

## **Analytik von Biopharmazeutika – Vom Bioreaktor bis zum finalen Produkt**

Gemeinsames Symposium des PVZ und der DPhG Fachgruppe  
Arzneimittelkontrolle/Pharmazeutische Analytik

**Braunschweig, 12. März 2015**

Christian Hunzinger

# Agenda

## **1 Introduction**

- Analytics of Biopharmaceuticals
- Process Analytics as a Specific Segment

## **2 Application Examples for Process Analytics**

- Cell Culture & mAb Analysis by Mid-infrared Spectroscopy (MIR)
- Glycosylation Analysis by CGE-LIF
- Host Cell Protein Analysis by Simple Western™ Technology

## **3 Outlook**

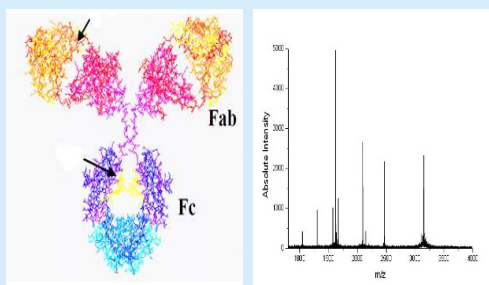
# Biopharma Analytics Segments Have Different Requirements

## Characterization

Product focus

High-end & detailed methods

Low throughput

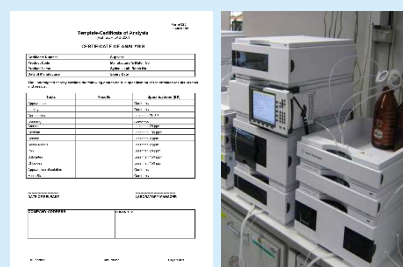


## QC Testing

Product focus

Robust & precise methods

Medium throughput



## Process Analytics

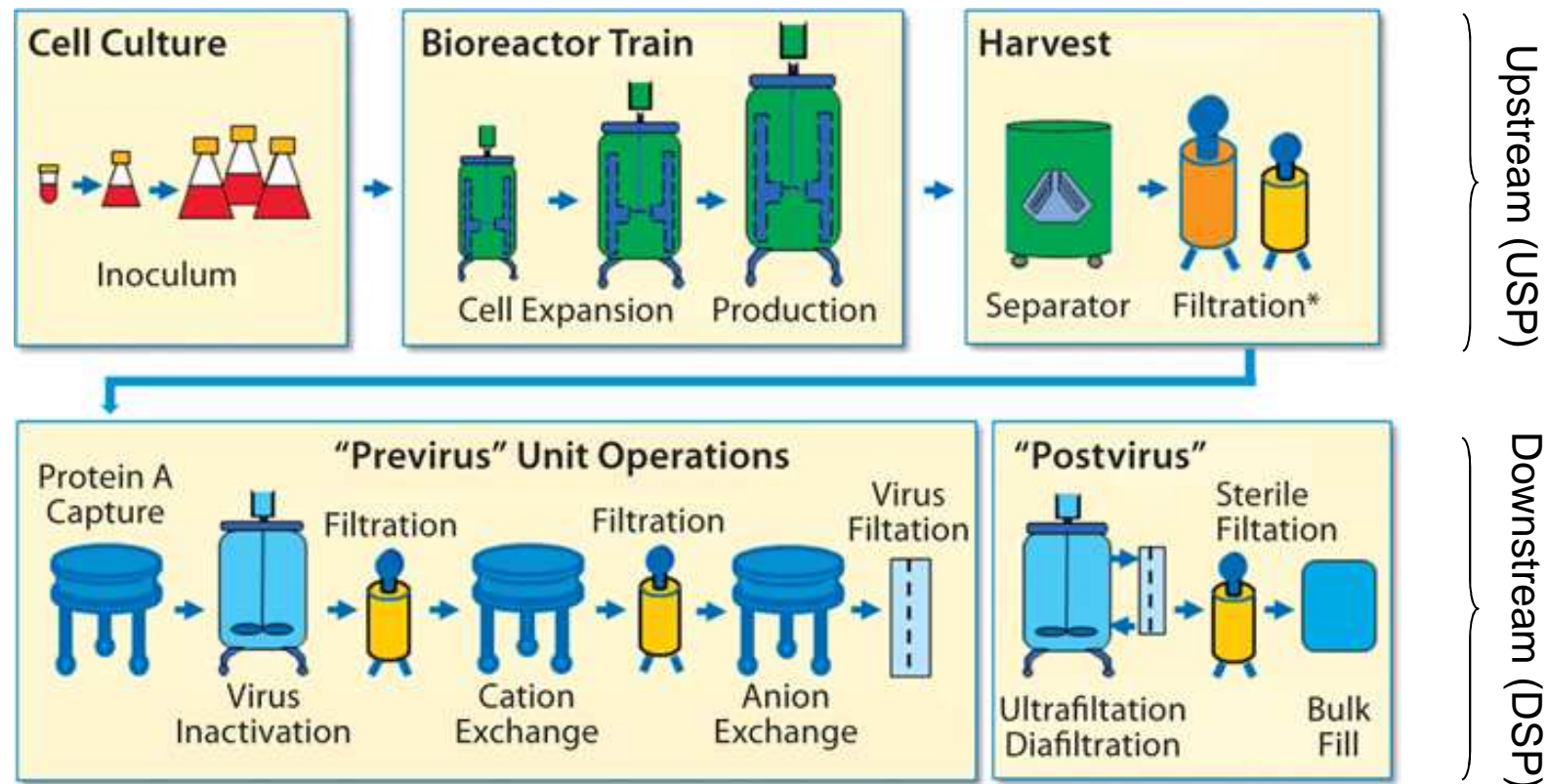
Process & Product focus

Fast & simple methods

High throughput









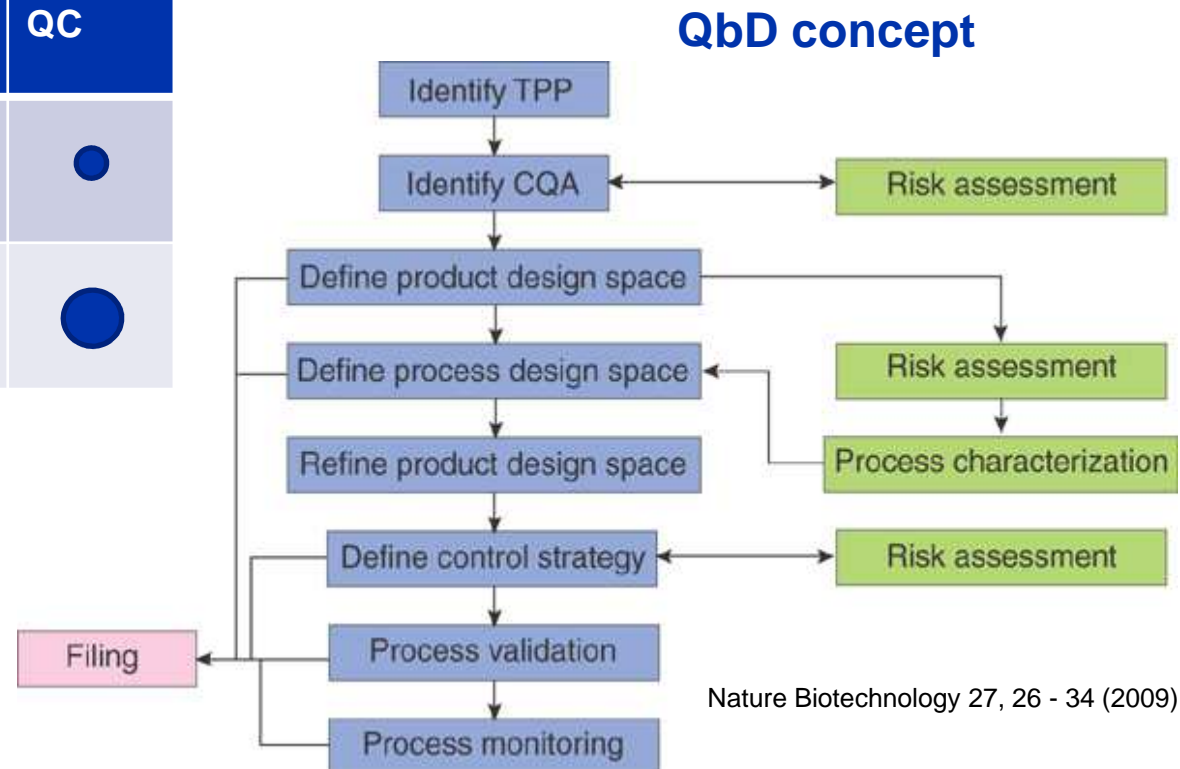
# The Classical mAb Manufacturing Process



