Characterization of Intact Monoclonal Antibodies (mAb) and their fragments using Novel Reversed Phase Columns Suresh Babu C.V.<sup>1</sup>, Phu T Duong<sup>2</sup>, Andrew Coffey<sup>3</sup>, and Meenakshisundaram Palaniswamy<sup>1</sup> <sup>1</sup>Agilent Technologies, Inc. Bangalore, India, <sup>2</sup>Agilent Technologies, Inc. Wilmington, DE 19808, <sup>3</sup>Agilent Technologies, Inc. Church Stretton, UK



### Introduction

With the continued importance of monoclonal antibodies biotherapeutics, (mAbs) as comprehensive characterization is a prerequisite. It is critical at discovery, development and manufacturing stages to confirm that the antibody drug has the correct primary structure (number, location and order of amino acids) and to monitor variants and other potential post translational modifications that can impact safety and efficacy. Due to the complexity of the molecules, the characterization method with high resolution for mAb primary structure by reversed-phase liquid chromatography can be very lengthy and time consuming. In this presentation, the data analysis of intact mAb and fragments such as heavy/light chains and Fc/Fab regions with high speed and high resolution are presented. These data are performed by using the novel, unique bonding chemistries-C4, C8 and Diphenyl on a new particle design of 3.5 µm Poroshell technology. The data from the LC/UV and LC/MS methods will be included here in this presentation.

### Therapeutic monoclonal antibodies were purchased from a local pharmacy and stored according to the manufacturers' instructions.

Experimental

**LC/UV:** For intact mAb analysis, mAb samples were diluted to 2 mg/mL using PBS. For the separation of the light and heavy chains, an aliquot of 0.5 M TCEP stock was added to the mAb samples to obtain a final concentration of 10 mM. The mixture was held at 60 °C for 30 minutes.

**LC/MS**: For intact mAb analysis, mAb samples were diluted to 1  $\mu$ g/ $\mu$ L using 0.1% formic acid in 3% ACN, For the separation of the light and heavy chains, an aliquot of 1M DTT stock was added to the mAb samples and the mixture was held at 37 °C for 1 hr. Digestion with Papain and FabRICATOR was performed at 37 °C for 3 hr and 1 hr respectively.



For LC/UV and LC/MS conditions,

refer Agilent application notes:

### LC/UV: 5991-6274EN

#### LC/MS: 5991-6296EN

# LC-UV

### Intact mAb analysis on a AdvanceBio RP-mAb Diphenyl, 2.1 x 50 mm, 3.5µm column



Intact mAb analysis on a AdvanceBio RP-mAb C4, 2.1 x 50 mm, 3.5µm column

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### **Reduced mAb analysis on a AdvanceBio RP-mAb column**

Diphenyl, 2.1 x 50 mm, 3.5µm		Retention time		Peak area		
LC HC Innovator	Samples	Mean (min)	RSD	Mean (mAU/min)	RSD	
rituximab	Agilent AdvanceBio RF	Agilent AdvanceBio RP-mAb, C4, 2.1 × 50 mm, 3.5 µm				
	Innovator rituximab	1.96	0	71.61	1.98	
Biosimilar rituximab LC HC	Biosimilar rituximab	1.95	0.26	77.3	0.47	
	Agilent AdvanceBio RF	Agilent AdvanceBio RP-mAb, Diphenyl, 2.1 × 50 mm, 3.5 µm				
	Innovator rituximab	2.51	0.20	66.7	0.458	
	Biosimilar rituximab	2.51	0	73.3	1.86	
4.1 x 50 mm, 3.5μm		Retention til Mean	me	Peak area Mean		



Intact mAb mass analysis on a AdvanceBio RP-mAb C4, 2.1 x 100 mm, 3.5µm column

mAb fragment analysis on AdvanceBio RP-mAb C4, 2.1 x 100 mm, 3.5µm column



## Conclusions

- AdvanceBio RP-mAb columns: Fast and superior separation power for both intact and fragments of mAb
- Demonstration of LC-UV-based approach to define the molecular similarity between a biosimilar and its innovator reference
- Area and RT precision of intact and reduced analysis using AdvanceBio RP-mAb columns were excellent, and show the reliability of the method
- The C4 and Diphenyl AdvanceBio RP-mAb columns, with an MS-compatible  $\bullet$ method, delivered fast and high-resolution analysis for intact and ADC mAbs Publication Number 5991-6626EN



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- Agilent Technologies, Inc. Publication number 5991-4266EN, 2014.
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