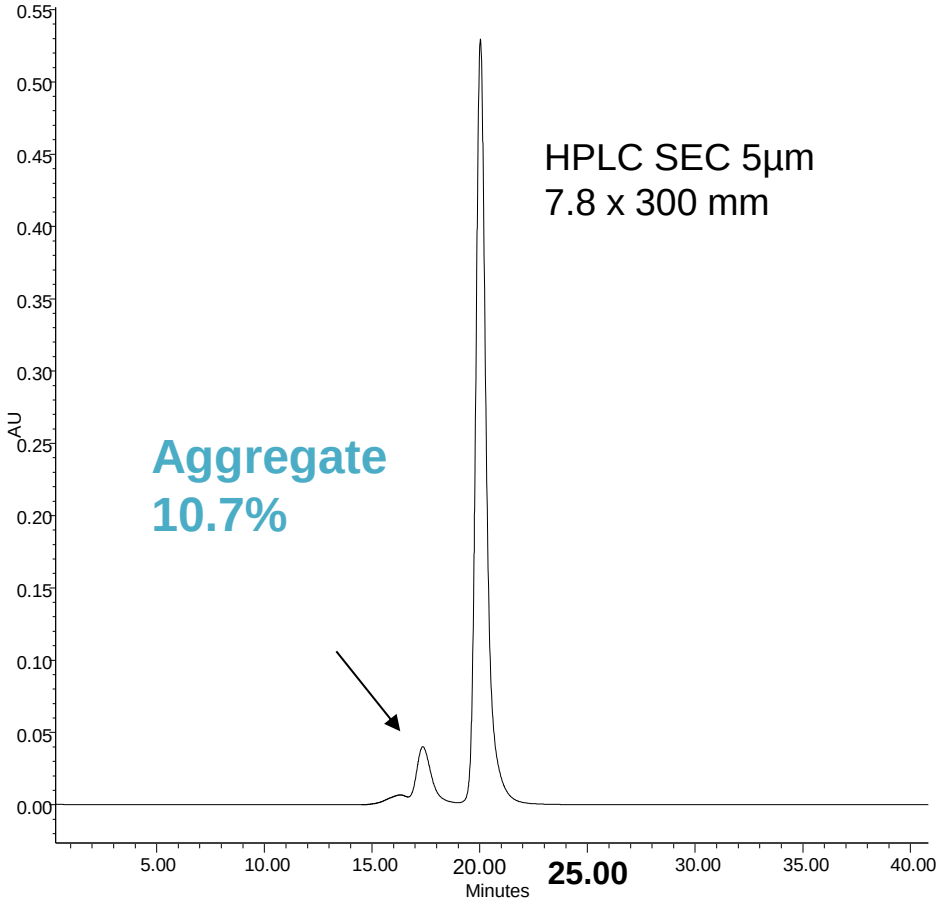
More Resolution

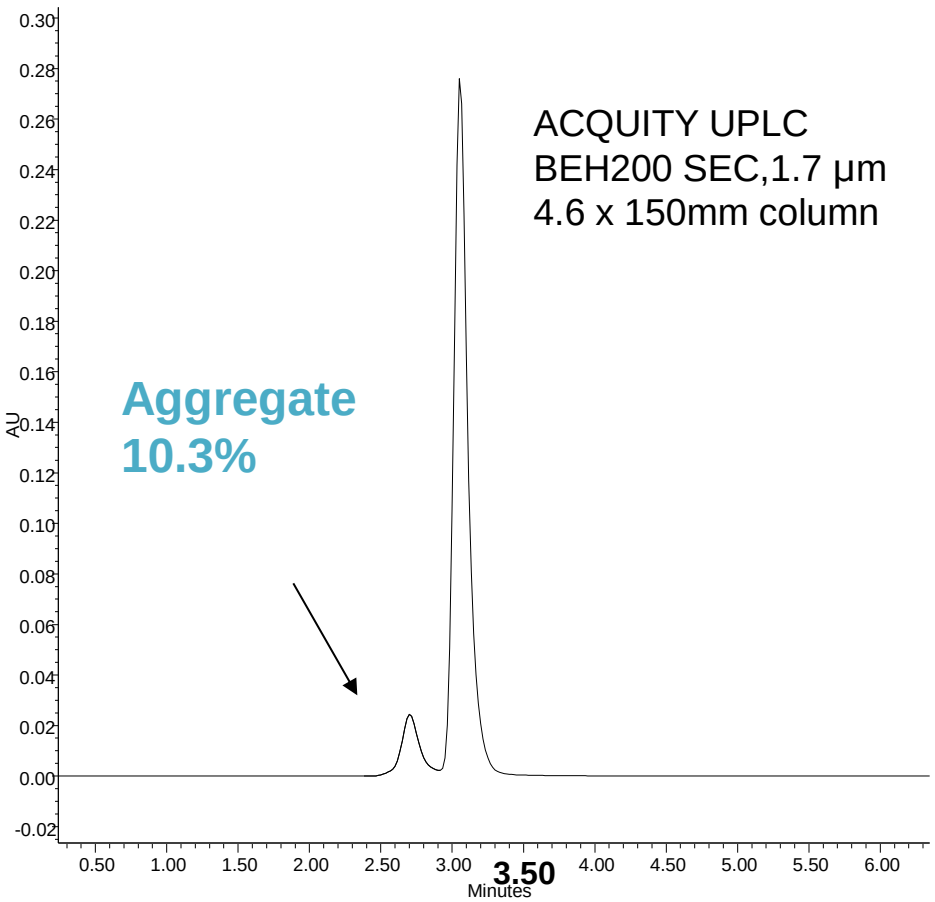


More Speed



Traditional SEC Comparison

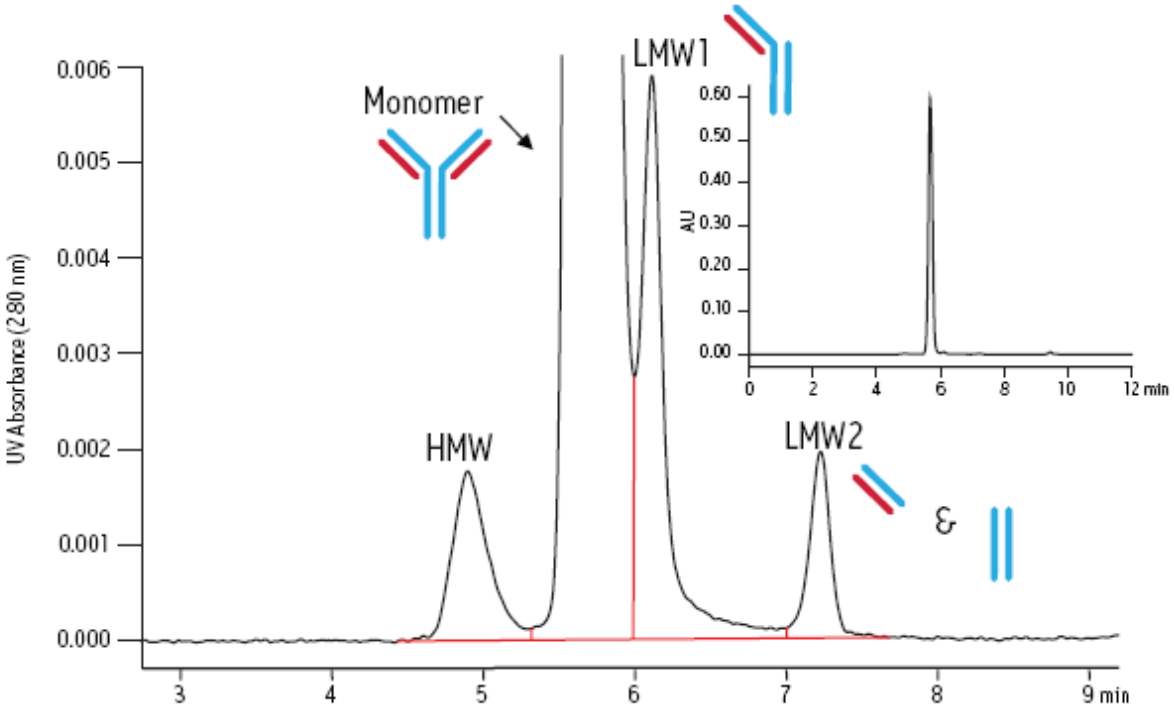




- Systems: HPLC- 2796 with 2497 Dual λ Wavelength Detector; ACQUITY UPLC® with TUV Detector, SS Flow Cell
- Flow rate: 0.4 mL/min; Mobile phase: 25mM Sodium phosphate, pH 6.8, 0.15M NaCl

Optimized separation of trastuzumab and its fragments in SE-UPLC

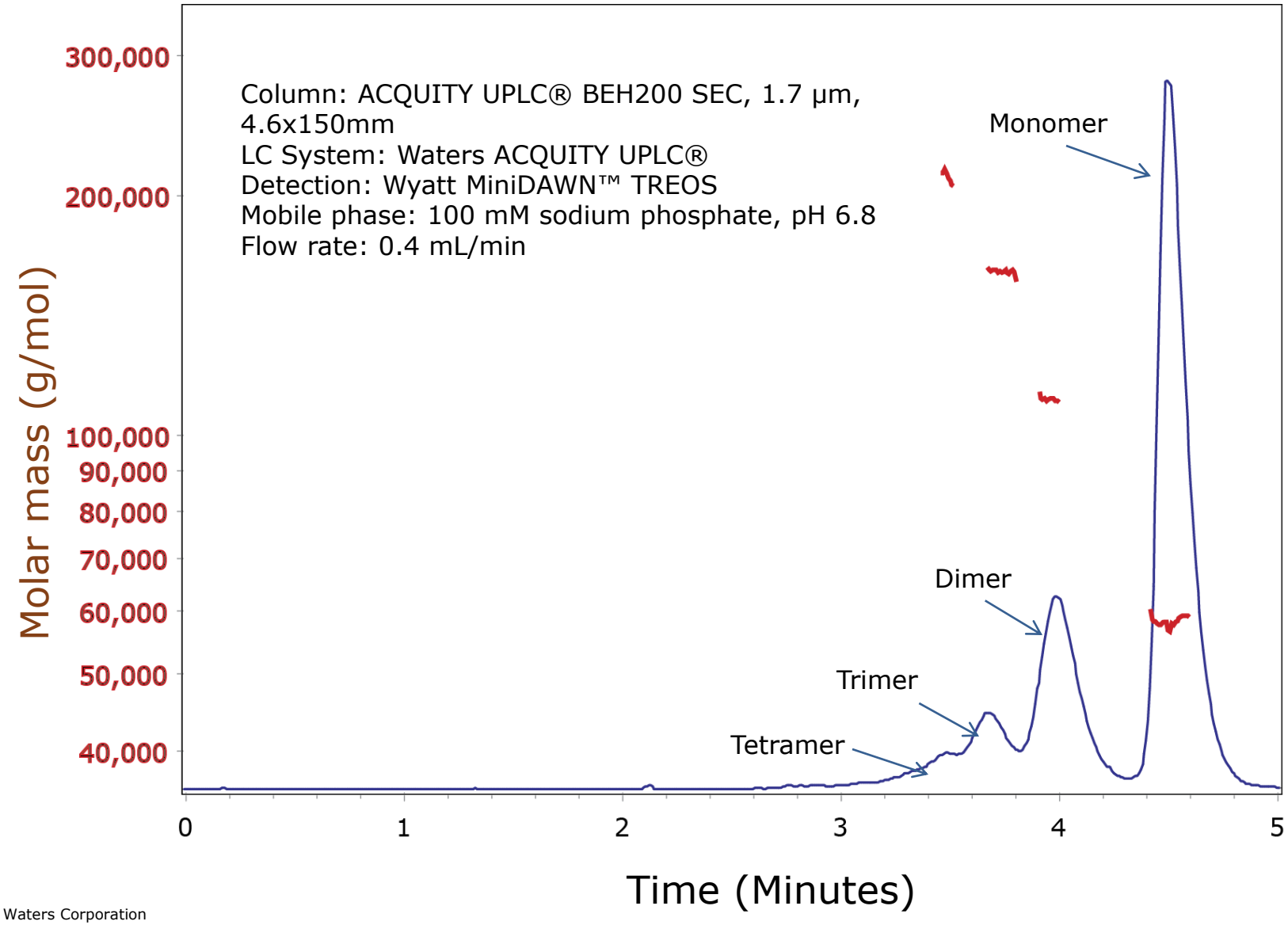
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Evaluation (n=4)		HMW	Monomer	LMW1	LMW2
Average Peak	Area (%)	0.51	98.02	1.15	0.33
%RSD	Area (%)	0.98	0.03	1.31	3.08

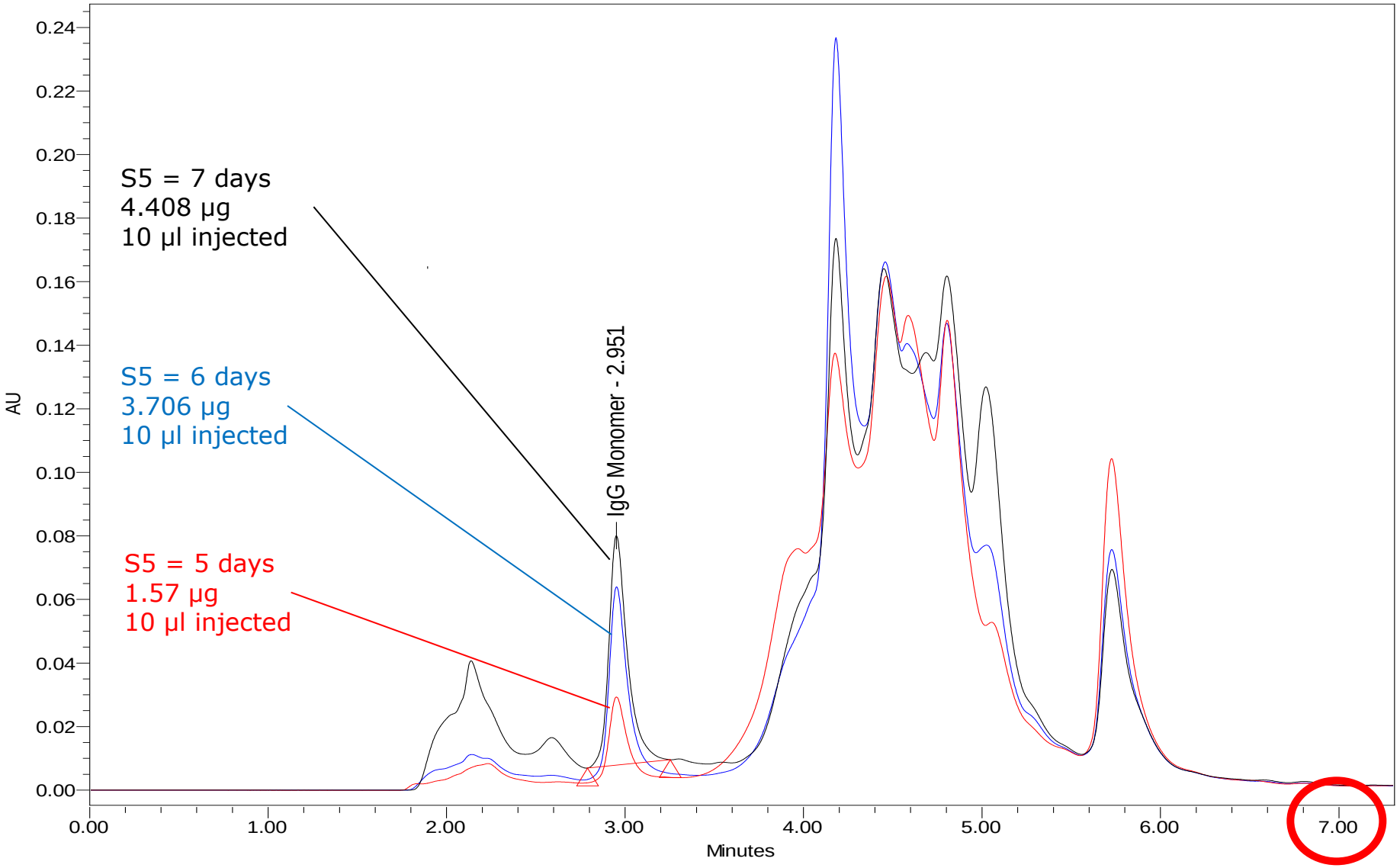
Separation of BSA and its Aggregates on ACQUITY With MALS Detection

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



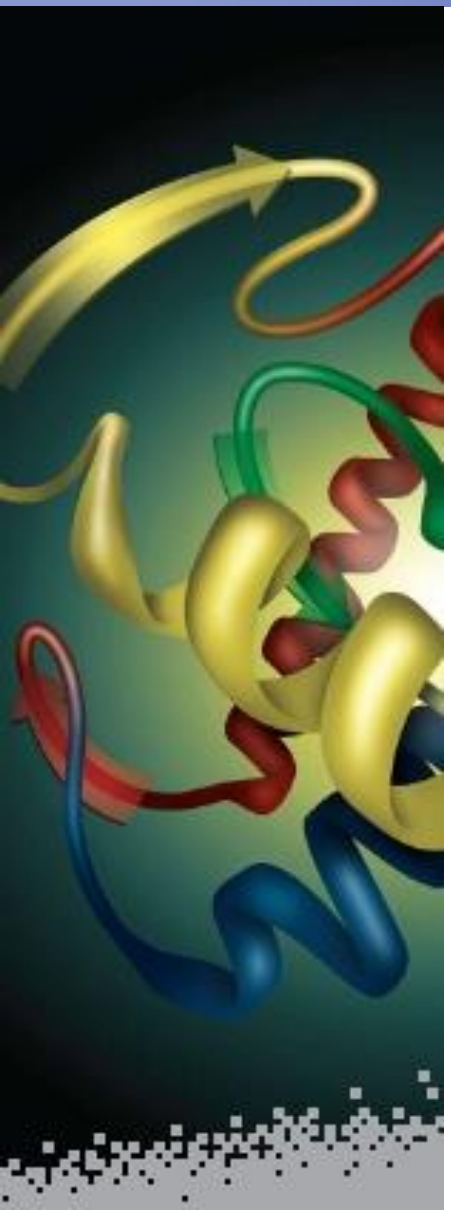
Exemple of SEC with TUV detector
IgG quantification in cell supernatant
Kinetics of IgG production