*BioProcess International, Vol. 10, No. 6, June 2012, pp. 48–57*

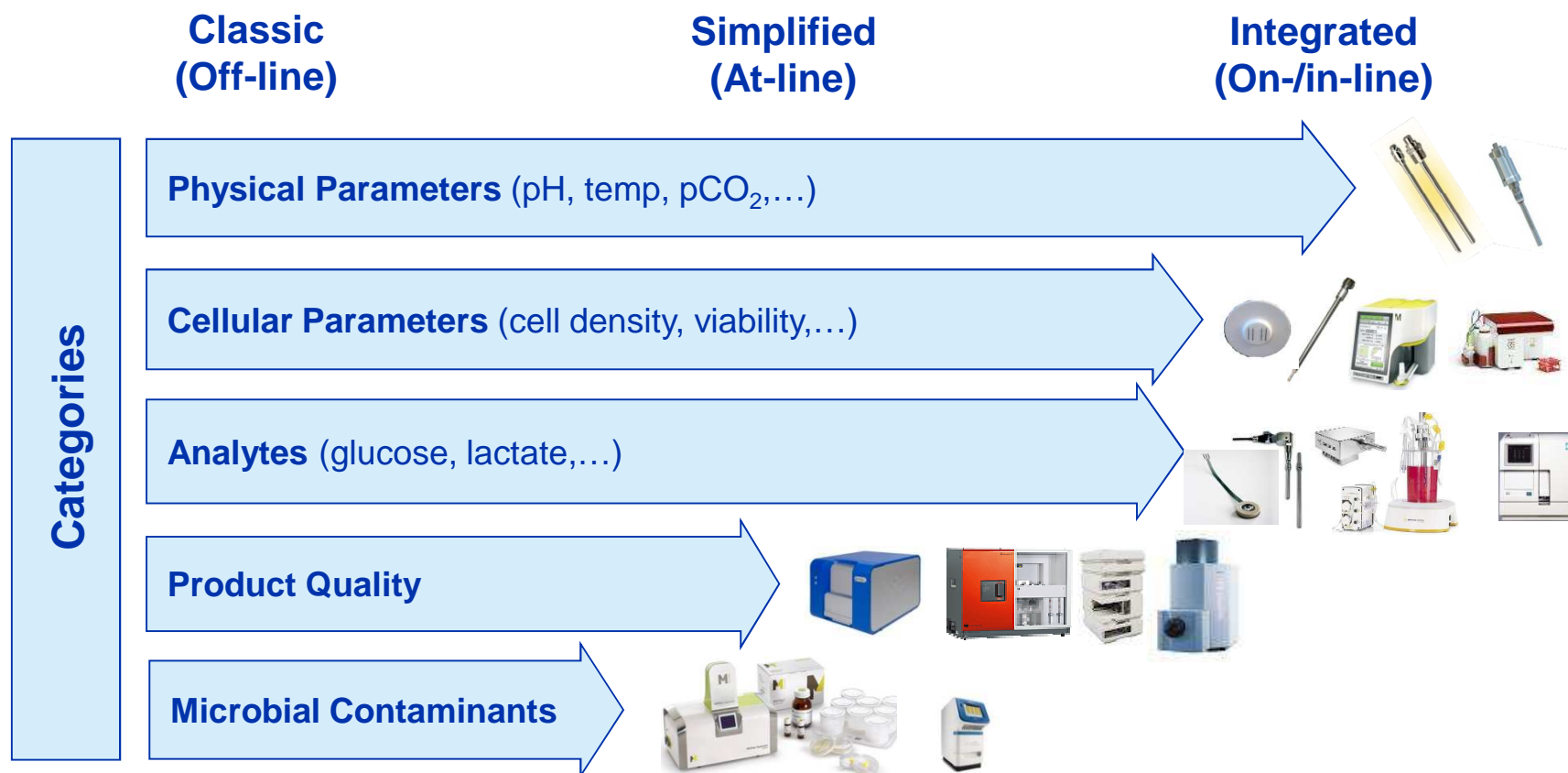
# Quality by Design (QbD) Concept Builds on Process Analytics (PAT initiative)

	Char	PAT	QC
Testing parameter			
Testing volume			



Nature Biotechnology 27, 26 - 34 (2009)

# Process Analytics Categories Differ in Technological Maturity



# Holistic Process Analytics Concept Demands Differentiated & Tailored Solutions

## Upstream Example



Process Development

Production

Preference for at-line setups

- High Testing Volume
- Flexibility
- More CQAs

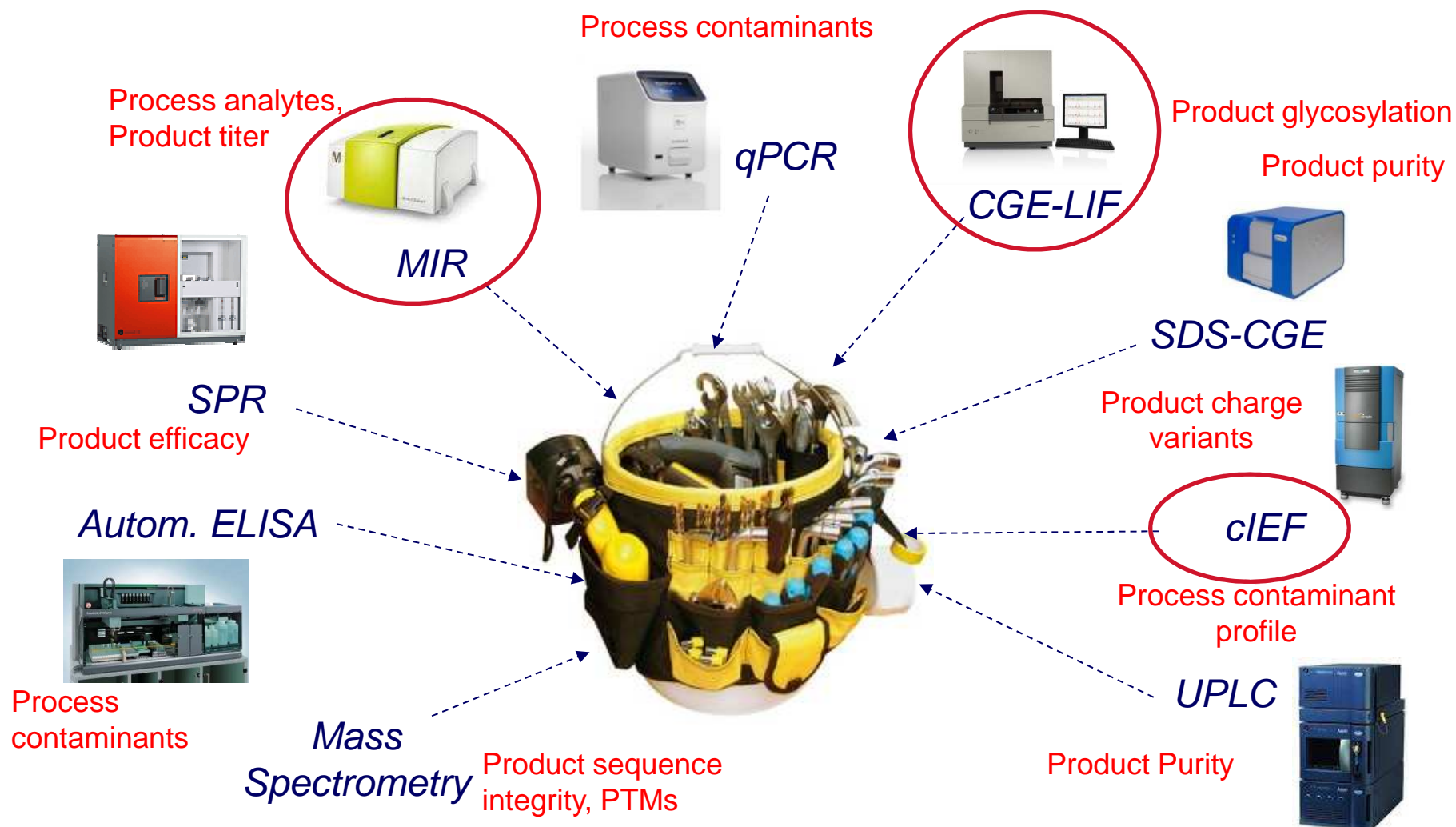
- More Detail
- Focus on „Understanding“

