

EBF 2021 Cyberconnect Events:

Focus Workshop: Peptides & Proteins with (LC-)MS

17-18 June 2021

12:30 12:45 Coming online Getting started - Welcome Philip Timmerman - EBF 13:00 13:20 Introduction to the workshop Matthew Barfield - on behalf of the EBF Why this workshop? 13:20 14:40 Session 1 - Scientific Challenges (e.g. reagents, free total, intact vs digested) 13:40 14:00 Daniel Vidler - Arcinova – A Quotient Sciences Business Identifying Peptide Markers From Mycobacterial Protein Digests – Development of a High-Resolution LC-MS Assay 14:00 14:20 Matthias Sury - Celerion Key Reagent Release Testing by LC-HRMS 14:20 14:40 Office Williams - OPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 15:30 Julien Petiter - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short QsA Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Biognalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	Day 1 (all t	imes in (CET, Brussels Time Zone)
Philip Timmerman - EBF Introduction to the workshop Matthew Barfield - on behalf of the EBF Why this workshop?			
13:00 13:20 Introduction to the workshop Matthew Barfield - on behalf of the EBF Why this workshop?	12:45	13:00	
13:20 14:40 Session 1 - Scientific Challenges (e.g. reagents, free total, intact vs digested) 13:20 13:40 Carsten Krantz - Novartis	42.00	42.20	·
13:20 14:40 Session 1 - Scientific Challenges (e.g. reagents, free total, intact vs digested) 13:20 13:40 Carsten Krantz - Novartis	13:00	13:20	·
13:40 13:40 Carsten Krantz - Novartis Hybrid LBA-LCMS for ADA detection 13:40 14:00 Daniel Vidler - Arcinova - A Quotient Sciences Business Identifying Peptide Markers From Mycobacterial Protein Digests - Development of a High-Resolution LC-MS Assay 14:00 14:20 Matthias Sury - Celerion Key Reagent Release Testing by LC-HRMS 14:20 14:40 Chris Williams - QPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 8ession 2 Q&A			
13:40 14:00 Daniel Vidler - Arcinova — A Quotient Sciences Business Identifying Peptide Markers From Mycobacterial Protein Digests — Development of a High-Resolution LC-MS Assay 14:00 14:20 Matthias Sury - Celerion Key Reagent Release Testing by LC-HRMS 14:20 14:40 Chris Williams - QPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:40 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 8ession 2 Q&A	13:20	14:40	
13:40 14:00 Daniel Vidler - Arcinova - A Quotient Sciences Business Identifying Peptide Markers From Mycobacterial Protein Digests - Development of a High-Resolution LC-MS Assay 14:20 14:40 Matthias Sury - Celerion Key Reagent Release Testing by LC-HRMS 14:20 14:40 Chris Williams - QPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) Julien Petiter - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monocional Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:40 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 8:00 18:00 18:00 Session 2 Q&A	13:20	13:40	Carsten Krantz - Novartis
Identifying Peptide Markers From Mycobacterial Protein Digests – Development of a High-Resolution LC-MS Assay 14:20 14:20 Matthias Sury - Celerion Key Reagent Release Testing by LC-HRMS 14:20 14:40 Chris Williams - QPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Petiter - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Kiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:40 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 8:00 18:00 18:30 Session 2 Q&A			•
14:20 14:40 Chris Williams - QPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC Session 2 Q&A	13:40	14:00	Identifying Peptide Markers From Mycobacterial Protein Digests – Development
14:20 14:40 Chris Williams - QPS Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC Session 2 Q&A	14:00	14:20	Matthias Sury - Celerion
Development of a hybrid method for quantification of a therapeutic protein differing by a single amino acid from the endogenous form 14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A			
14:40 15:10 Break 15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	14:20	14:40	
15:10 18:30 Session 2: Scientific developments (new tools) 15:10 15:30 Julien Peltier - GlaxoSmithKline			
15:10 15:30 Julien Peltier - GlaxoSmithKline Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	14:40	15:10	Break
Characterisation and Quantification of Therapeutic Antibodies by Incorporating Response Bias Correction using Affinity Capture and Intact Protein LC-MS. 15:30 15:50 Ke Li - Frontage Labs Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A			
Development and validation of a LC/MS method for the quantification of fascin in human serum 15:50 16:10 Thomas Schneider - BiognoSYS AG	15:10	15:30	Characterisation and Quantification of Therapeutic Antibodies by Incorporating
15:50 16:10 Thomas Schneider - BiognoSYS AG	15:30	15:50	Development and validation of a LC/MS method for the quantification of fascin
Context of Use Validation of a Data Independent Acquisition based Deep Proteome Quantification Approach 16:10 16:30 Lei Xiong - Sciex Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	15:50	16:10	
Improved LC-MRM workflow for cyclic peptide quantification on natriuretic peptide family 16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	10.50	10.10	Context of Use Validation of a Data Independent Acquisition based Deep
16:30 16:40 Short Q&A Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	16:10	16:30	Improved LC-MRM workflow for cyclic peptide quantification on natriuretic
Short logistic break 17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	16:30	16:40	
17:00 17:20 James Marr - MSD Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A			
Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal Antibodies in Pharmacokinetic Studies using LC-MS/MS for Analysis 17:20 17:40 Szabolcs Szarka - LGC Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A			Short logistic break
Utilizing high-resolution mass spectrometry to improve the sensitivity of a therapeutic protein assay 17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	17:00	17:20	Improvements in Immunoprecipitation and Digestion Efficiencies for Monoclonal
17:40 18:00 Anton Rosenbaum - AstraZeneca Comparison of Bioanalytical Methods for Pharmacokinetic Assessments of ADC 18:00 18:30 Session 2 Q&A	17:20	17:40	Utilizing high-resolution mass spectrometry to improve the sensitivity of a
18:00 18:30 Session 2 Q&A	17:40	18:00	
18:30 End of Day 1	18:00	18:30	·
	18:30		End of Day 1

