

## **Characterization and Quantitation of Antibody Drug Conjugates**

Matthew Blatnik, Ph.D. and Chris Turck, Ph.D.

Pharmaceutical Interest Group Workshop, ASMS Vancouver

Monday, 21 May 2012, 5:45-7:25, Room 109

**Number of Attendees:** ≥125 people

### **Workshop Format**

Chris and I decided to run the workshop differently this year. We did not like the original format (which we used in 2011) that included three short panelist lead presentations followed by open discussion (we were coached on using this format). Our panelists in 2011 talked longer than their allocated 10 mins, interest decreased and we agreed that most folks were tired of listening to talks by the end of the day.

We altered our 2012 survey to include open ended questions along with solicitation for panelists willing to share and engage an audience. From the names provided, ~ 50 people were interested in participating. We cross referenced these individuals using Medline and LinkedIn to find experts. We asked Ola Saad (Genentech) to provide a 25 min presentation overview of the topic and asked the remaining experts to provide a statement of intent by email for participating as discussion panelists. Ryan Preston (Pfizer CovX), Jennifer Nemeth-Seay (J & J) and Jinzhi Chen (Takeda) provided very nice responses and joined Ola after her presentation as panelists. We asked the panelists to discuss the topic between them to keep dialog going if the audience was silent.

### **Workshop Discussion**

Ola gave a 30 min overview of the topic which included: characteristics of ADC biologics, conjugation sites/load and fit-for-purpose assay strategies including ELISA and LC-MS as complimentary tools. The panel/audience led discussion included: peptide mapping of ADC's, selecting conjugation sites (working around IP/patents), differentiating conjugation sites and drug antibody ratio (DAR) in vivo/ex vivo, linker stability/toxicity and preclinical species radio labeling experiments. One of the biggest issues in the ADC space is the translation between ELISA and LC-MS (with DAR and free payload) and PK-PD modeling.

The discussion following Ola's overview was very constructive. There was a lot of participation and we ran over 20 mins.

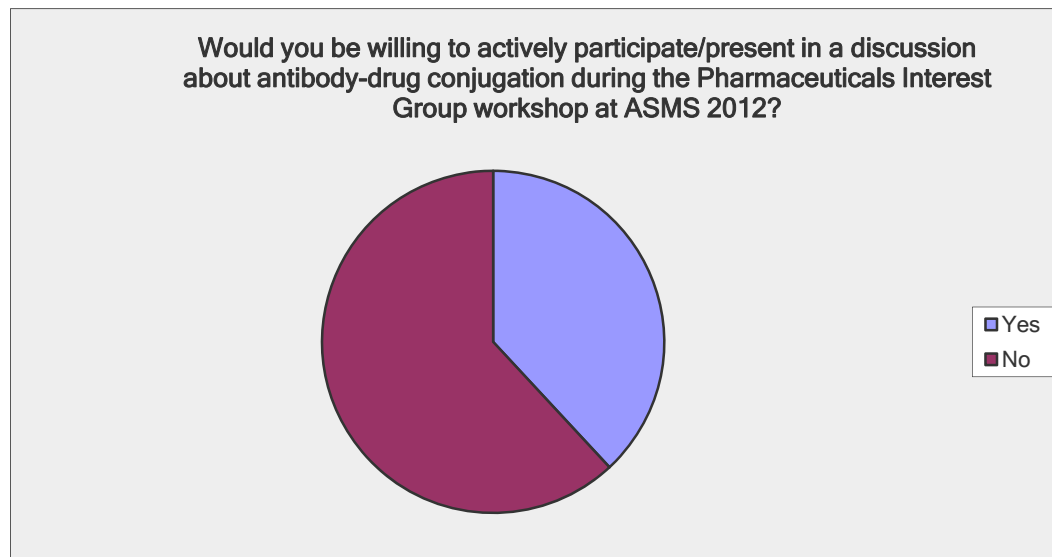
### **Succession Plan**

Using more of an Egalitarian approach to the workshop, Chris and I want to submit a call for workshop leaders to all the members of the pharma group via email (including the ~ 30 new members we picked up this year) and ask them to write a statement of intent (no more than 100 words). We have made positive impacts with this group over the last two years and want to make certain it continues to thrive by choosing people interested in putting some time. Therefore, we want to identify our successors but stay on as workshop leads for 2013 to properly coach and mentor the new leaders. We will introduce them as our successors at next year's workshop (if we are allowed to have one).