Preference for in/on-line setups

- Validated Systems
- Minimal Approach
- Focus on Control



# Selected Process Analytics Tools Used at Merck





# Agenda

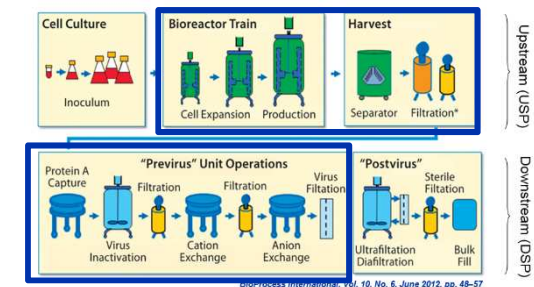
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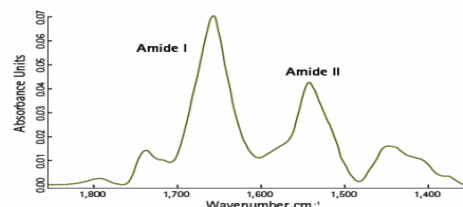
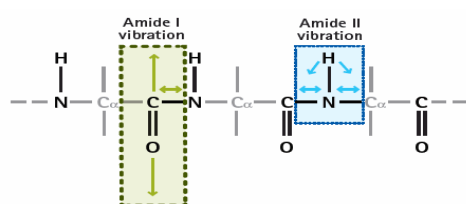
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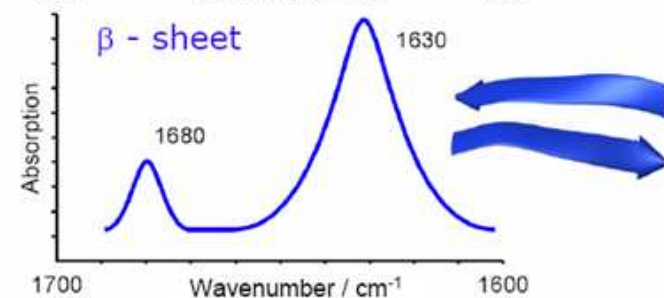
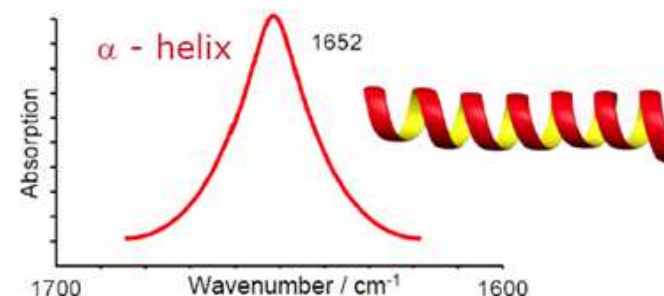
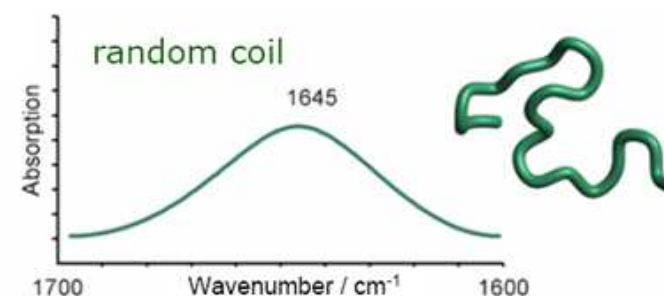


# Mid-Infrared (MIR) Based Protein Analysis and Quantification



Fabian et al., Encyclopedia of Analytical Chemistry, Wiley & Sons, pp. 5779-5803.

wavenumber area in cm <sup>-1</sup>	assigned protein secondary structure
~ 1615	aggregated strands
1620- 1635	beta-sheet
1640- 1650	irregular
~ 1640	3 <sub>10</sub> - helix
1650- 1658	alpha-helix
~ 1660	3 <sub>10</sub> - helix
1655- 1685	turns+ loops
1675- 1695	antiparallel beta-sheet
~ 1685	aggregated strands



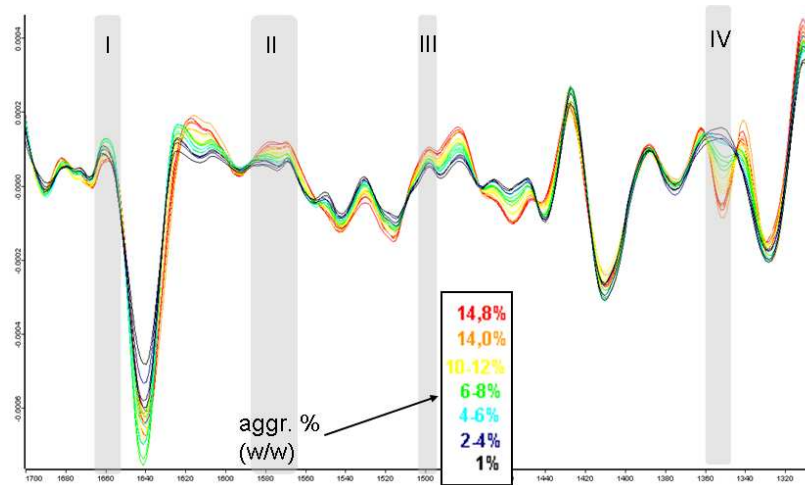
# MIR - Technical Approach



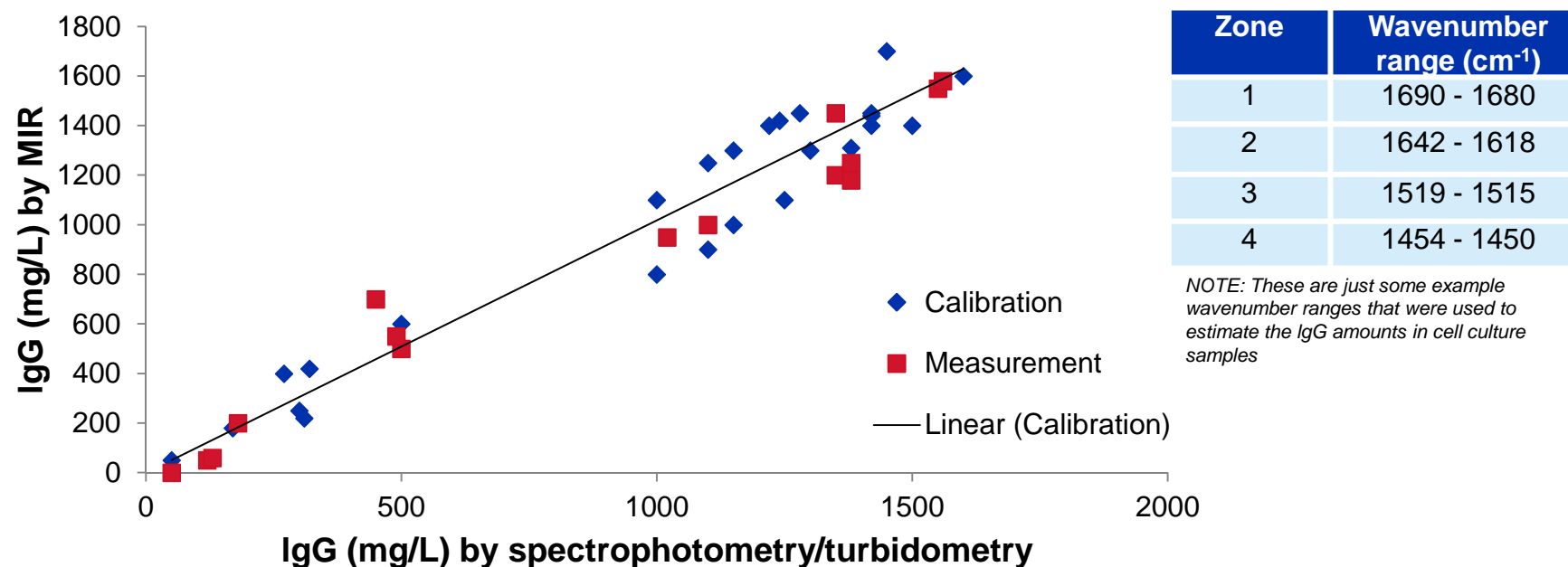
- Prepare samples with known parameter concentration
- Identify wavenumber ranges showing correlation of band intensity with parameter
- Optimize wavenumber ranges by automated processing (Bruker OPUS software)
- Design quantification models based on optimized wavenumber ranges

## *IgG Aggregation Example*

Zone	Wavenumber range (cm <sup>-1</sup> )	Assigned
1	1665 - 1654	Amide I
2	1579 - 1567	Amide II
3	1502 - 1496	Amide II
4	1360 - 1355	C-O Carboxy