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Chromatography of proteins

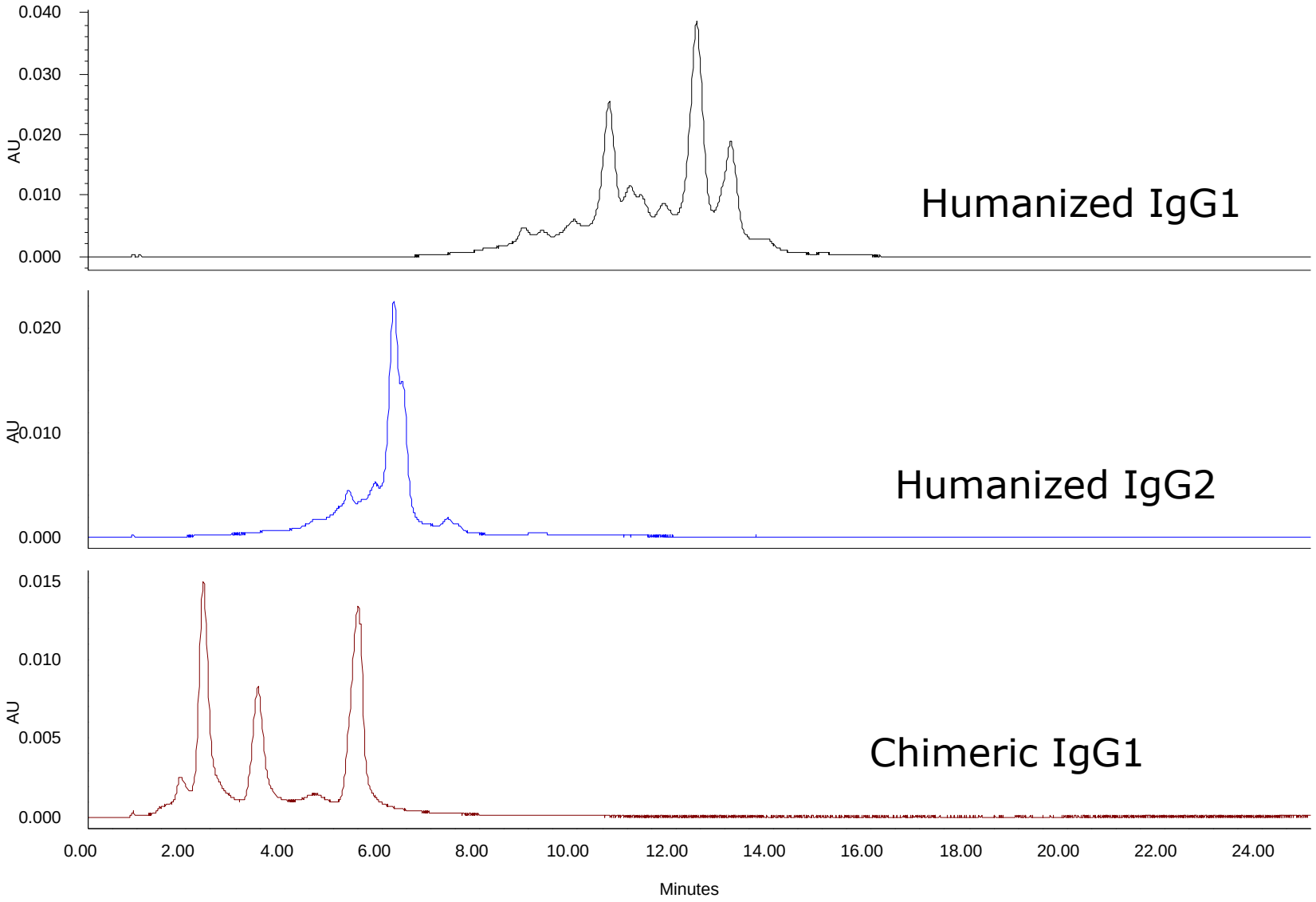
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



- Size Exclusion Chromatography :
  Aggregation, Fragmentation, Separation, Isolation, Quantification
- Ion Exchange Chromatography :
  Charge variants, fractionnation of complexe samples
- Reverse Phase Chromatography :
  Hydrophobicity separation, Intact Mass Analysis, Quantification

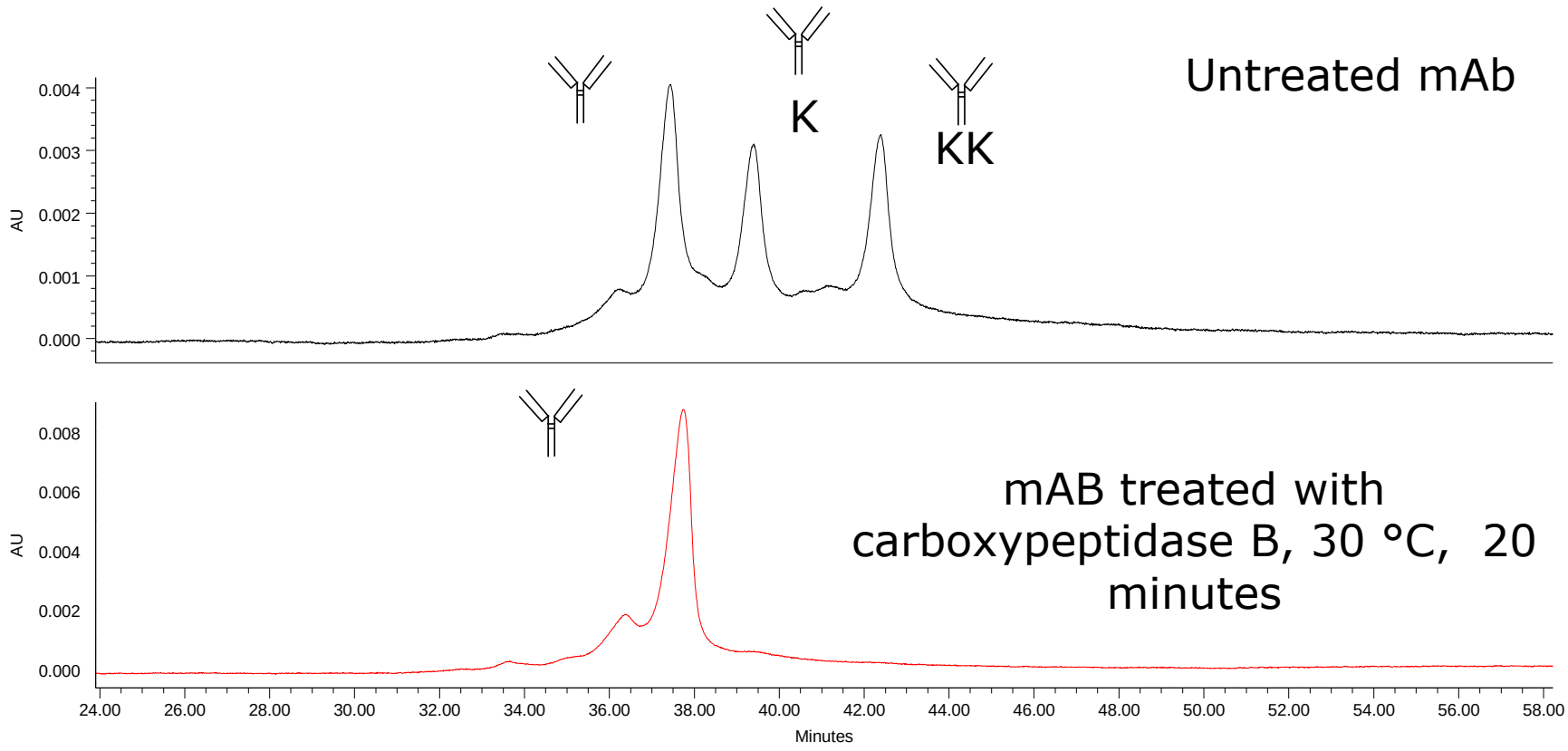
Ion-Exchange Analysis of Antibodies on Protein-Pak Hi Res CM Column

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Confirmation of c-terminal Lysine Variants of mAb

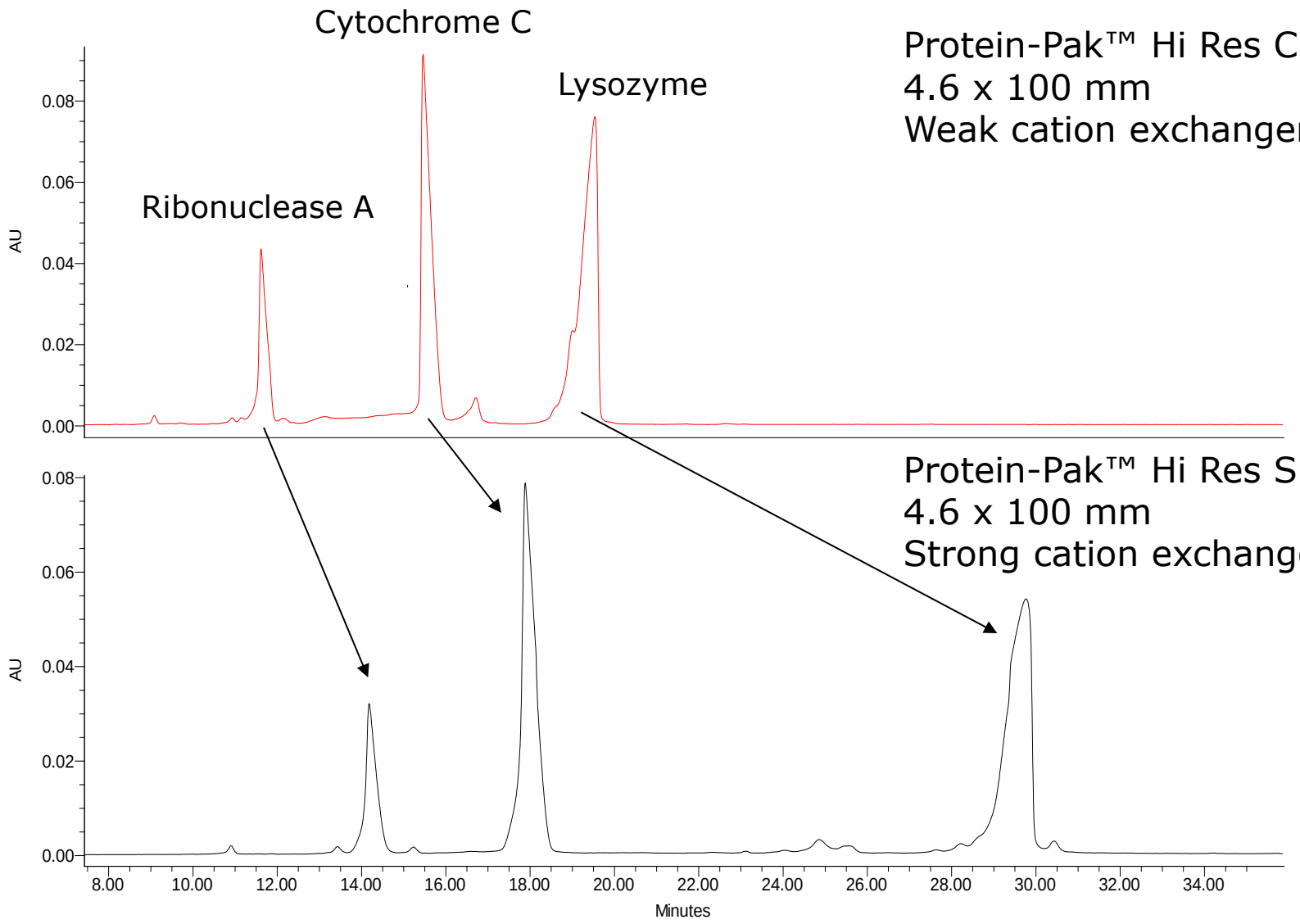
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



- IEX can be used to confirm the presence of mAb lysine variants
- Column: Protein-Pak Hi Res CM, 4.6 x 100mm

Protein-Pak Hi Res CM and SP Column Comparison

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

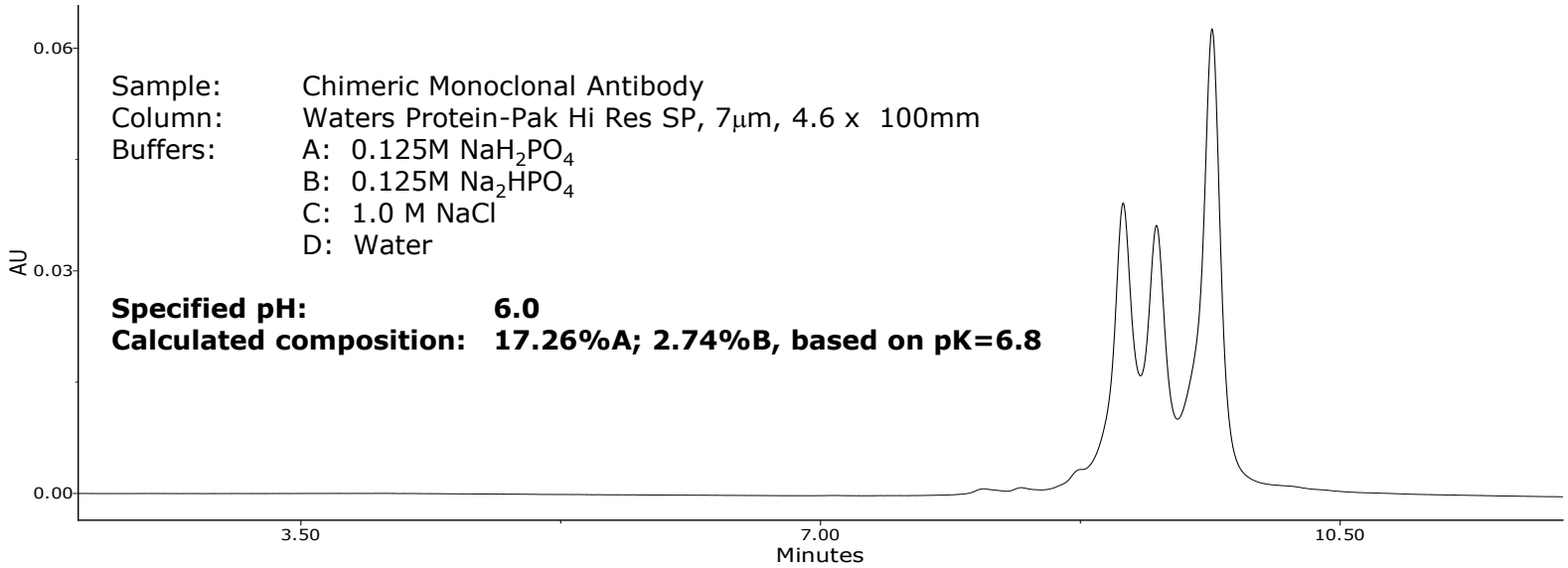


Protein-Pak™ Hi Res CM, 7 µm
4.6 x 100 mm
Weak cation exchanger

Protein-Pak™ Hi Res SP, 7 µm
4.6 x 100 mm
Strong cation exchanger

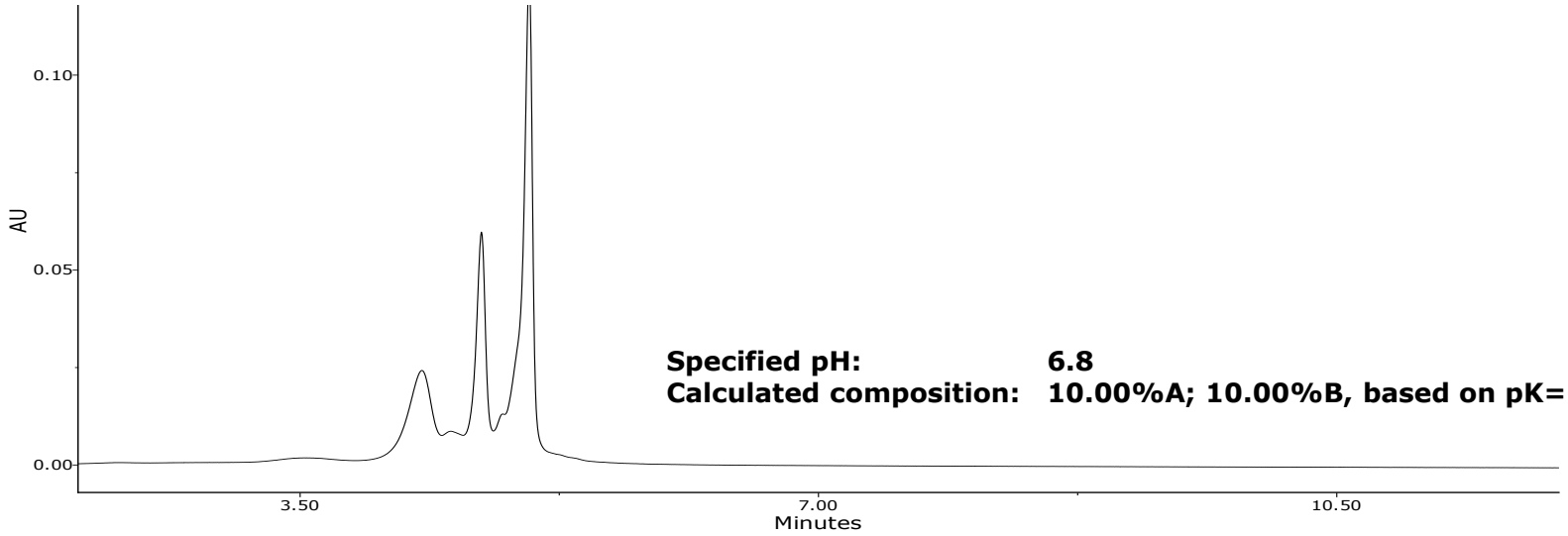
IEX of Chimeric Monoclonal Ab
Effect of AutoBlend Plus pH Adjustment

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Sample: Chimeric Monoclonal Antibody
Column: Waters Protein-Pak Hi Res SP, 7μm, 4.6 x 100mm
Buffers: A: 0.125M NaH_2PO_4
B: 0.125M Na_2HPO_4
C: 1.0 M NaCl
D: Water