Day 2 (all times in CET, Brussels Time Zone)

12:45	13:00	Coming online
13:00	14:30	Session 3: how to interpret the data (e.g. biological specificity vs. analytical specificity, which data are 'true'?
13:00	13:10	Philip Timmerman - EBF Introduction to the session: Turning Scientific challenges challenges into
13:10	13:30	opportunities Oriol Peris Serrano - Charles River Laboratories
13:30	13:50	The Impact of Assay Acceptance Criteria on Derived Data – Pharmacokinetic Assessment Through Simulation Gregor Jordan - F. Hoffmann-La Roche
		Is correct quantification of free/active drug concentrations by hybrid LC-MS possible? An evaluation applying the "free analyte QC concept"
13:50	14:10	Nico van de Merbel - PRA-HS/U. Groningen Analytical consequences of the in vivo deamidation of trastuzumab and
14:10	14:30	pertuzumab: comparison of the results of three bioanalytical platforms Session 3 Q&A and panel discussion
14:30	14:50	Break
14:50	16:20	Session 4 - Defining a bioanalytical strategy for peptide/protein: which assay when and why?
14:50	15:00	lain Love - on behalf of the EBF Introduction to the session: Questions to consider when building a bioanalytical strategy for proteins
15:00	15:20	Rita Martello - Merck KGaA How to develop a bionalaytical strategy for therapeutic proteins
15:20	15:40	Shashank Gorityala - Covance
15:40	16:00	LCMS-based strategies for the quantitation of protein biotherapeutics Emmanuel Njumbe Ediage, Janssen R&D Challenges in developing an LC-MS/MS assay for the quantification of Pegasys;
16:00	16:20	what are we measuring? Session 4 Q&A and panel discussion
16:20	16:40	Break
16:40	18:20	Session 5 - Regulatory challenges - experience and industry recommendations
16:40	17:00	Amanda Wilson - on behalf of the EBF Introduction to the session: EBF FB from the survey
17:00	17:20	Case studies & scientific and regulatory challenges on combining MS and LBA
		Tsvetelina Ivanova, Comac-Medical Pharmacokinetic analysis using LBA and MS concentration data – was this a real challenge?
17:20	17:40	William Mylott, PPD Bioanalytical Method Validations: Taking a 'Hybrid Approach'
17:40	18:00	Eric Thomas, Covance by Labcorp Perspectives on Performance and Requirements for Protein MS Assays
18:00	18:20	Closing Panel discussion: where regulatory and scientific challegens for protein analysis meet.
18:20		Closing comments and Adjourn



Organising Committee:

Matthew Barfield (F. Hoffmann-La Roche), Iain Love (Charles River Laboratories), Amanda Wilson (AstraZeneca), Nico van de Merbel (PRA-HS) and Philip Timmerman (EBF)