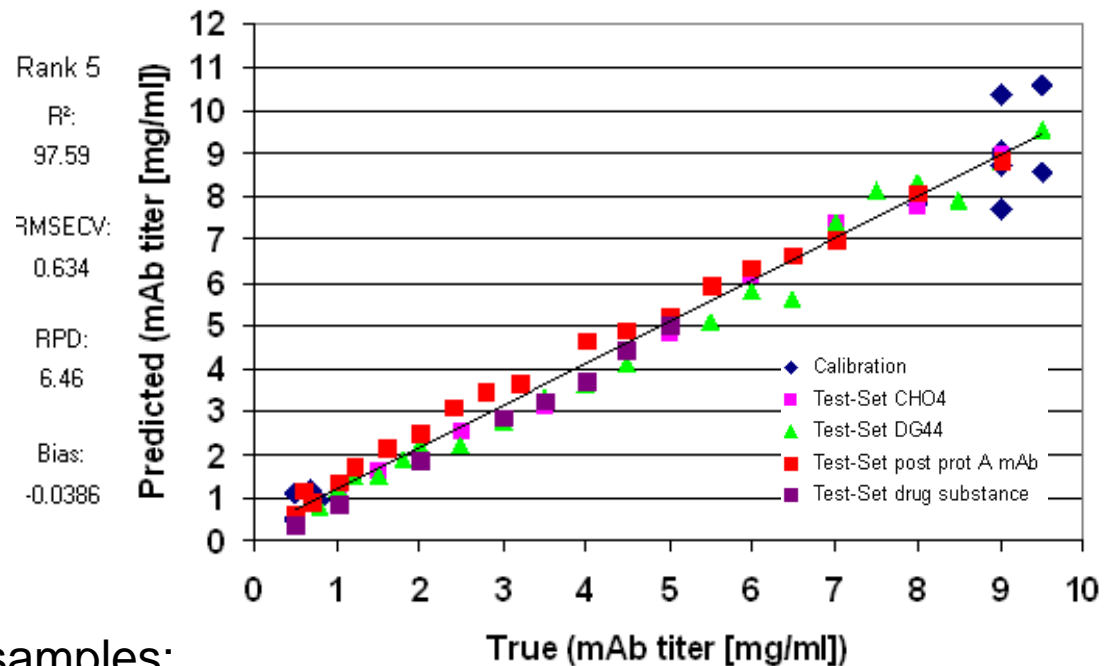
## mAb Quantification in Cell Culture by MIR



- Measured samples with known IgG concentration (e.g. estimated by spectrophotometry);
- Identified wavenumber ranges showing correlation of band intensity with IgG;
- Obtained good agreement for the range >400 mg/L of IgG;
- 75% of all measured samples of >400mg/L IgG concentration are in 10% range of reference values.

## mAb Quantification in Different Matrices by MIR

- 1 IgG
- Different IgG concentrations
- 4 matrices (2 cell culture fluids, post-prA pool, drug substance)

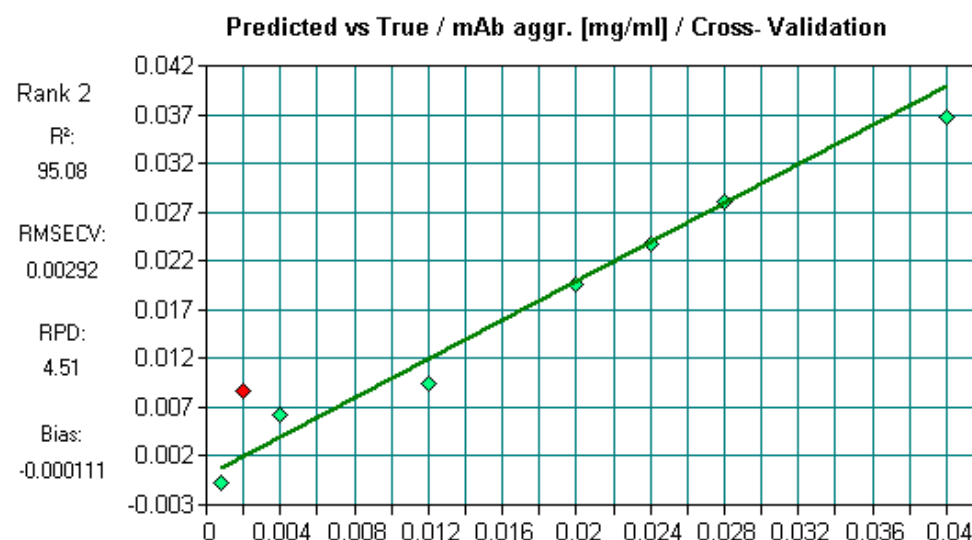


- Results from 61 test-set samples:
  - 72% with CV < 10%
  - 86% with CV < 20%
- A single mAb in various matrices can be quantified with one model

# mAb Aggregate Quantification by MIR

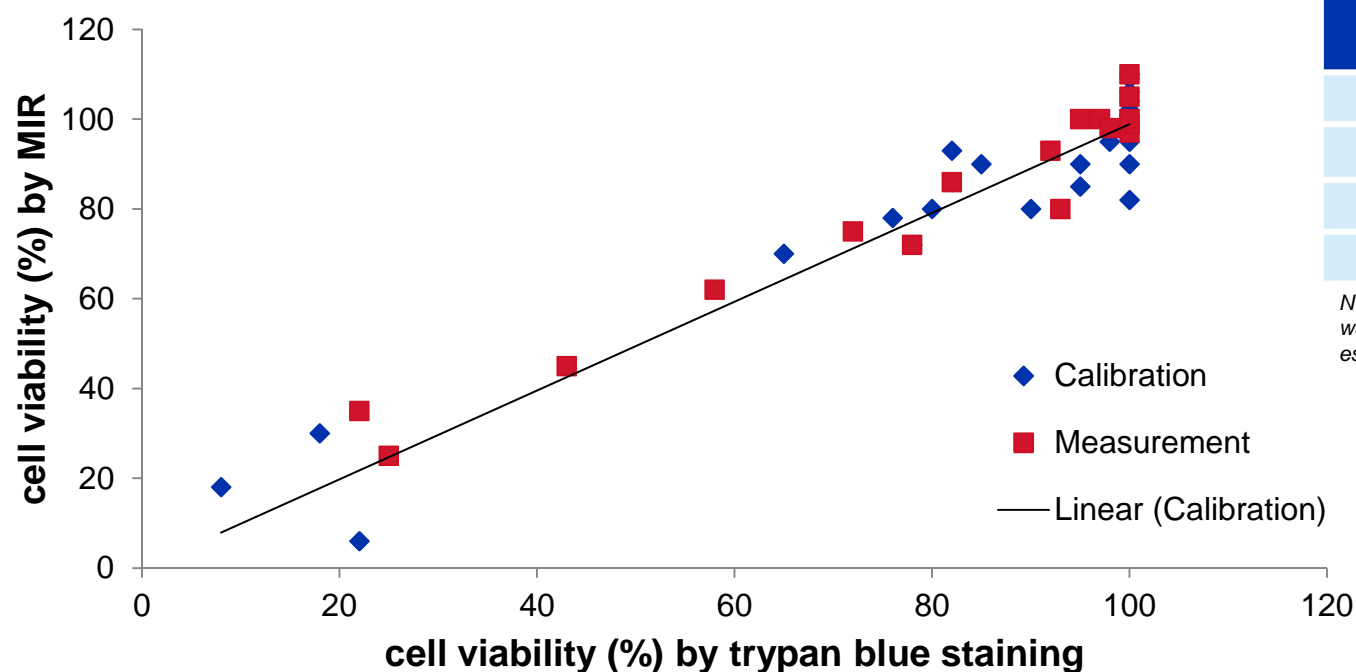
- 1 mAb
- Different mAb conc.
- Different mAb aggr. Conc.
- 1 matrix (cell culture fluid)

mAb A in CHO-DG44 CCF		
True [mg/ml]	Predicted [mg/ml]	CV %
0,0008	-0,0032	355,0
0,0020	0,0096	270,1
0,0040	0,0068	48,7
0,0080	0,0078	2,0
0,0120	0,0098	13,0
0,0160	0,0231	31,5
0,0200	0,0183	6,0
0,0240	0,0230	2,8
0,0280	0,0288	2,1
0,0400	0,0348	9,1



- Using models for small quantification windows, mAb aggregates down to 0,02 mg/ml can be quantified
- Corresponds to 0.2 – 2 % of mAb aggregates (10-1 g/L titer)