Specified pH: 6.0
Calculated composition: 17.26%A; 2.74%B, based on pK=6.8



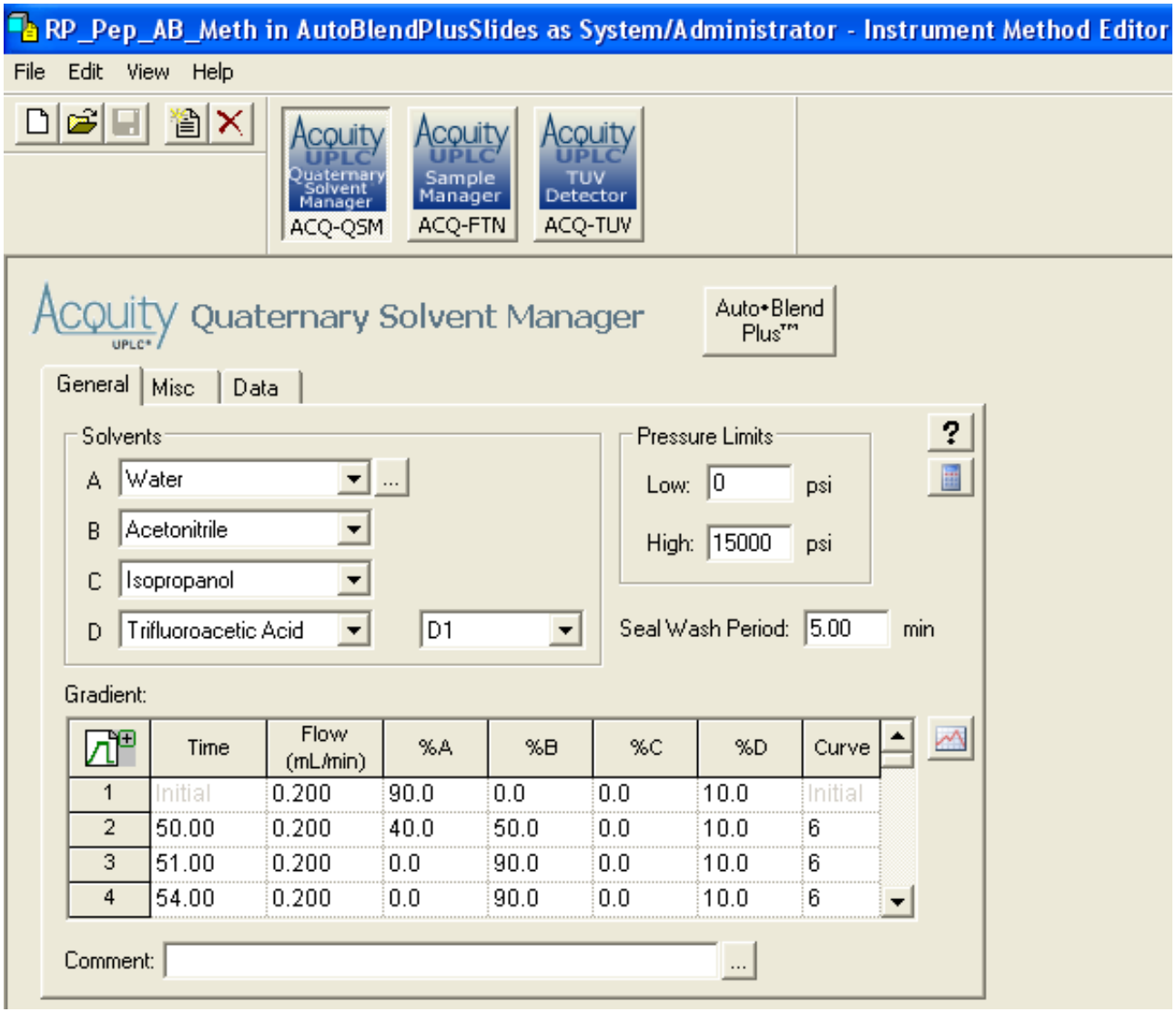
Specified pH: 6.8
Calculated composition: 10.00%A; 10.00%B, based on pK=6.8

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Auto●Blend™ and Auto●Blend Plus™ Technology

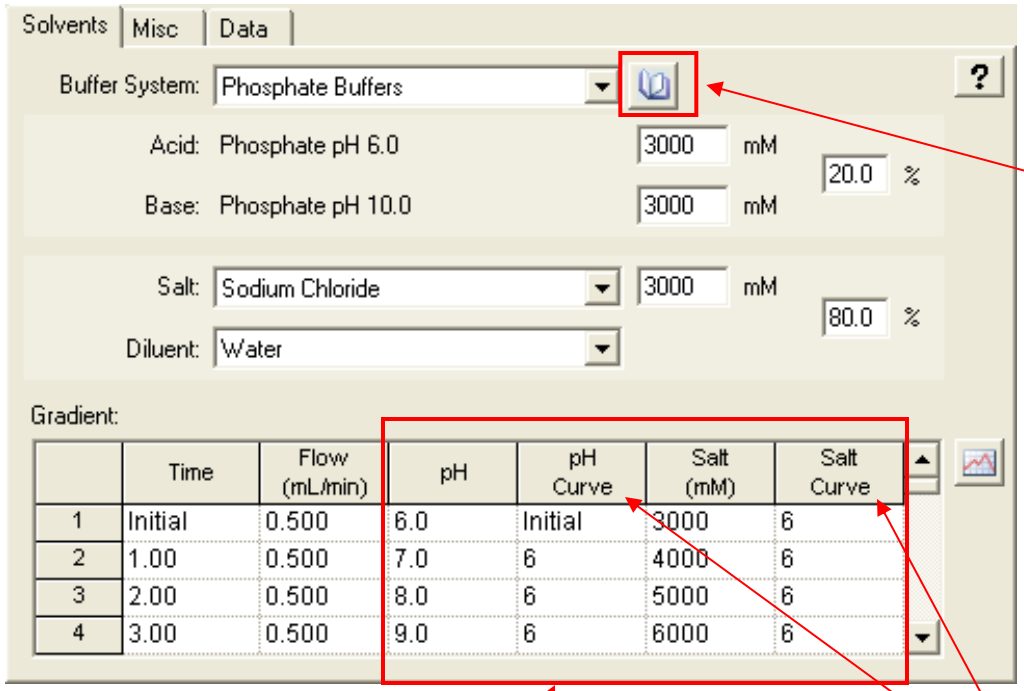
Conventional Method Editor Program Percentage Flow

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

"Auto•Blend Plus"



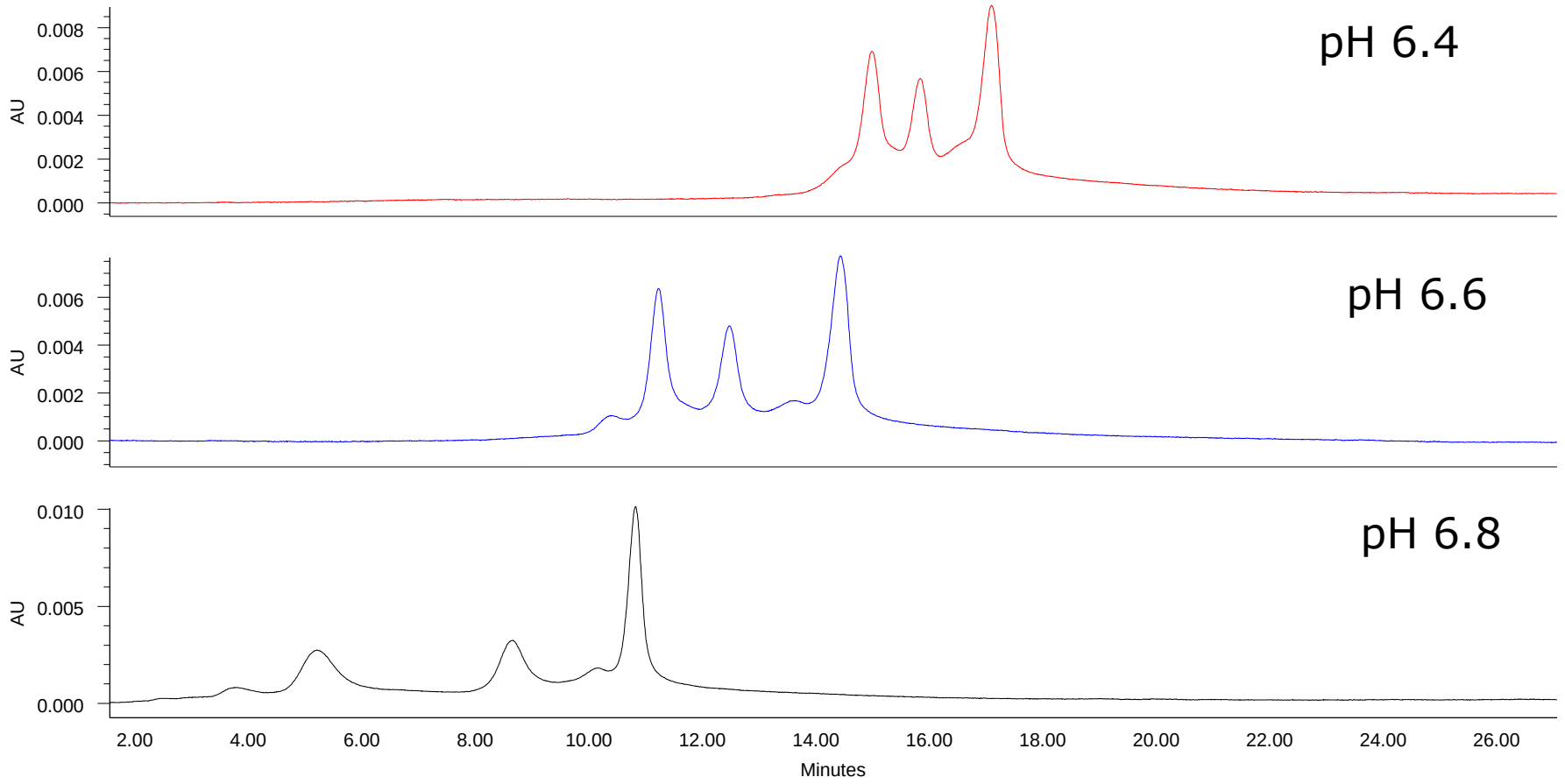
Solvent library with pH & other solvent characteristics

User now programs 'Gradient' profile in pH & Salt strength

Two independent Waters Curves

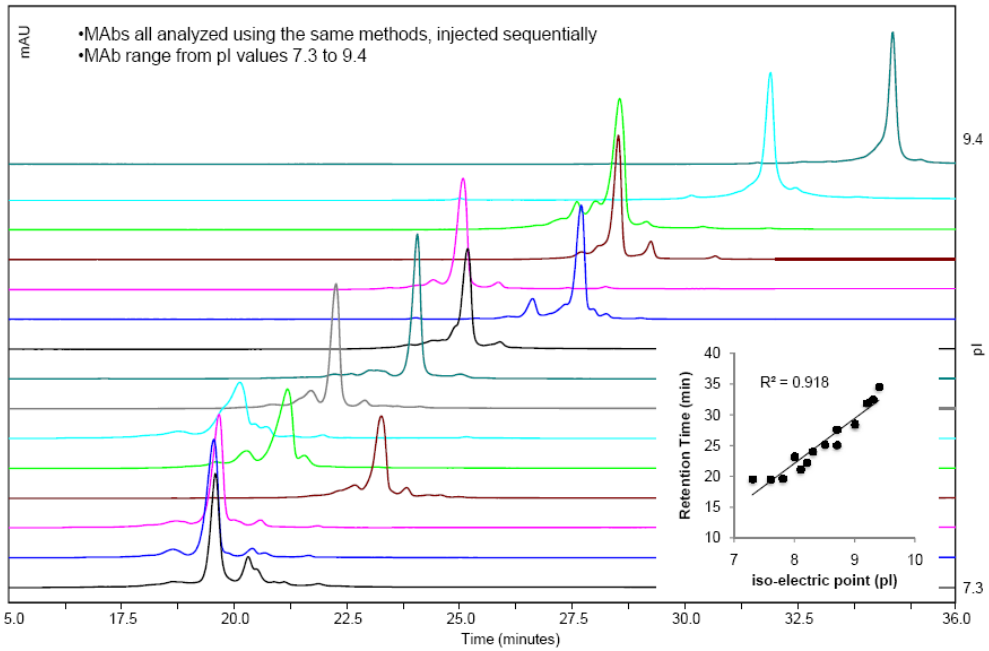
pH Effect on mAb Separation

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



- pH can be used to optimize separation of mAb variants
- Column: Protein-Pak Hi Res CM 4.6 x 100 mm column

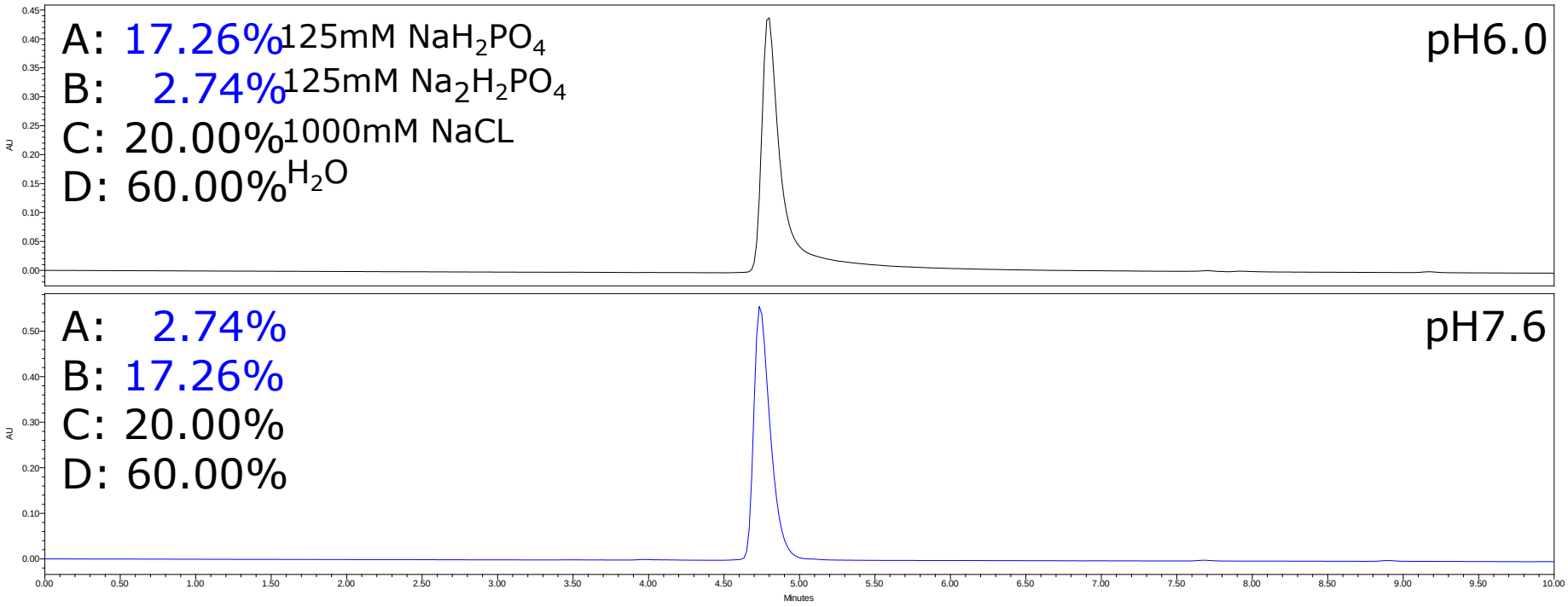
Interest of pH gradients



- Retention time is pI dependant.
- One method for acidic and basic degradants
- More robust method regarding the sample composition

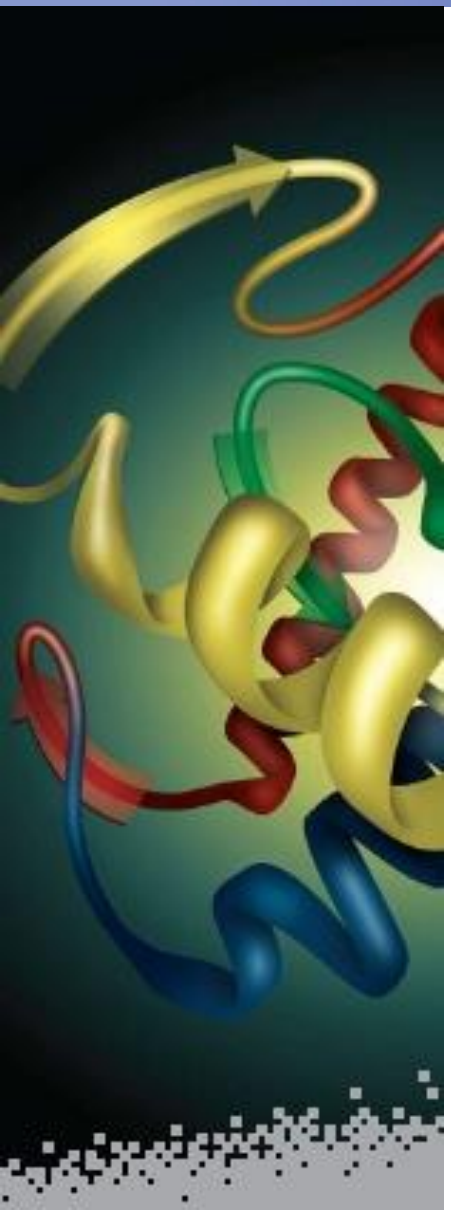
SEC of Humanized Monoclonal Ab
Effect of AutoBlend Plus pH Adjustment