# Relative Cell Viability in Cell Culture by MIR



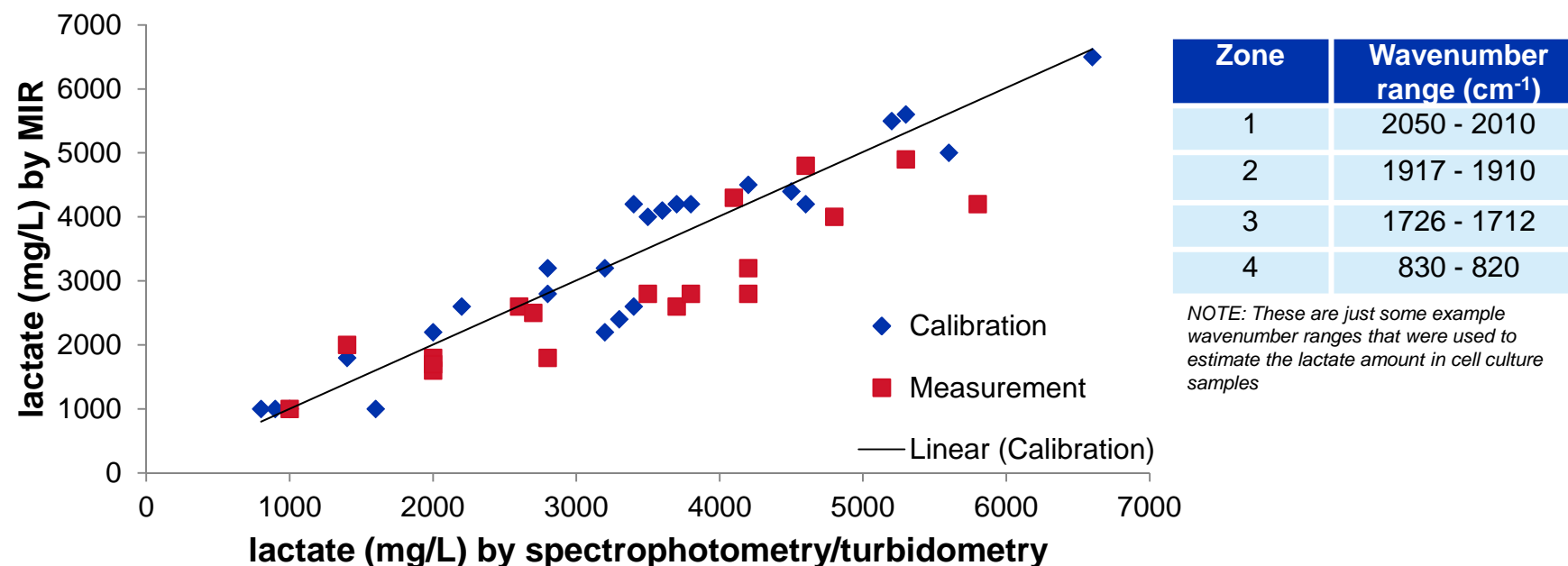
Zone	Wavenumber range (cm <sup>-1</sup> )
1	3538 - 3536
2	2360 - 2350
3	1491 - 1487
4	776 - 770

NOTE: These are just some example wavenumber ranges that were used to estimate the relative cell viability

- Measured samples with known cell viability (%) (e.g. estimated by the trypan blue staining);
- Identified wavenumber ranges showing correlation of band intensity with cell viability;
- Obtained good agreement for the range between 20 and 95% of relative cell viability;
- If cell viability was 100% according staining method, MIR-based values deviated up to 20%.



# Lactate Quantification in Cell Culture by MIR



- Measured samples with known lactate amount (e.g. estimated by spectrophotometry);
- Identified wavenumber ranges showing correlation of band intensity with lactate amount;
- Obtained larger deviations between reference values and predicted values, indicating a potentially indirect calibration. More calibration samples are necessary for better correlation.

# Agenda

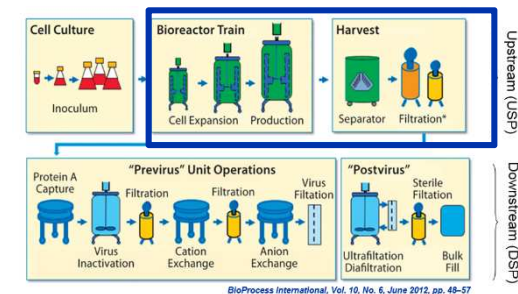
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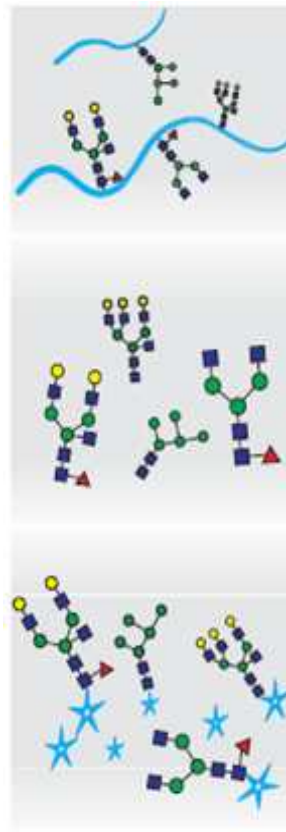
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- Host Cell Protein Analysis by Simple Western™ Technology

## 3 Outlook



# CGE-LIF N-Glycan Analysis Workflow



*Protein purification  
(prA )*

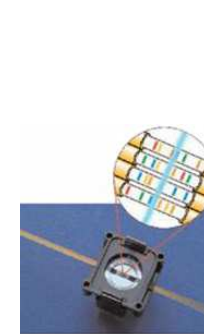
Protein reduction  
(DDT and IAA)

Glycan release with  
**PNGase F**

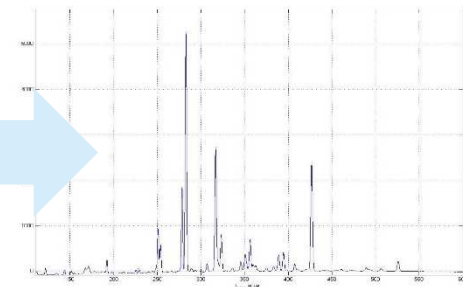
Glycan extraction and  
reconcentration

Glycan labeling with  
**APTS**

*Removal of excess  
APTS optional*

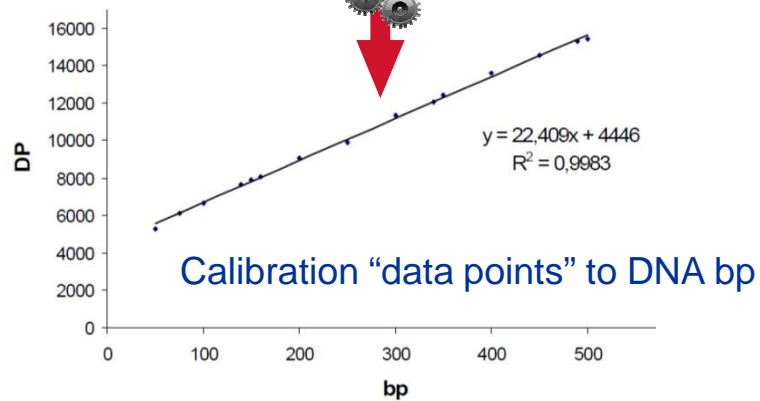
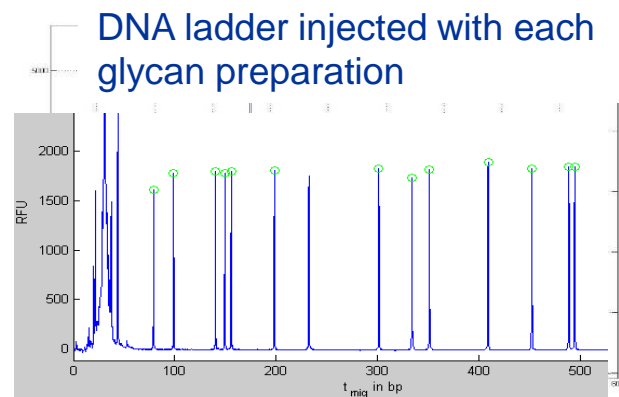


*DNA Sequencer*



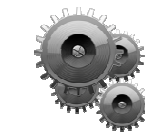
*Method adapted from Papac et al., Glycobiology , 1998 and Laroy et al. Nature Method, 2006*

# CGE-LIF N-Glycan Data Processing



Glycan to DNA bp "conversion"

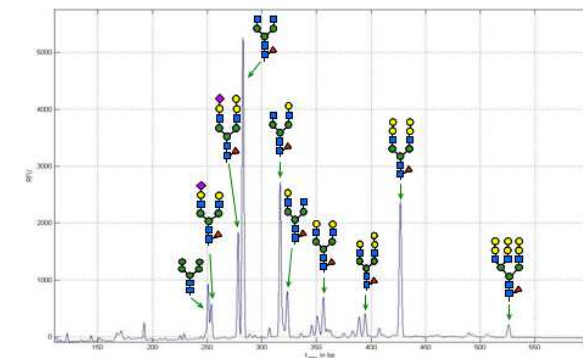
standard N-glycan		t <sub>mig</sub> (bp)
	FA2 / (NGA2F)	200
	FA2G2 / (NA2F)	264



**"glyXtool"**  
by glyXera\*



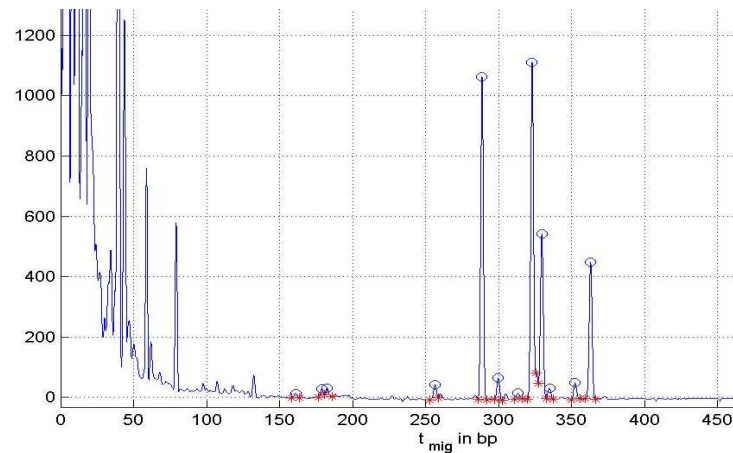
**N-**  
oligosaccharides  
identification



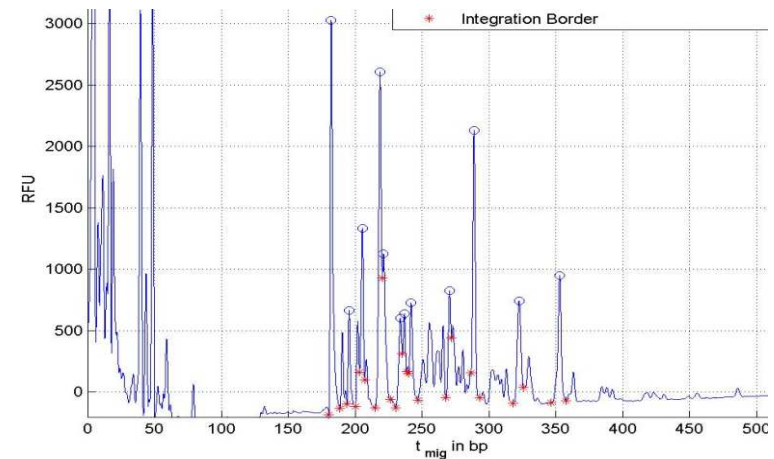
\*Access to "glyXtool" granted within the framework of a collaboration with E. RAPP, Max Planck Institute, Magdeburg, Germany

# CGE-LIF Shows Wide Application Range

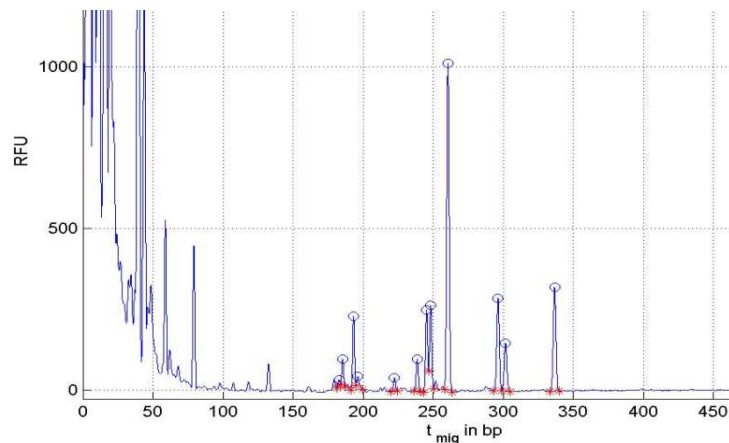
*Classical h-mAb*



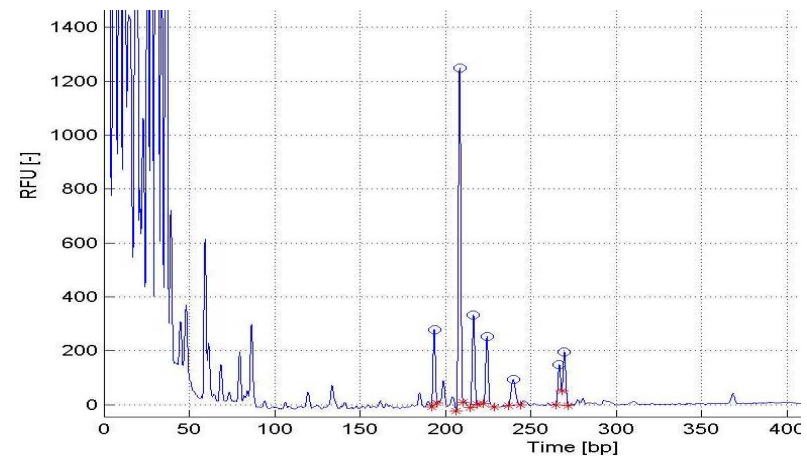
*Highly glycosylated Fc-fusion*



*Highly glycosylated h-mAb*



*Small glycoprotein*

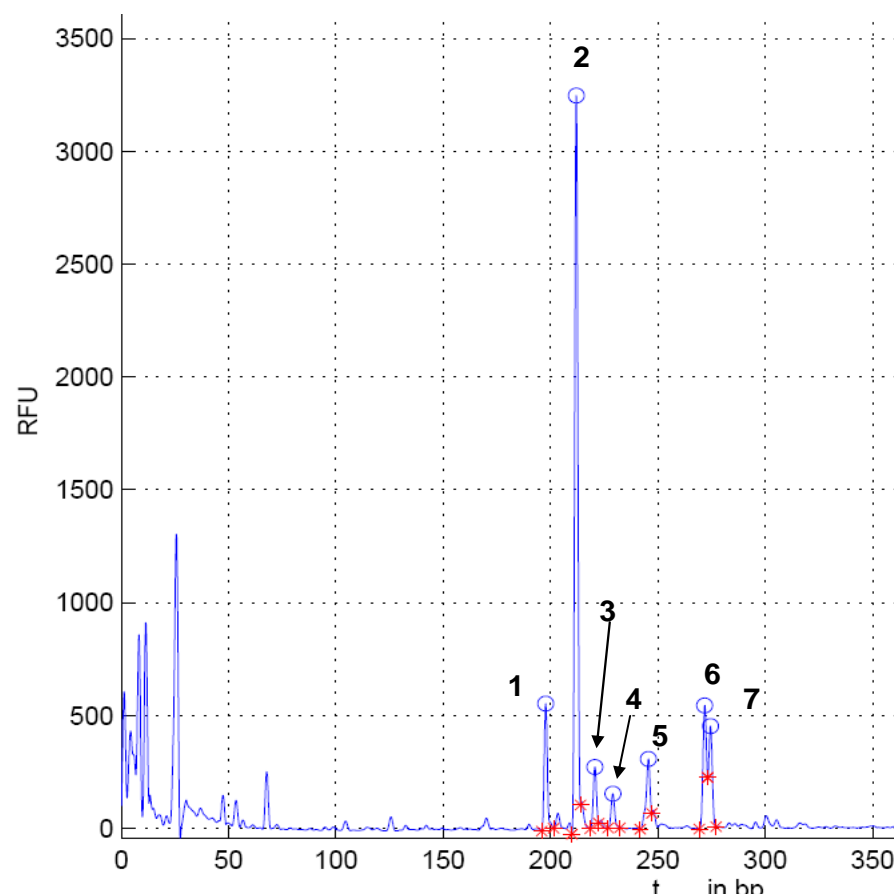


# CGE-LIF Yields Excellent Reproducibility

Glycoprotein with 7 main N-oligosaccharides, 12 preparations per run, 3 independent runs.

Migration Time		
Peak	AVG	STDEV%
1	198.16	0.17
2	212.44	0.17
3	221.11	0.17
4	229.49	0.17
5	246.13	0.17
6	272.44	0.17
7	275.10	0.17

Relative Peak Height %		
Peak	AVG	STDEV%
1	10.18	1.82
2	58.79	0.35
3	4.89	1.06
4	2.79	2.62
5	5.55	1.26
6	9.73	1.66
7	8.08	1.47



# Agenda

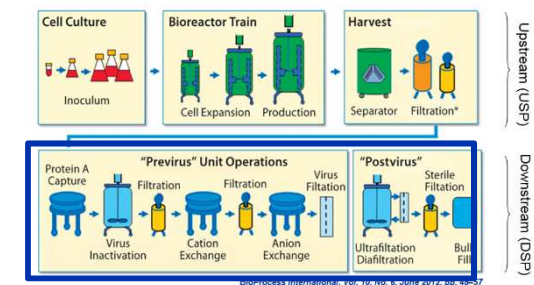
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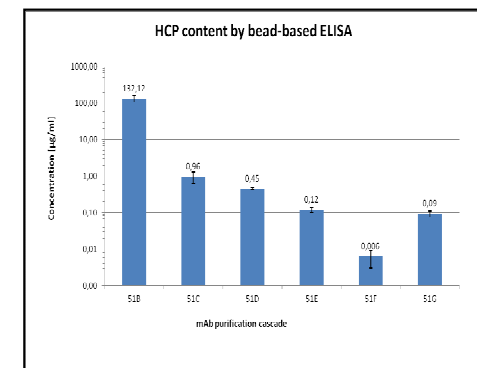
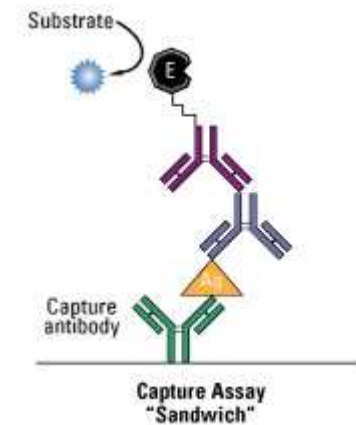
## 3 Outlook