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Chromatography of proteins

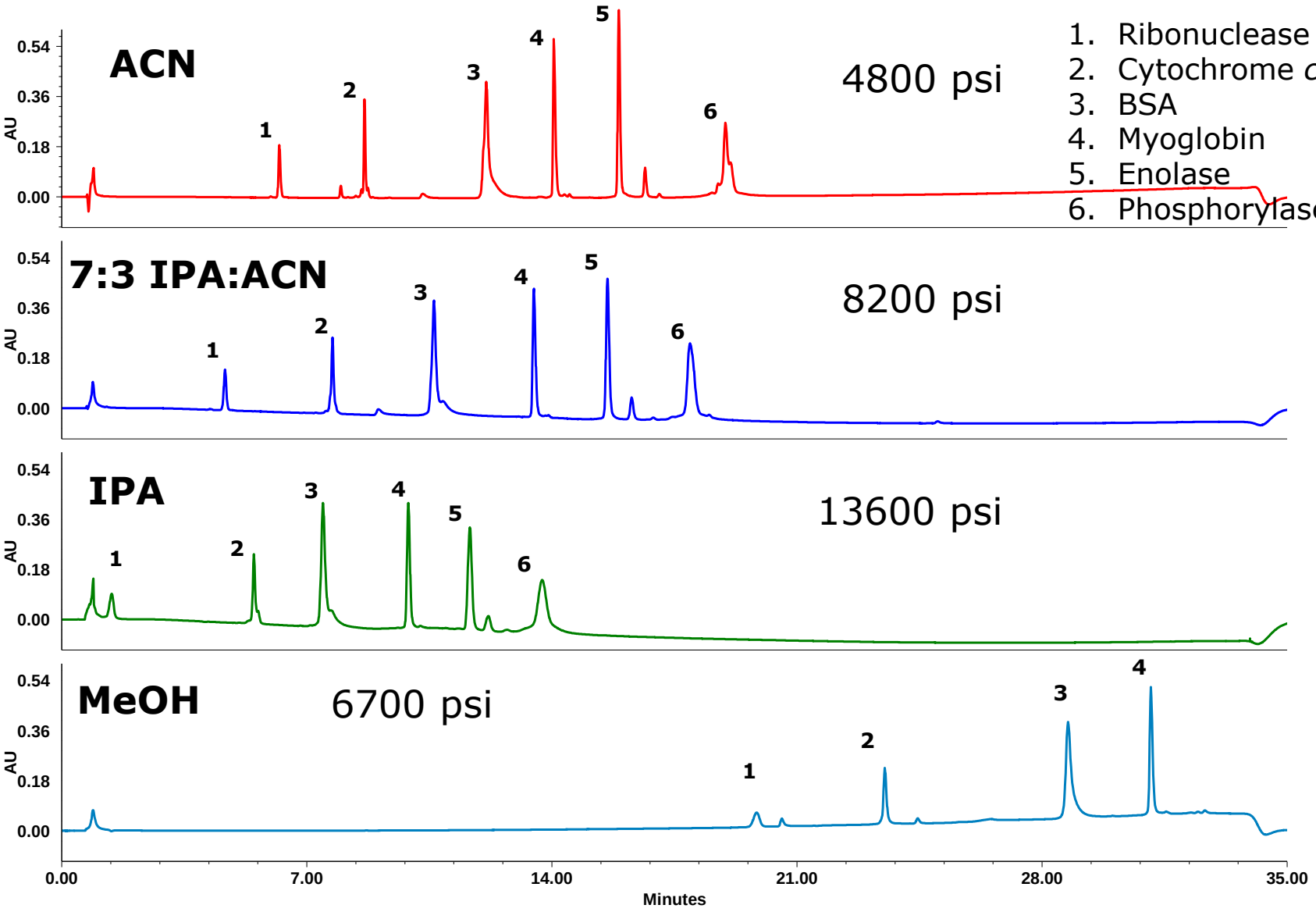
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



- Size Exclusion Chromatography :
  Aggregation, Fragmentation, Separation, Isolation, Quantification
- Ion Exchange Chromatography :
  Charge variants, fractionnation of complexe samples
- Reverse Phase Chromatography :
  Hydrophobicity separation, Intact Mass Analysis, Quantification

Protein Mix
Effect of Solvent on Separation @ 40 °C

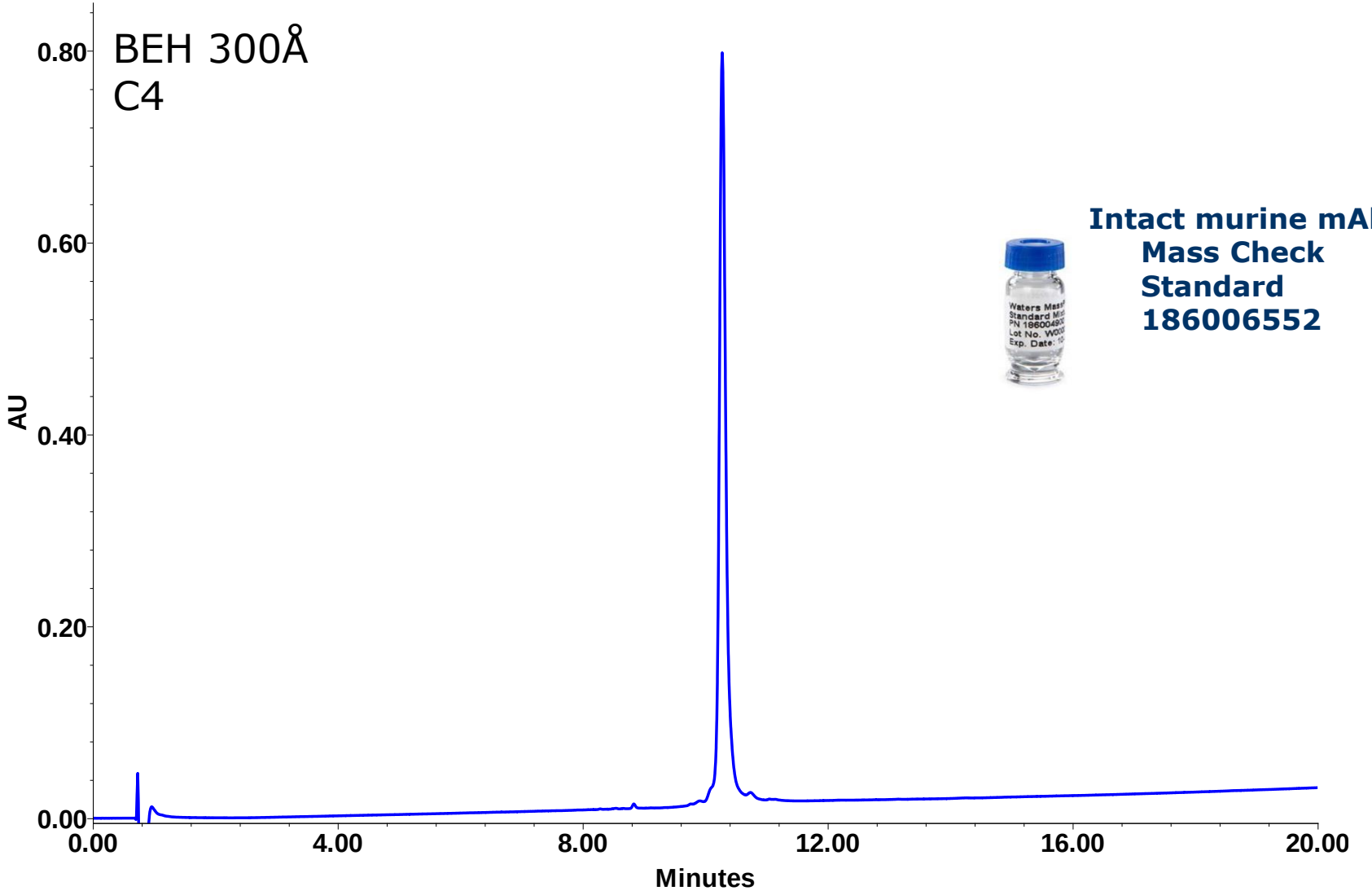
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



1. Ribonuclease
2. Cytochrome *c*
3. BSA
4. Myoglobin
5. Enolase
6. Phosphorylase b

Murine Monoclonal IgG

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

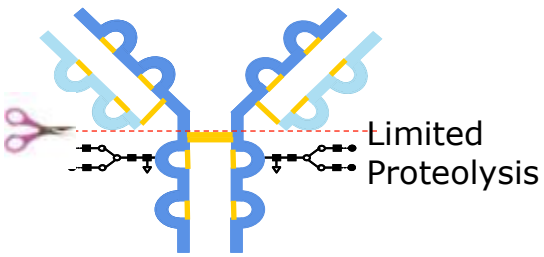


Intact murine mAb Mass Check Standard 186006552

The large IgG molecule elutes as a narrow, symmetrical peak.

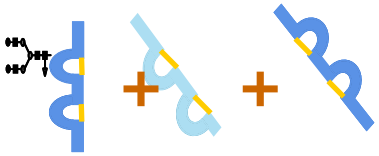
Better chromatography also with MS friendly eluents

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Total:
20 min

Partial
Reduction



Fc/2 LC Fd

Fd: 23960.5 Da

LC: 23437.5 Da

Fc/2: 26502.5 Da
26648.5 Da
26810.5 Da
26973.0 Da

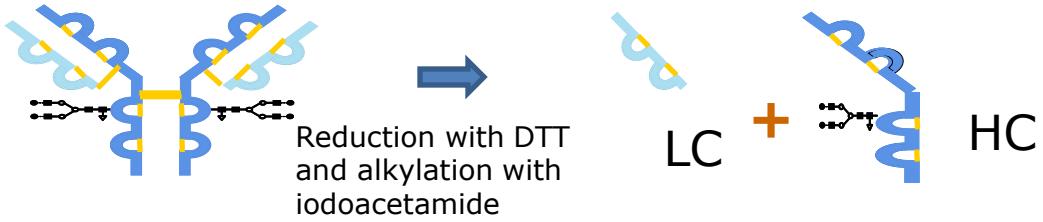
Fc/2 clip 1:
14488.5 Da
14650.5 Da
14812.5 Da

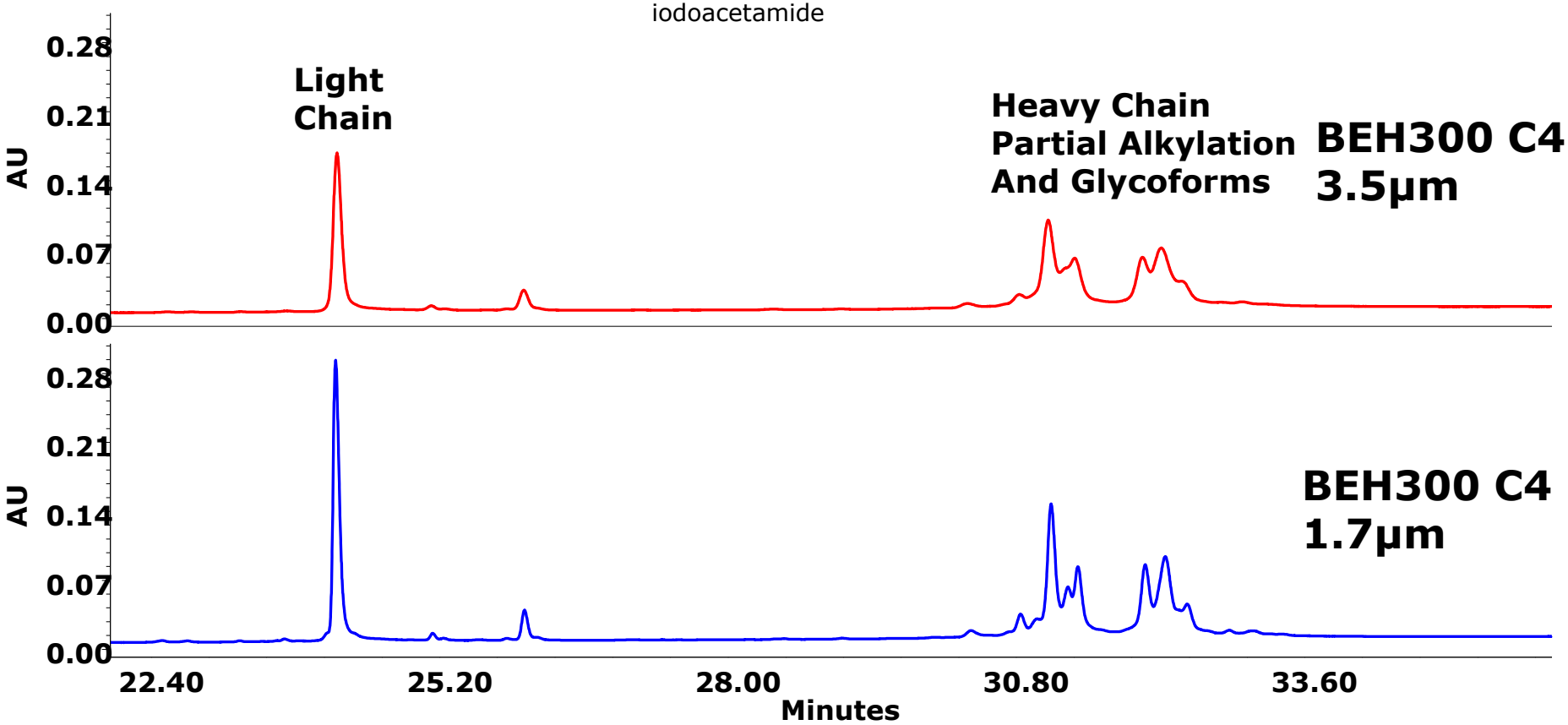
Fc/2 clip 2:
12178.0 Da

BEH300 C4 separations can be directly coupled to LC/MS Tof detectors.

Separation of antibody fragments IgG Heavy and Light Chains

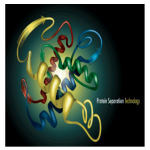
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

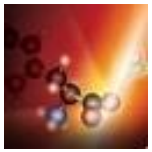




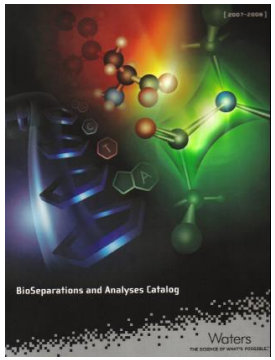
The improved resolution UPLC® protein analysis absolutely preserves the selectivity across particle sizes.

Overview of Waters solutions for Biomolecules

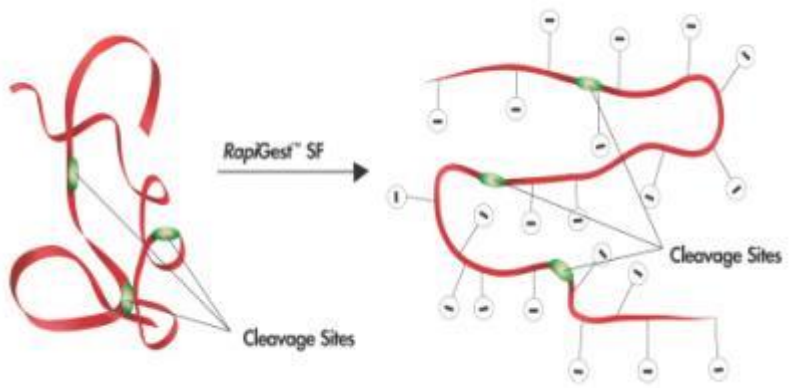





- Protein Characterization, Analysis and Purification (PrST)
  SEC, IEX, RP, HIC
- Peptide Separation Technology (PST)
  RP, HILIC
- Amino Acid Analysis (AAA)
  AccqTag Ultra
- Oligonucleotide Separation Technology (OST)
  IP-RP, IEX
- Glycan Separation Technology (GST)
  HILIC, RP
  Carbohydrates : SEC, IEX, HILIC, RP
- Sample preparation solutions and MS consumables
  - Phosphopeptide extraction
  - Digestion of proteins
  - Desalting devices
  - **Standards**



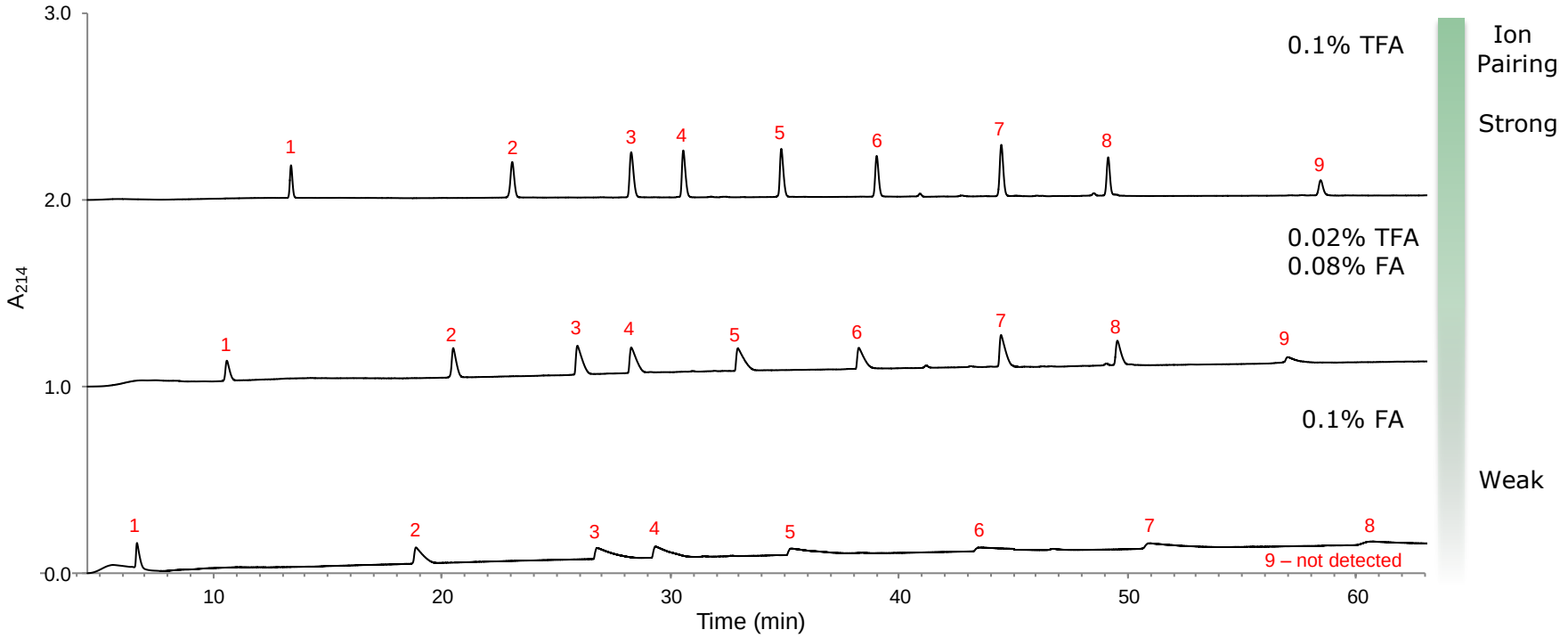
What's RapiGest™ SF



- It's compatible with current protein digestion sample prep protocols.
- It is an anionic detergent that improves solubility (i.e., unfolding) and digestion of proteins for improved enzymatic digests.
- Unlike conventional denaturants, RapiGest SF does not inhibit enzyme activities so it reduces digestion times and reduces the amount of enzyme used.
- It does not cause protein modifications (e.g., deamidation) unlike some other protein denaturants.
- It's an acid labile surfactant whose degradation products do not interfere with LC/MS or MALDI MS analysis.

Competitor's "Industry Standard" 5 µm Porous Silica C18

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Competitor's "Industry Standard" C18
2.1 x 250 mm, Porous 5 µm, 300Å
ACQUITY UPLC® H-Class Bio

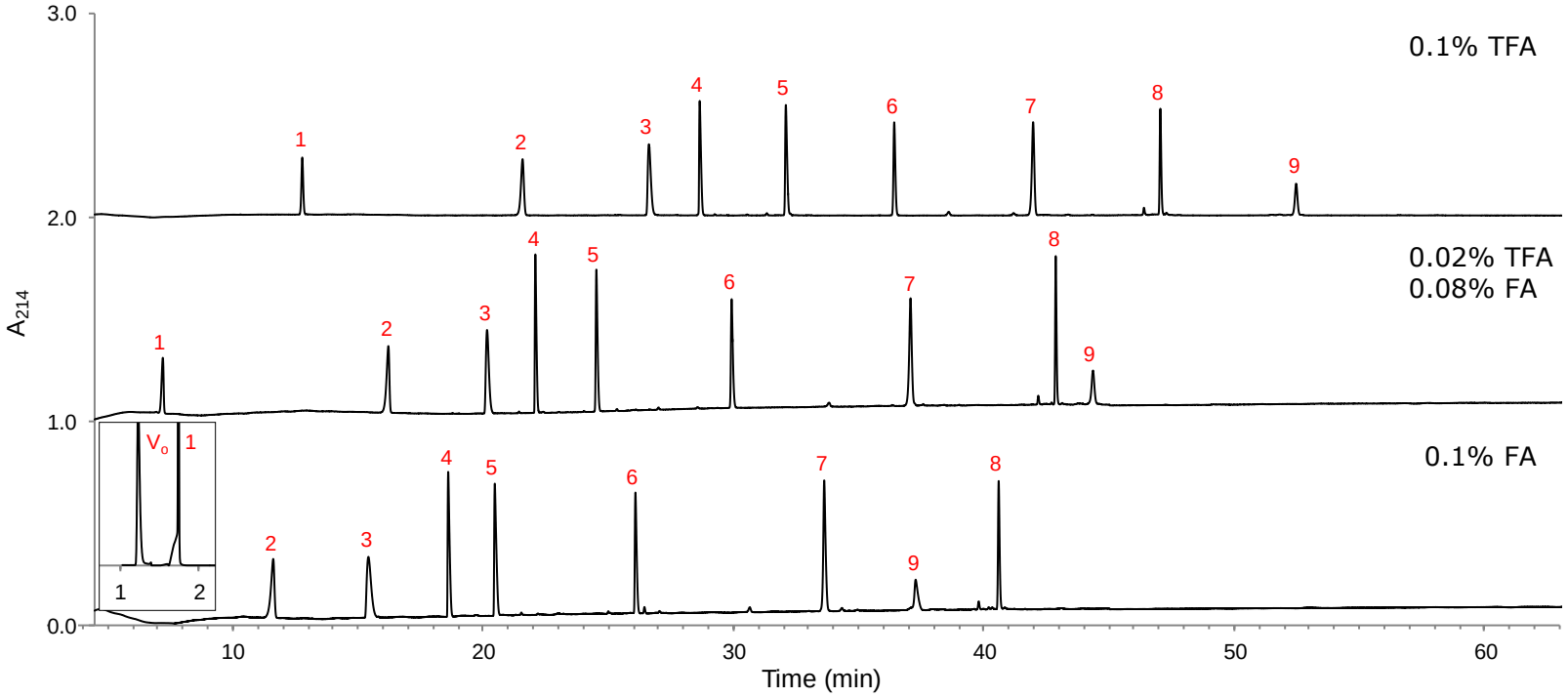
2% ACN for 1 min,
then to 50% ACN over 60 min
0.3 mL/min
40°C
UV @ 214 nm / Xevo® G2 QTOF
5.6 µg MassPREP Peptide Mixture

MassPREP™ Peptide Mixture

	Peptide	Sequence
1	RASG-1	RGDSPASSKP
2	Angiotensin 1-7	DRVYIHP
3	Bradykinin	RPPGFSPFR
4	Angiotensin II	DRVYIHPF
5	Angiotensin I	DRVYIHPFHL
6	Renin Substrate	DRVYIHPFHLLVYS
7	Enolase T35	WLTGPQLADLYHSLMK
8	Enolase T37	YPIVSIEDPFAEDDWEAWSHFFK
9	Melittin	GIGAVLKVLTTGLPALISWIKRKRQQ

A New Column Chemistry – CSH130 C18

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

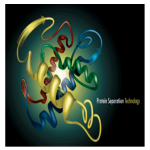


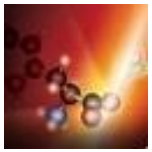
Waters ACQUITY UPLC CSH130 C18
2.1 x 150 mm, Porous 1.7 µm, 130Å

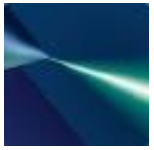
CSH™ Technology

	Peptide	Sequence
1	RASG-1	RGDSPASSKP
2	Angiotensin 1-7	DRVYIHP
3	Bradykinin	RPPGFSPFR
4	Angiotensin II	DRVYIHPF
5	Angiotensin I	DRVYIHPFHL
6	Renin Substrate	DRVYIHPFHLLVYS
7	Enolase T35	WLTGPQLADLYHSLMK
8	Enolase T37	YPIVSIEDPFAEDDWEAWSHFFK
9	Melittin	GIGAVLKVLTTGLPALISWIKRKRQQ

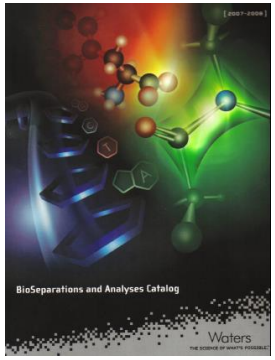
Overview of Waters solutions for Biomolecules





- Protein Characterization, Analysis and Purification (PrST)
  SEC, IEX, RP, HIC
- Peptide Separation Technology (PST)
  RP, HILIC
- Amino Acid Analysis (AAA)
  AccqTag Ultra
- Oligonucleotide Separation Technology (OST)
  IP-RP, IEX
- Glycan Separation Technology (GST)
  HILIC, RP
  Carbohydrates : SEC, IEX, HILIC, RP
- Sample preparation solutions and MS consumables
  - Phosphopeptide extraction
  - Digestion of proteins
  - Desalting devices
  - **Standards**



Chemistry of AQC Derivatization

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

AQC Reagent

Derivatized Amino Acid

- Reacts readily with both primary and secondary amines
- Forms stable derivatives
- Requires no vacuum drying, sample prep or extraction
- Amendable to automation

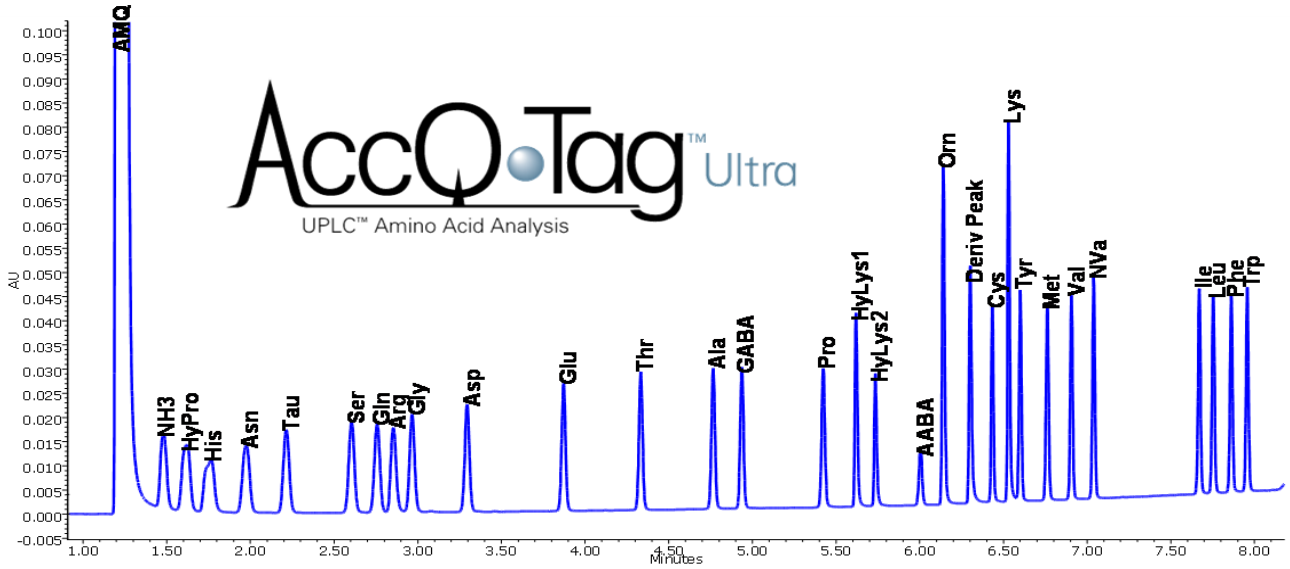
AccQ·Tag™ Ultra
UPLC™ Amino Acid Analysis

AAA for monitoring cell culture media

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

MONITORING CELL CULTURE MEDIA WITH THE WATERS AMINO ACID ANALYSIS SOLUTION

Paula Hong, Thomas E. Wheat, Jeffrey R. Mazzeo, and Diane M. Diehl
Waters Corporation, Milford, MA U.S.



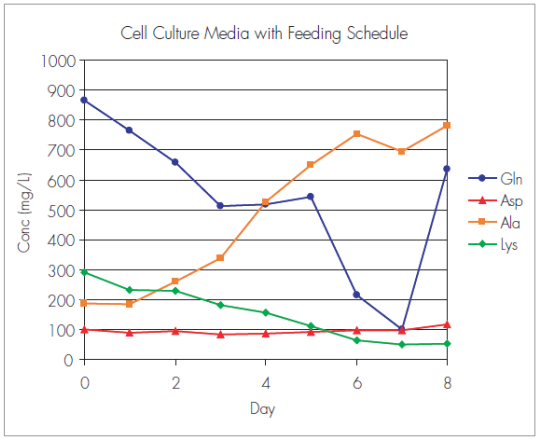


Figure 5. Quantitative trends in amino acid concentration during cell culture.

- ✓Cell media dilution
- ✓AccQ Tag derivatisation
- ✓UPLC with AccQ Tag Solvent
- ✓Column AccQ Tag (2.1X100)mm , 1.7um

→ **Monitoring cell culture**

AAA of hydrolysed protein

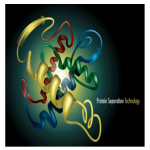
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

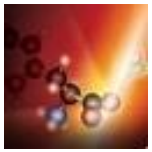
- Accurate protein concentration without interfering compounds coming from the sample matrix. (Bradford, BCA)
- Primary sequence confirmation by relative composition of each amino acids in a purified protein.

Sample ID	Total µg AA / mL Hydrolysate
BSA 1-1	699.64
BSA 1-2	694.09
BSA 1-3	697.88
BSA 1-4	698.21
BSA 1-5	695.43

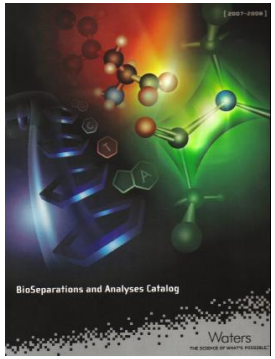
Amino Acid	Expected # Residues	*Observed # Residues
His	17	15.36 ± 0.19
Ser	28	26.00 ± 0.08
Arg	23	22.37 ± 0.08
Gly	16	17.68 ± 0.20
Asp	54	55.47 ± 0.21
Glu	79	80.68 ± 0.20
Thr	33	31.92 ± 0.06
Ala	47	47.51 ± 0.15
Pro	28	28.35 ± 0.14
Lys	59	57.78 ± 0.38
Tyr	20	20.19 ± 0.08
Met	4	4.16 ± 0.15
Val	36	35.67 ± 0.16
Ile	14	13.15 ± 0.15
Leu	61	63.13 ± 0.19
Phe	27	26.57 ± 0.13

Overview of Waters solutions for Biomolecules

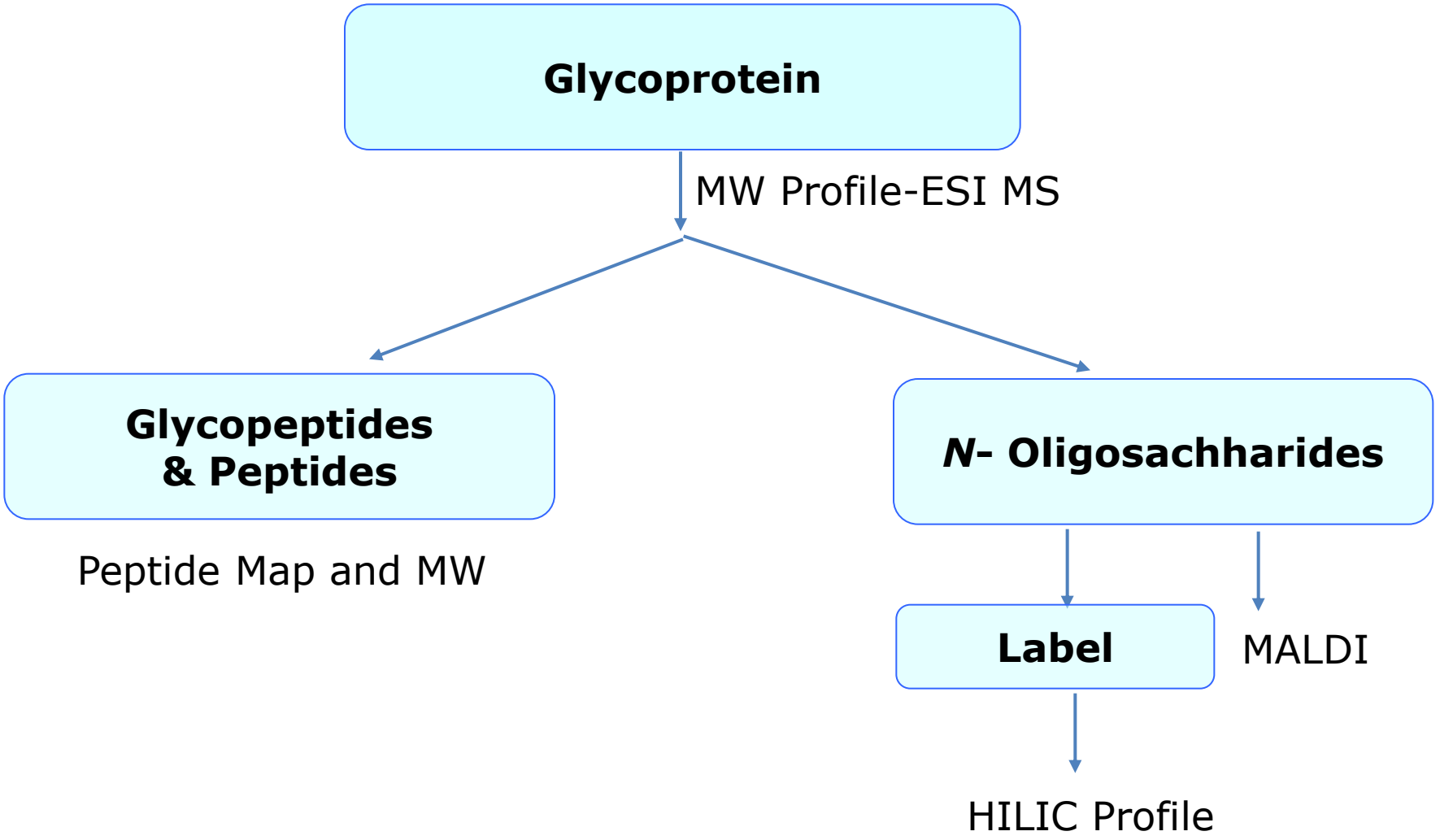





- Protein Characterization, Analysis and Purification (PrST)
  SEC, IEX, RP, HIC
- Peptide Separation Technology (PST)
  RP, HILIC
- Amino Acid Analysis (AAA)
  AccqTag Ultra
- Oligonucleotide Separation Technology (OST)
  IP-RP, IEX
- Glycan Separation Technology (GST)
  HILIC, RP
  Carbohydrates : SEC, IEX, HILIC, RP
- Sample preparation solutions and MS consumables
  - Phosphopeptide extraction
  - Digestion of proteins
  - Desalting devices
  - **Standards**