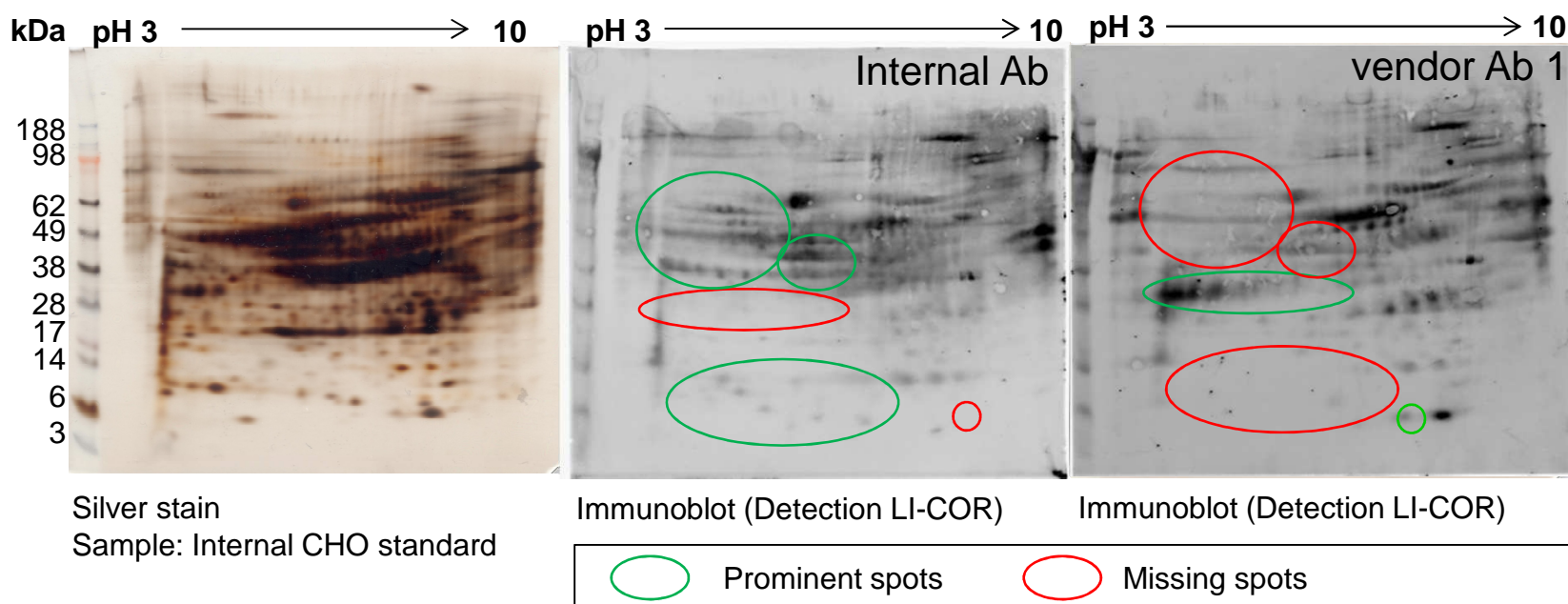


# Current Standard Host Cell Protein (HCP) Analysis is Limited

- Standard approach for detection of HCP is still ELISA based detection using polyclonal antisera against the host cell proteome
- Limitations of this approach
  - Gives only overall estimate of HCP content
  - Coverage of HCPs strongly depends on the quality of the antiserum (especially true for commercial assays)
  - Low or non immunogenic proteins are not captured
- Consequently, Health Authorities are requesting development of cell-line specific HCP assays including extensive characterization
- In addition, mass spectrometric (LC-MS) approaches are increasingly implemented as orthogonal approaches



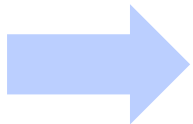
## Standard HCP Characterization by 2D-PAGE/ Immunoblotting



- 2D Immunoblotting technique still state of the art for mAb characterization, but limited in throughput and reproducibility/quality of results.

# Assessment of the Simple Western Technology for HCP Characterization

- Simple Western Technology developed for preclinical R&D to analyze individual target proteins in cell / tissue lysates