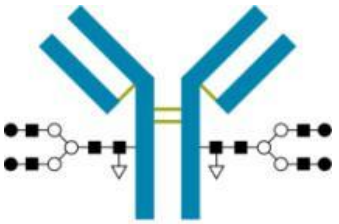
Waters Glycoprotein Work Flows



Waters Glycoprotein Work Flows

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

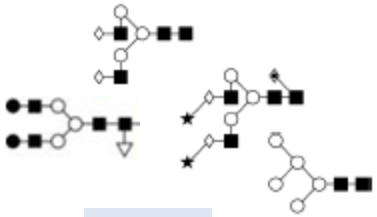
Glycoprotein



PNGase-F

RapiGest™ SF

MassPrep™
HILIC
µElution Plate

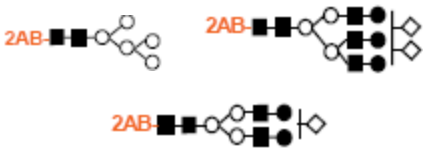


***N*- Oligosacharides**

2AB -Labelling

MALDI

MassPrep™
HILIC
µElution Plate

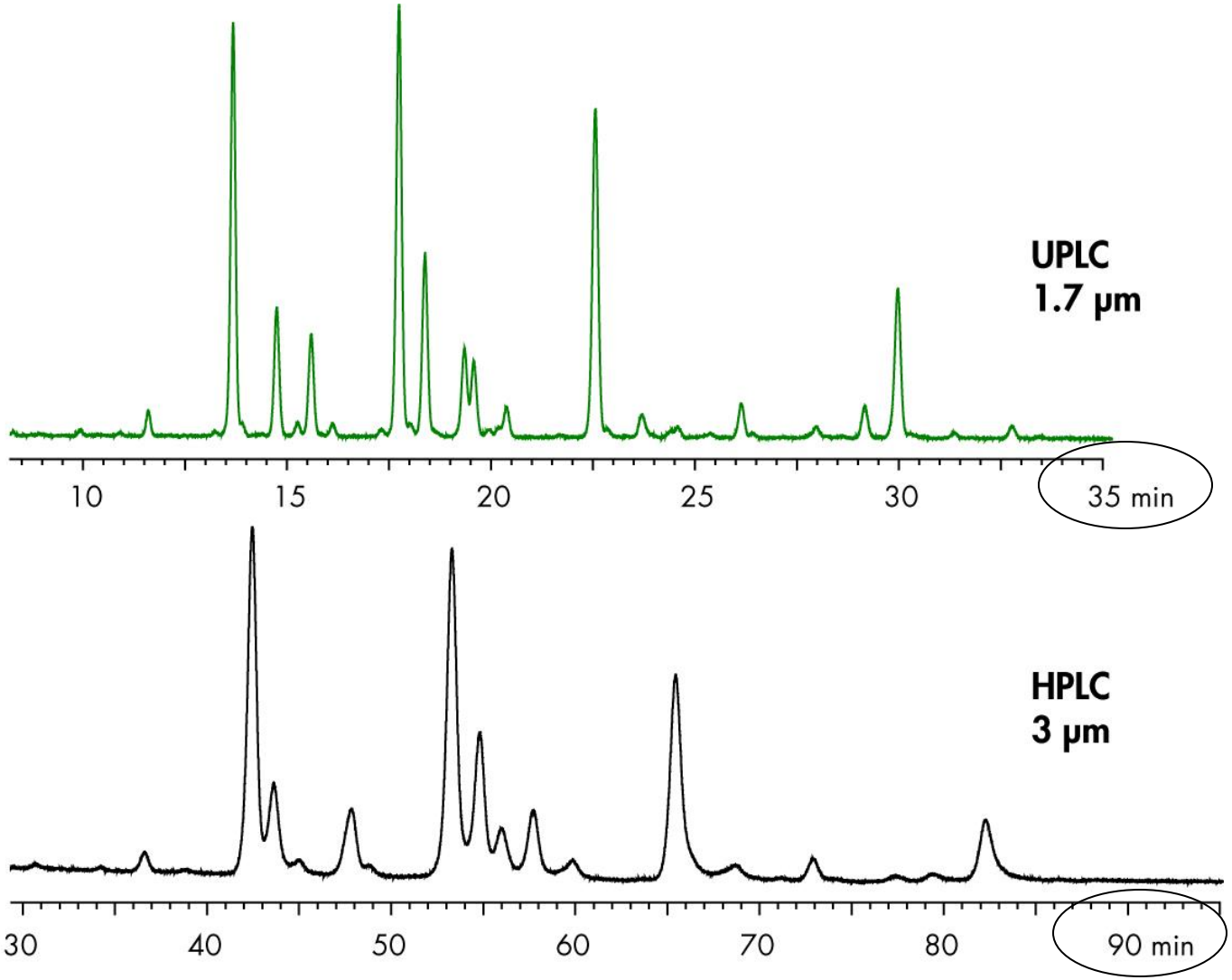


LC/Fluo analysis

BEH-Amide UPLC column

3µm HPLC column vs. 1.7µm ACQUITY UPLC® BEH Glycan column on an ACQUITY UPLC® System

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

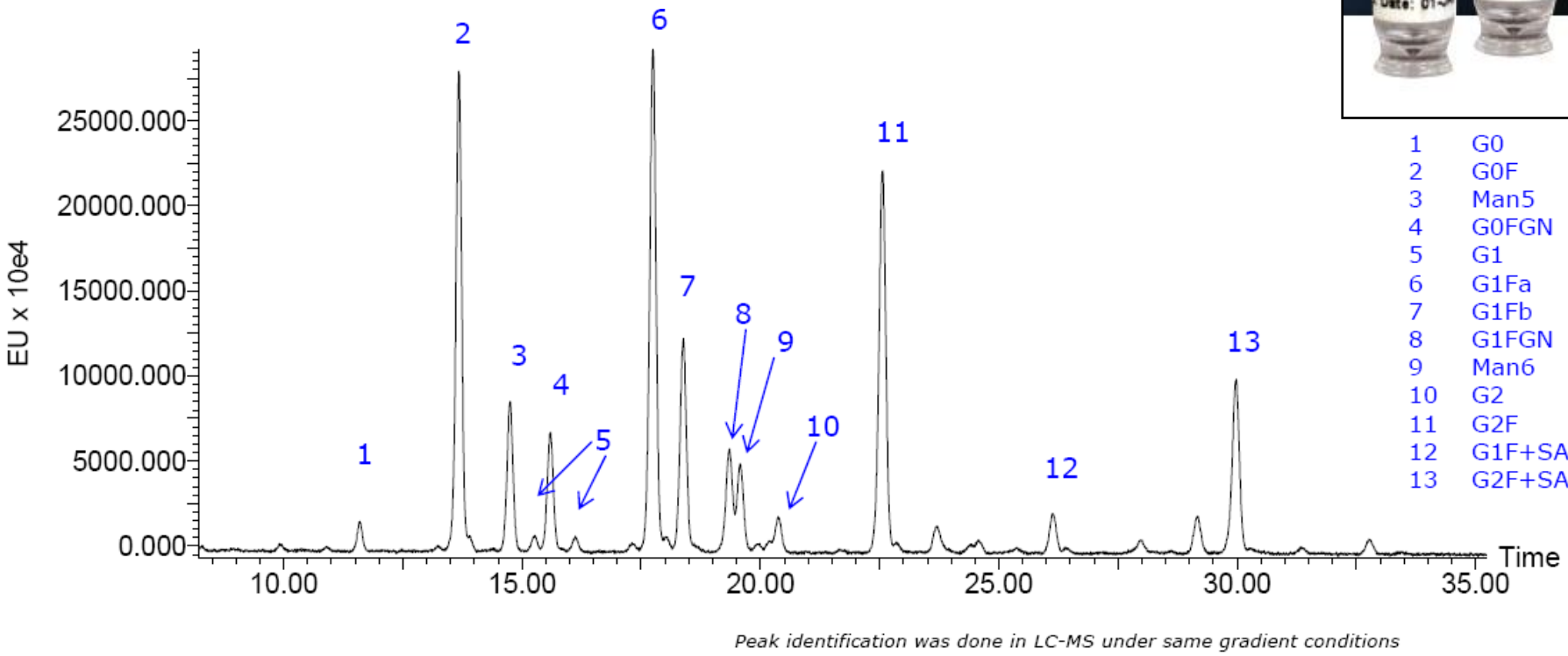


2AB-Labeled Glycans from Human IgG

UPLC FLD analysis of Human IgG 2AB-N-linked Glycans

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Glycan Performance Test Standard Mix :
PN : 186006349
Human IgG 2AB-Nlinked Glycans + Man5/6

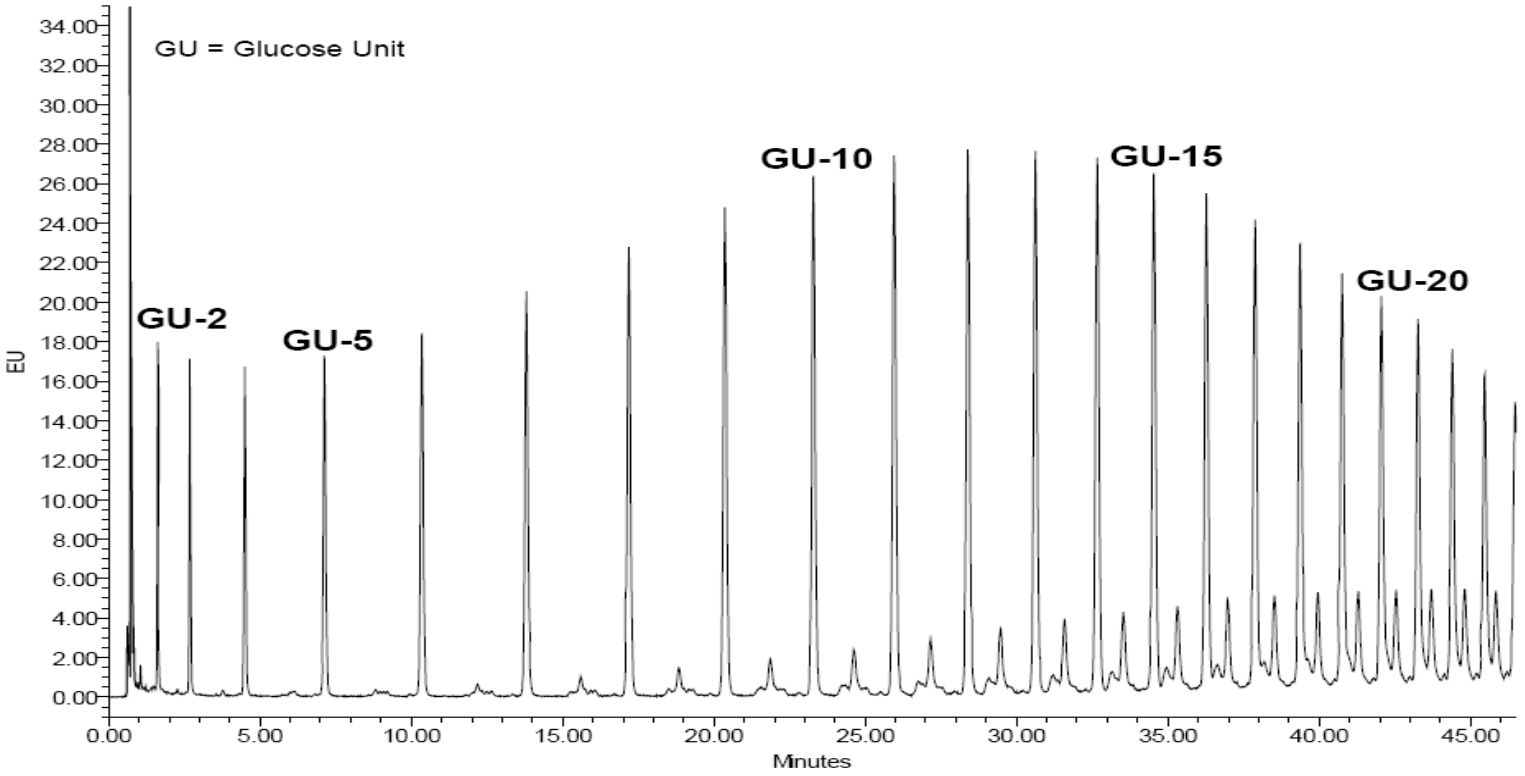


1	G0
2	G0F
3	Man5
4	G0FGN
5	G1
6	G1Fa
7	G1Fb
8	G1FGN
9	Man6
10	G2
11	G2F
12	G1F+SA
13	G2F+SA

Peak identification was done in LC-MS under same gradient conditions

UPLC® Separation
2-AB labeled Dextran Ladder

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

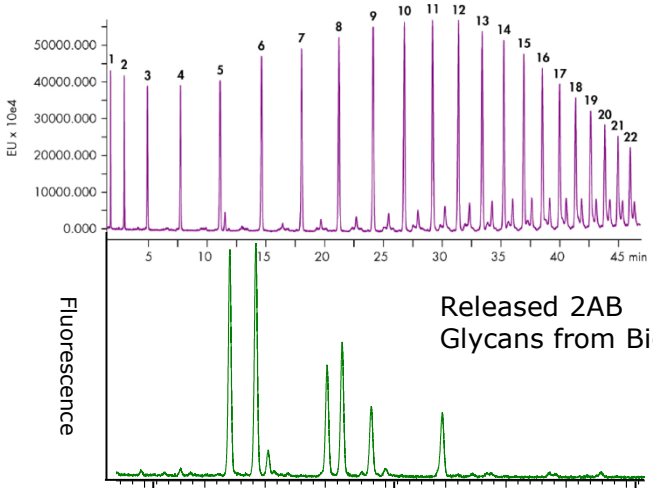


2AB Dextran Ladder Calibration Standards :
PN : 186006841
200µg/vial GU from 2 to 30

UPLC-FLR Released analysis complements mass data for glycan characterization

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

HILIC UPLC-FLR



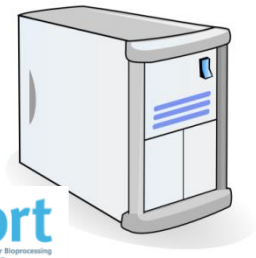
2AB Dextran Standard (GU)

Released 2AB Glycans from Biotherapeutic

Empower 3.0
UNIFI 1.6

GU Search

		GU HPLC	GU UPLC
F(3)XM3	avg.: 1189.080 mono: 1188.428		5.89 ±0.029
A3	avg.: 1520.402 mono: 1519.566	5.88 ±0.045	5.90 ±0.029
F(6)A2	avg.: 1463.351 mono: 1462.544	5.88 ±0.032	5.90 ±0.042
Galß1-4[Fucα1-3]GlcNAcß1-3Galß1-4GlcNAcß1-6[Galß1-3]GalNAc	avg.: 1260.158 mono: 1259.465		5.93



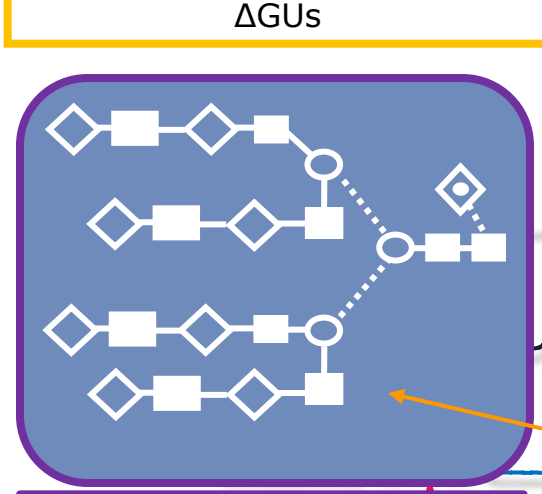
nibrt National Institute for Bioprocessing Research and Training

GLYCOBASE 3.0+

New Glycan Found in EPO Exoglycosidase Digestion with UPLC/FLR

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Same digestion pattern and ΔGUs



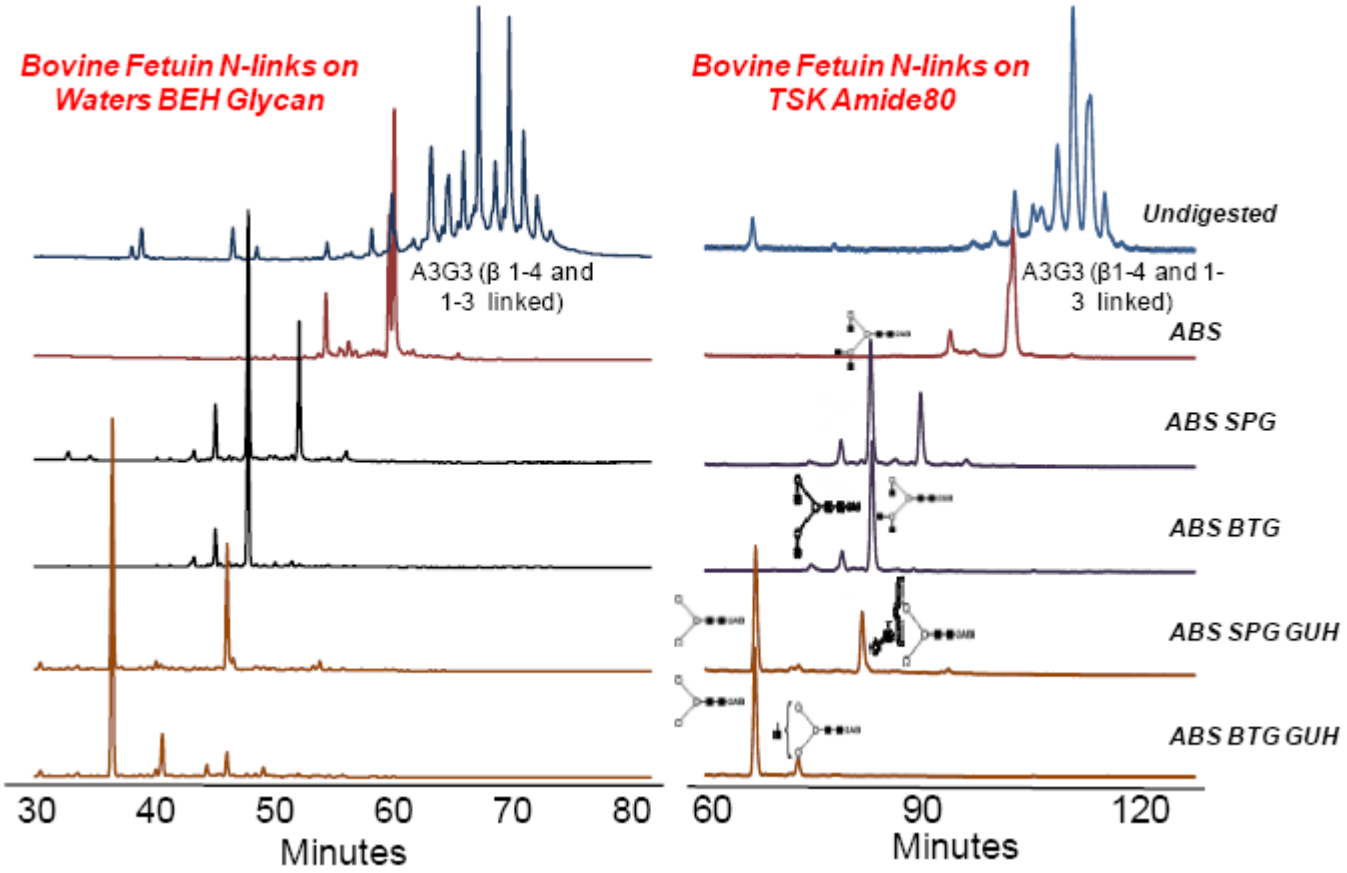
F(6)A4G4Lac4S4
GU ~ 14.8

GlycoBase V2.0
Developed by Pauline Rudd's group at the
Oxford Glycobiology Institute (Director Raymond A Dwek FRS)
and now at NIBRT, Ireland

nibrt

Glycan structure using exoglycosidase & Glucose unit libraries

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



GlycoBase V2.0

Developed by Pauline Rudd's group at the Oxford Glycobiology Institute (Director Raymond A Dwek FRS) and now at NIBRT, Ireland

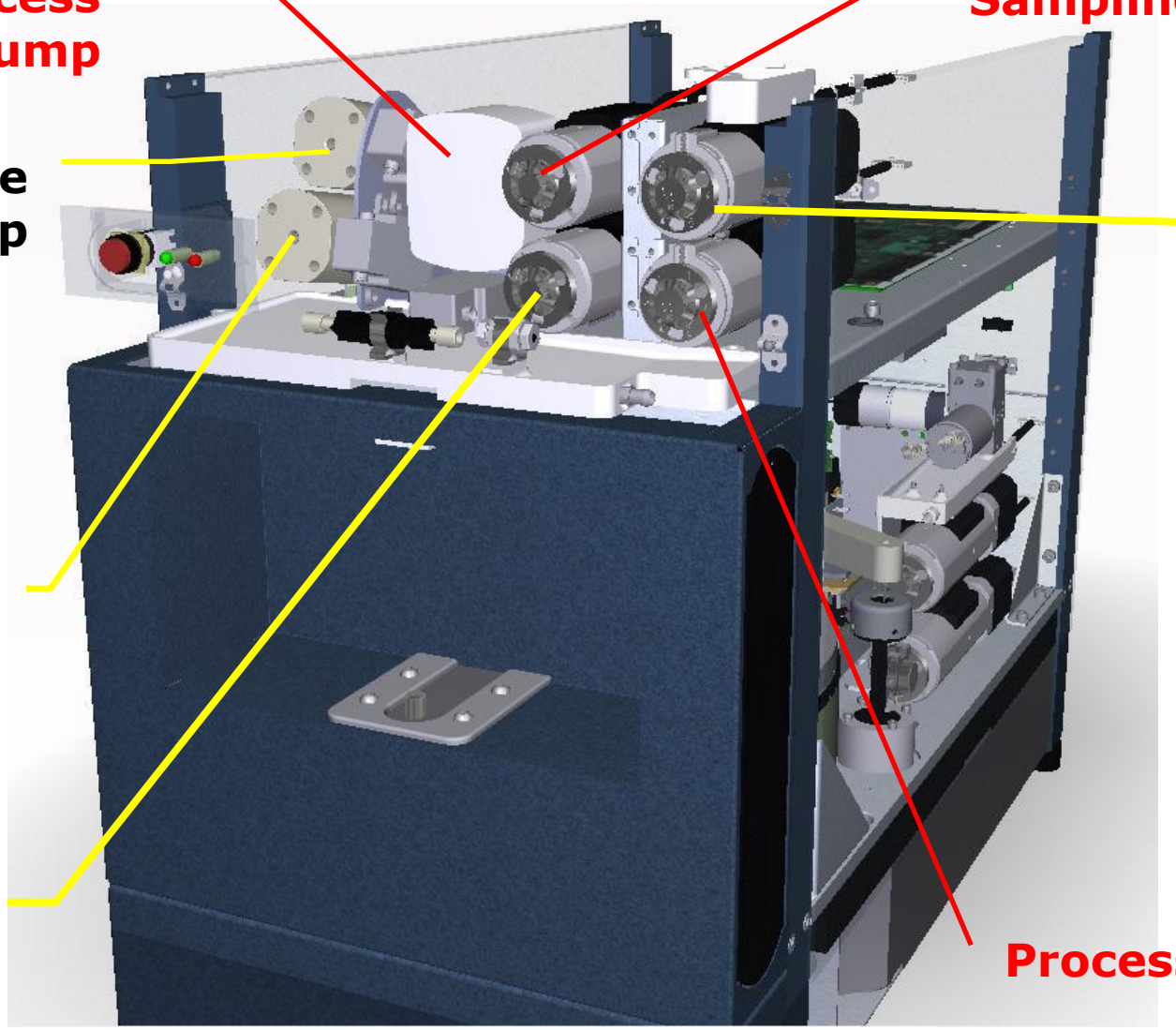
nibrt

ACQUITY UPLC® Family Tree

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

Online Process Sample Manager Fluidic Components

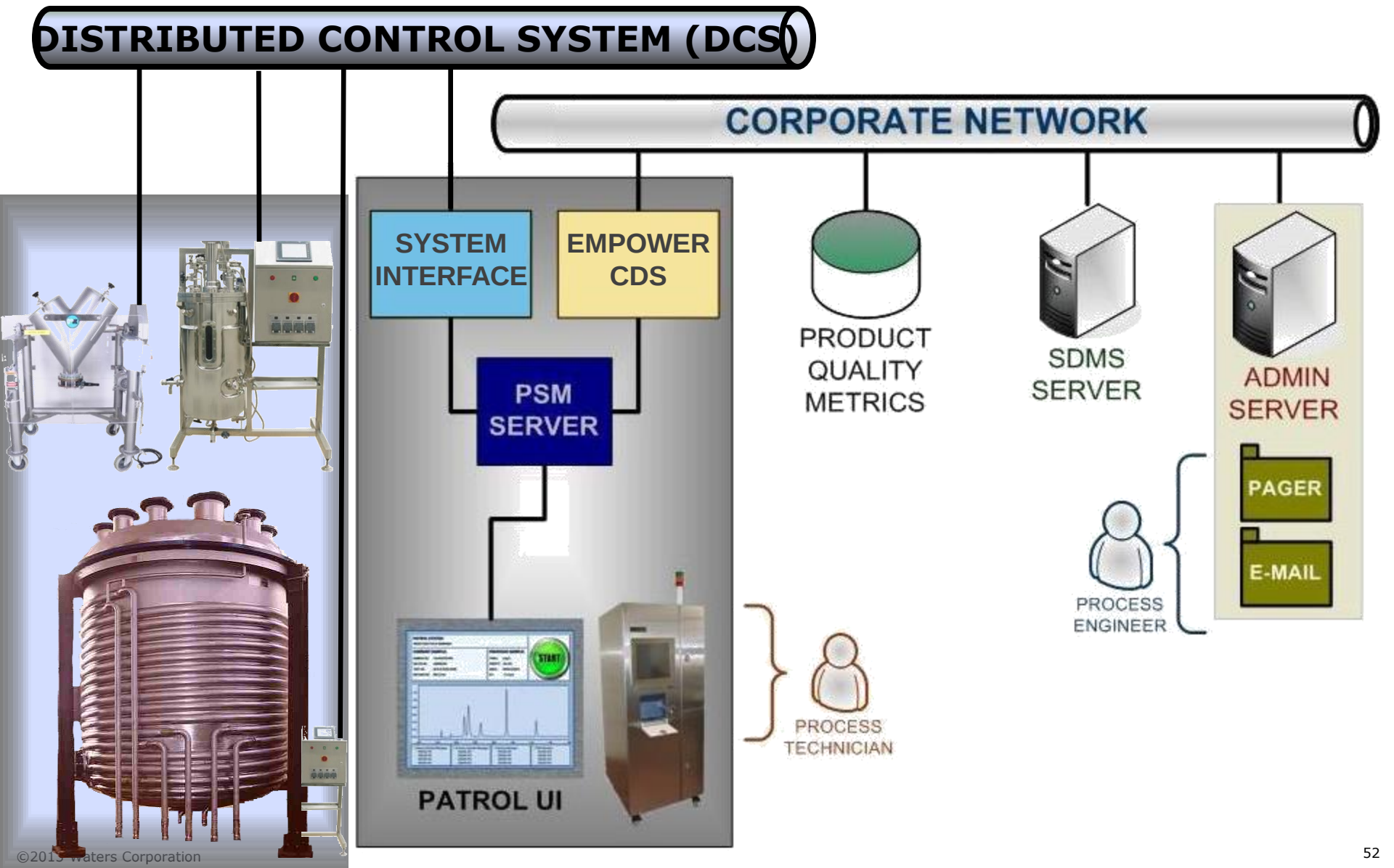
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Courtesy of Bob Tacconi