**Can the CE-based, HT Simple Western technology add value to the HCP characterization and assay development?**

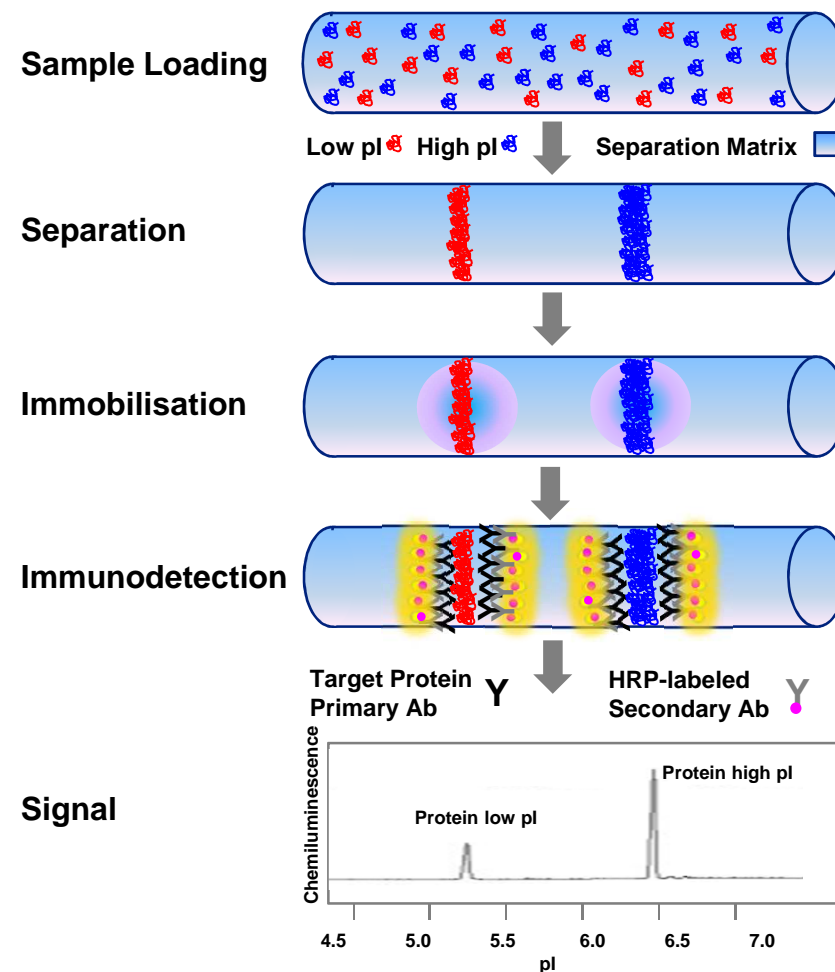


*Picture by courtesy of Protein Simple*

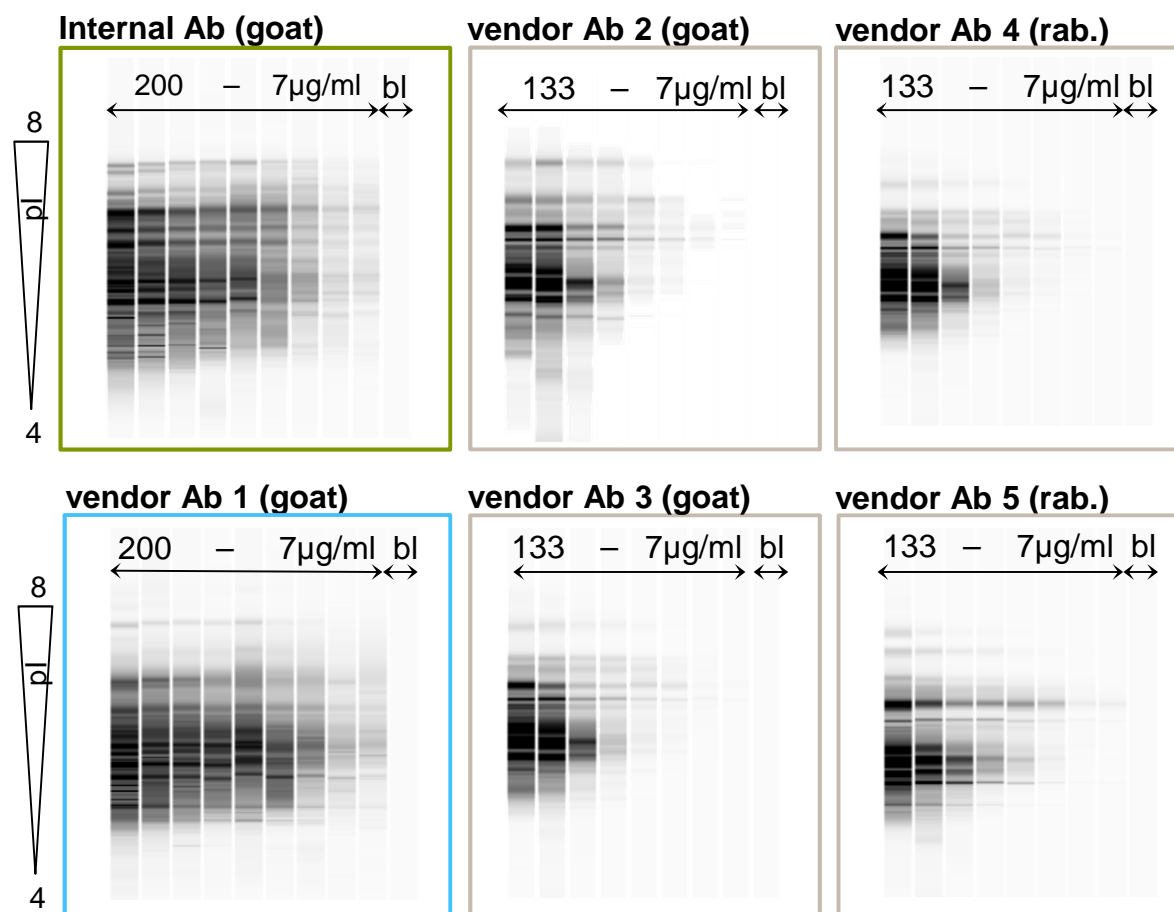
# The Simple Western™ Technology (Protein Simple)

## Technology

- Size- or charge-based separation of proteins by capillary electrophoresis (SDS-CGE / **cIEF**)
- UV-fixation of separated proteins to capillary wall
- Chemiluminescence immunodetection by in-capillary incubation with 1st Ab and HRP-labeled 2nd Ab / Luminol
- Analysis using electropherograms or visualization as gel-like pictures
- Throughput 88 samples per run (12-24 h)



# Multiple HCP Antibody Titrations can be Performed in one Experiment



## ◀ Gel-like pictures

Sample:  
Internal CHO standard

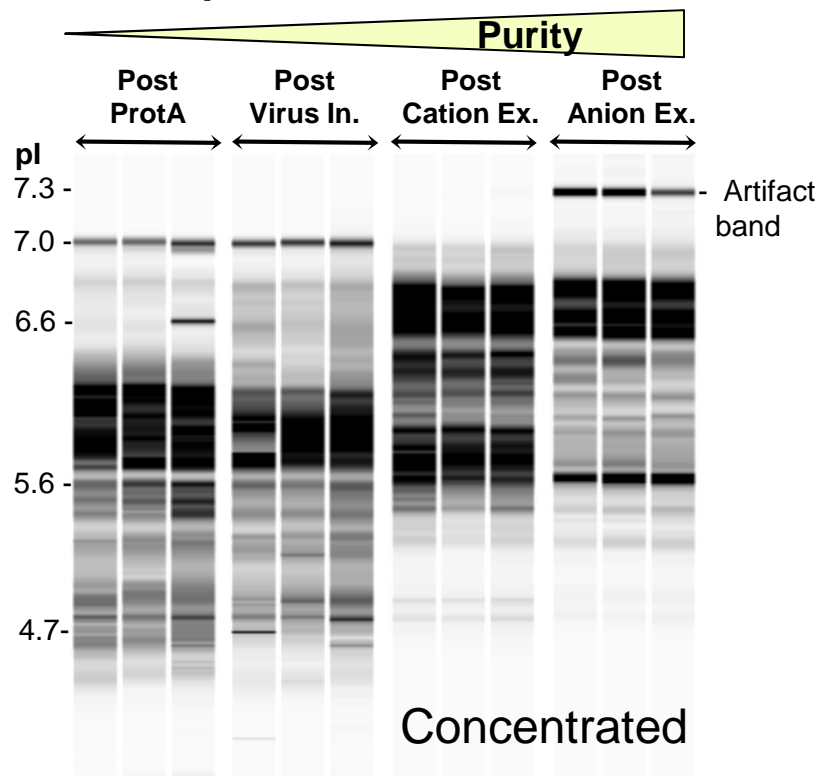
bl = blank (w/o 1<sup>st</sup> Ab)

## Benefits:

- Increased throughput
- Improved resolution
- Improved consistency

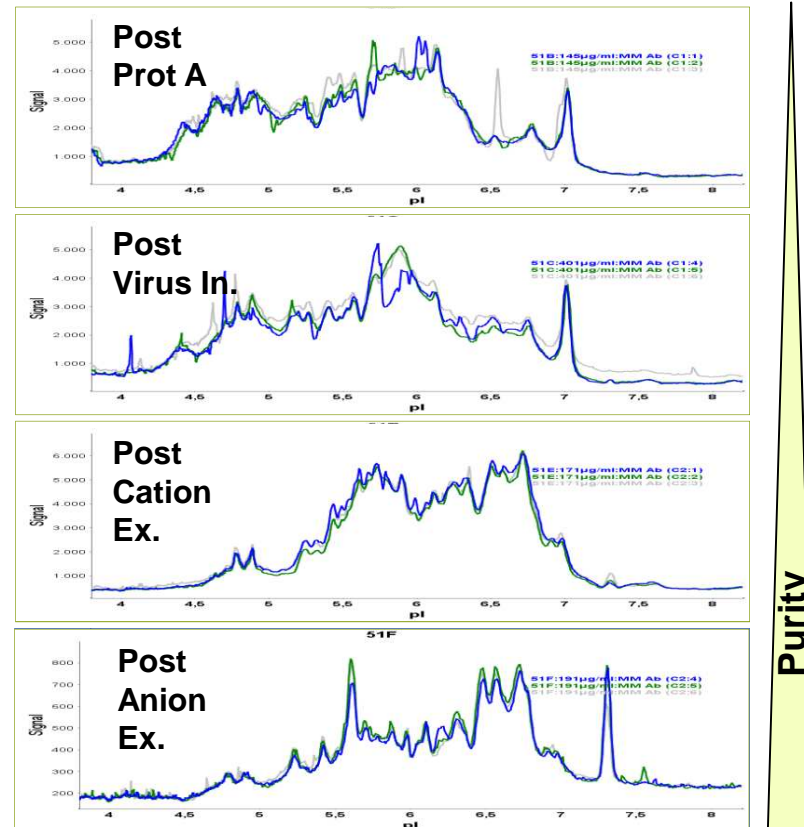
# Analysis of HCP pI Distribution in a mAb Purification Cascade can Guide DSP Development

## Gel-like picture



NOTE: Black-white intensities between different purification fractions do not represent quantitative relations, as the contrast was adjusted manually in order to obtain best possible qualitative data.

## Electropherograms



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1

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- Product Titer and Aggregation Analysis by MIR
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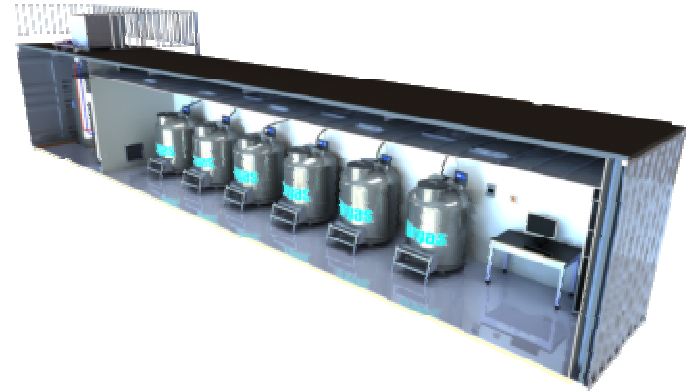
3

## Outlook



# Future Dimensions of Biomanufacturing

- Modular & flexible manufacturing concepts
- Continuous & closed processes
- Increased use of single-use equipment



[www.biologicsmodular.com](http://www.biologicsmodular.com)



# In the Future Analytics and Bioprocess Systems Merge to Create Revolutionary Products

- Technological advancement has proven a clear trend in the direction of “Smart Systems”. These will have integrated sensors to provide complete process and product information in real-time



# Acknowledgements

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- Florian Capito
- Harald Kolmar

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