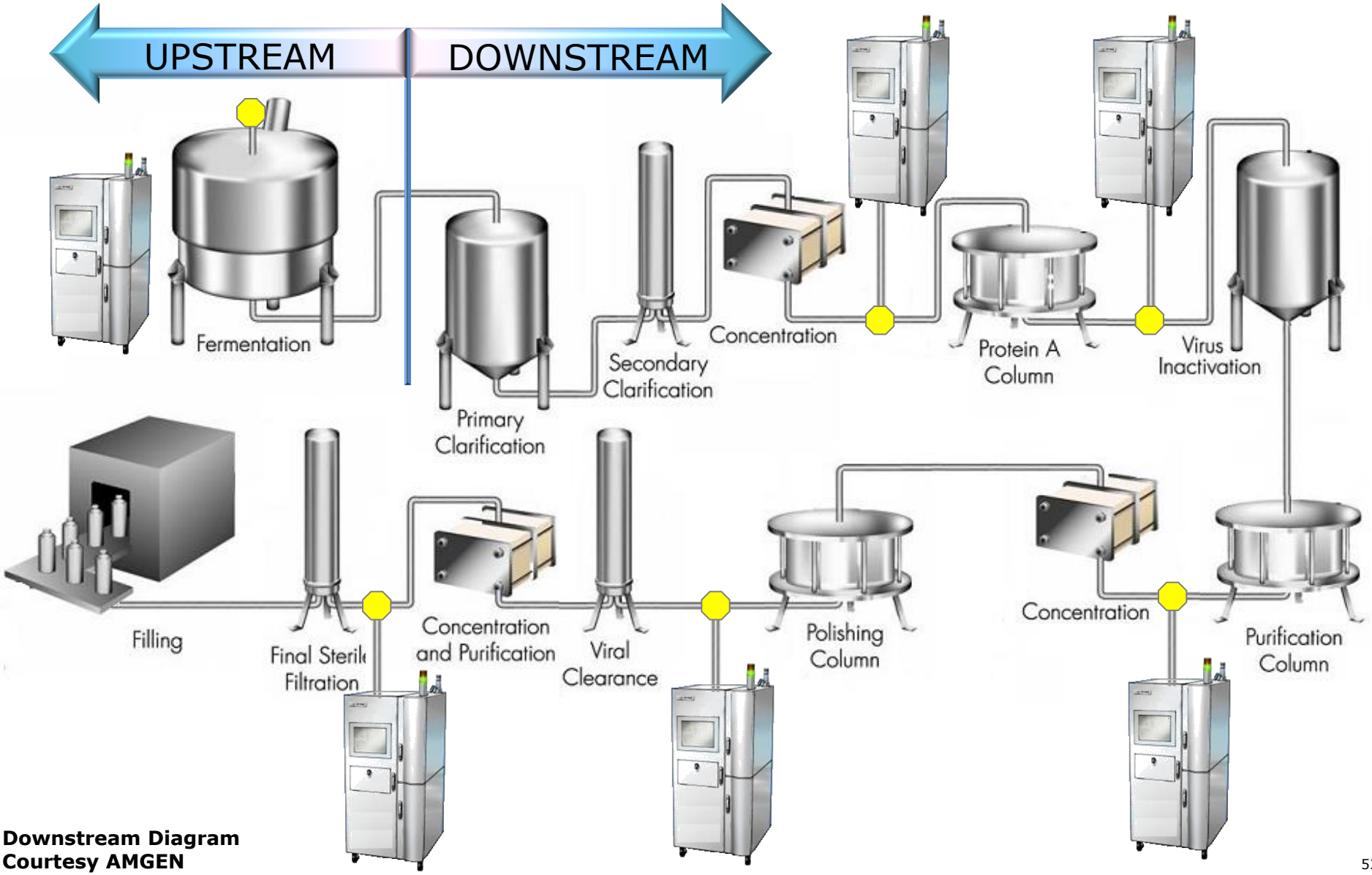
Data and Communication

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

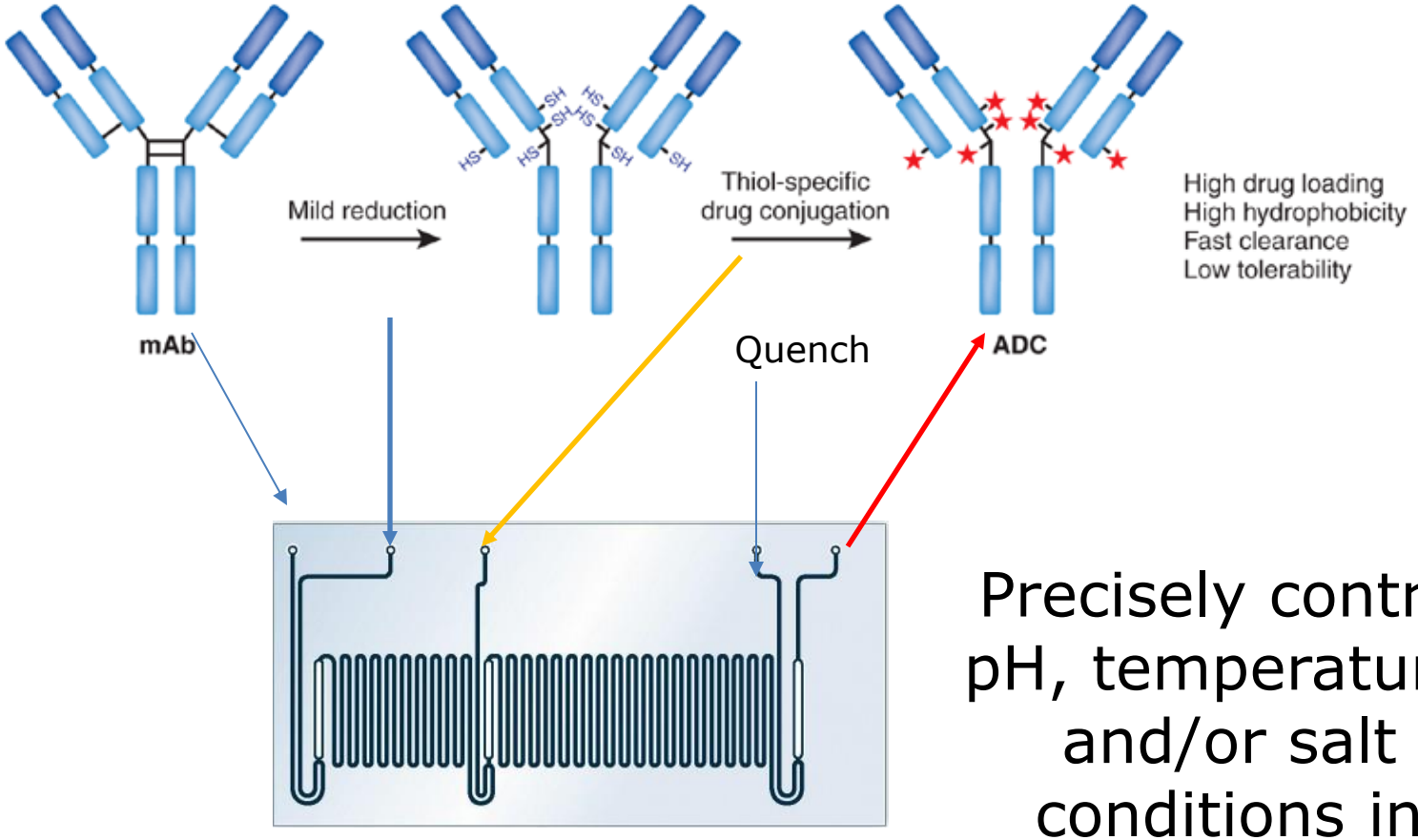


Automated Process Analysis
Biopharm Downstream Processing

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™



Downstream Diagram
Courtesy AMGEN

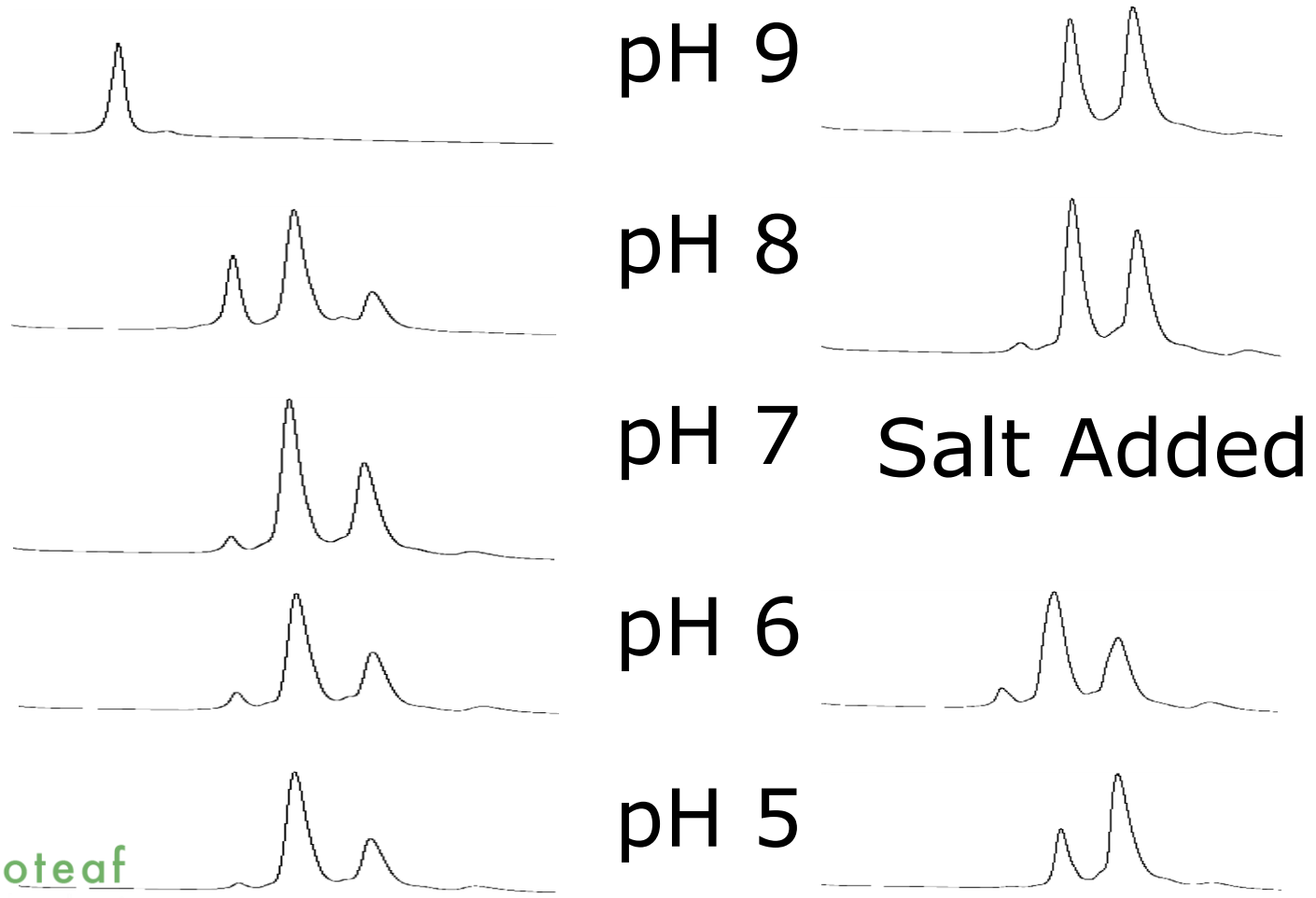


Precisely control pH, temperature, and/or salt conditions in seconds

Proteaf Technologies

Control Loading
Site Specific Conjugation

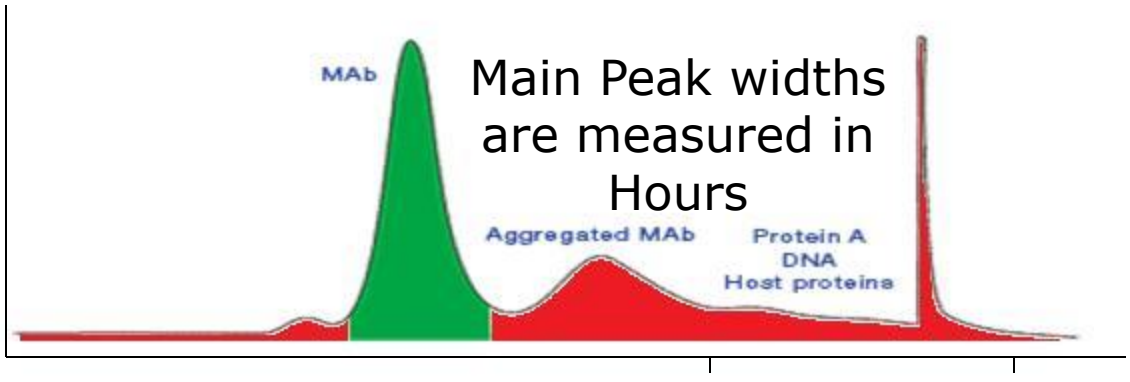
Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

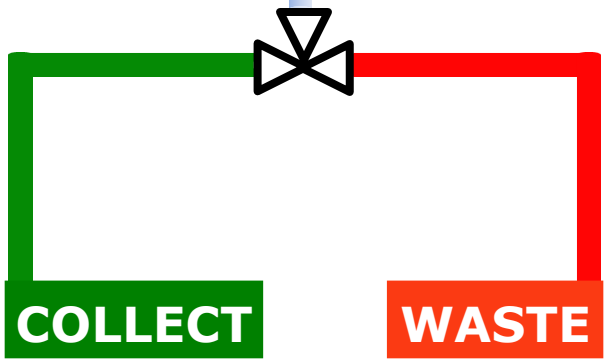


Proteaf Technologies

Opportunity: Downstream Processing Biopharmaceutical Purity Analysis

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

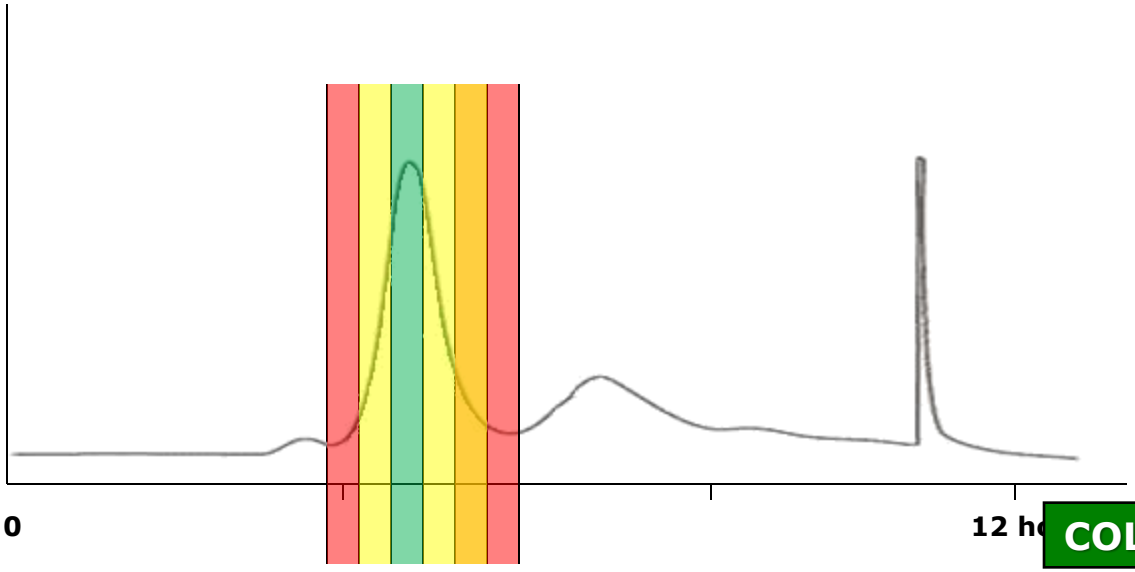


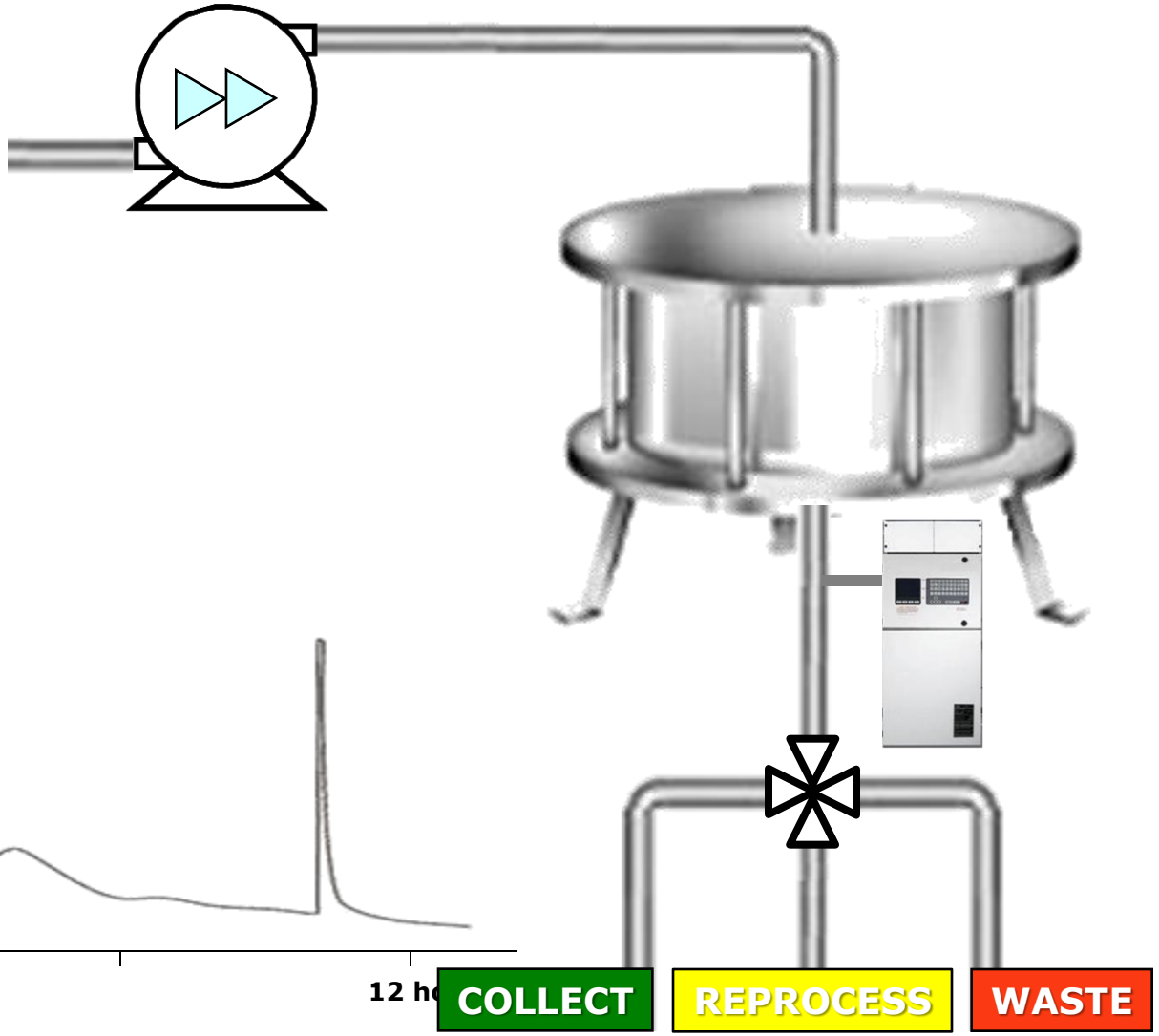


Opportunity: Downstream Processing Biopharmaceutical Purity Analysis

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

- 40 minute analysis
- A minimum of 160L requires reprocessing
- Initial process recovery yield 40%
- Final recovery yield after reprocessing 58%



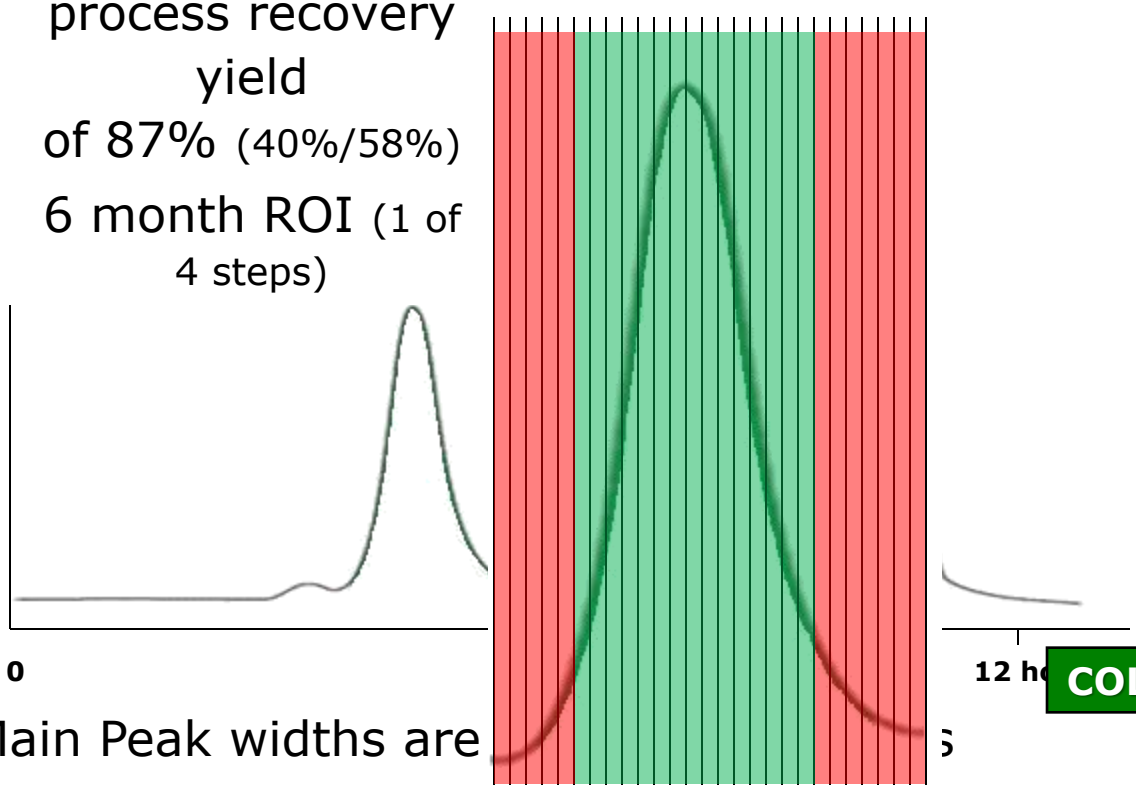


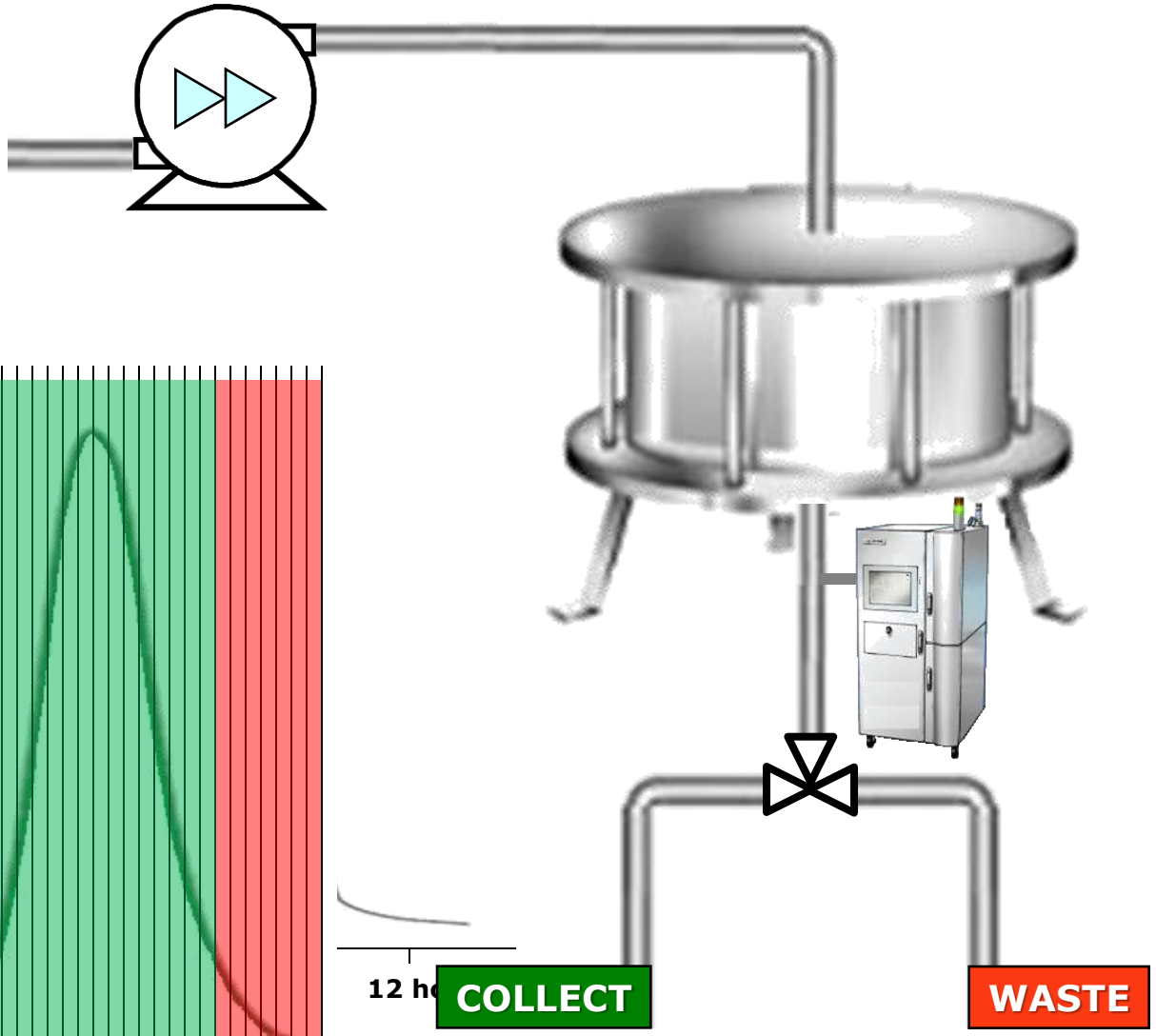
Main Peak widths are measured in Hours

Opportunity: Downstream Processing Biopharmaceutical Purity Analysis

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

- 3.5 minute analysis
- No fractions need to be reworked
- Total initial process recovery yield of 87% (40%/58%)
- 6 month ROI (1 of 4 steps)





Main Peak widths are s

Application-Specific Solutions
Biopharmaceutical market

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™

- UPLC
  - AAA
  - Peptide Mapping
  - Released Glycans
  - Intact RP
  - Intact SEC
  - Intact IEX
  - Oligonucleotides

Caractérisation des protéines thérapeutiques, transfert de méthodes sur des systèmes PAT

Questions?

Waters
THE SCIENCE OF WHAT'S POSSIBLE.™