## ASMS 2012 Pharma IG

Would you be willing to actively participate/present in a discussion about antibody-drug conjugation during the Pharmaceuticals Interest Group workshop at ASMS 2012?

Answer Options	Response Percent	Response Count
Yes	38.1%	56
No	61.9%	91
<i>answered question</i>		<b>147</b>
<i>skipped question</i>		<b>1</b>

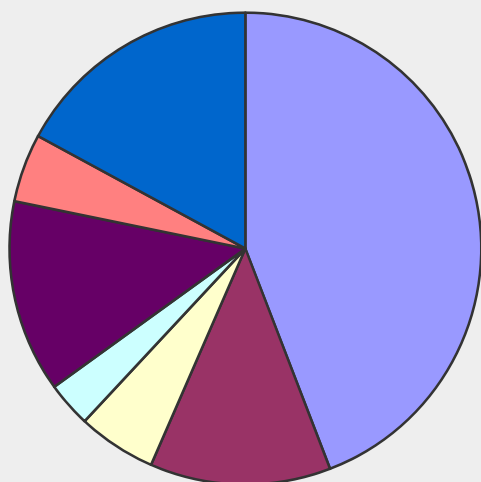


## ASMS 2012 Pharma IG

What is your organization's primary support function?

Answer Options	Response Percent	Response Count
Bioanalytical	44.2%	57
Large molecule	12.4%	16
ADME	5.4%	7
Biomarker	3.1%	4
Characterization/Purification/Formulation	13.2%	17
Biotransformation	4.7%	6
Other (please specify)	17.1%	22
<i>answered question</i>		<b>129</b>
<i>skipped question</i>		<b>19</b>

What is your organization's primary support function?



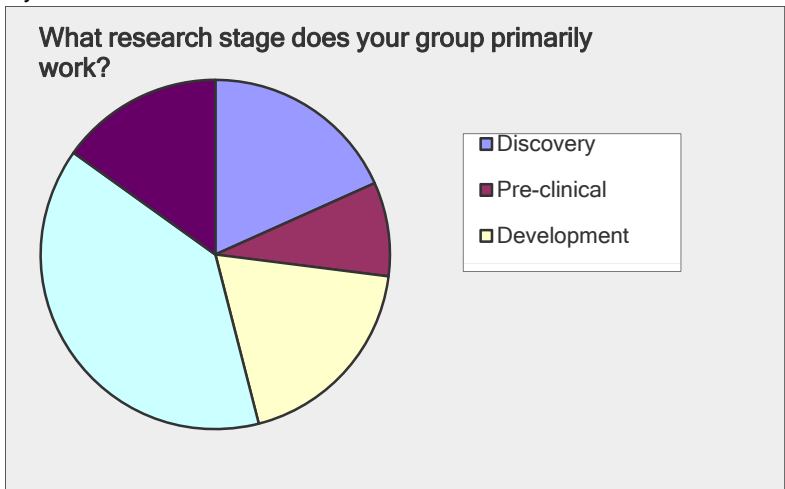
- Bioanalytical
- Large molecule
- ADME
- Biomarker
- Characterization/Purification/Formulation
- Biotransformation
- Other (please specify)

## ASMS 2012 Pharma IG

What research stage does your group primarily work?		
Answer Options	Response Percent	Response Count
Discovery	18.3%	23
Pre-clinical	8.7%	11
Development	19.0%	24
A combination of above	38.9%	49
Other (please specify)	15.1%	19
<i>answered question</i>		<b>126</b>
<i>skipped question</i>		<b>22</b>

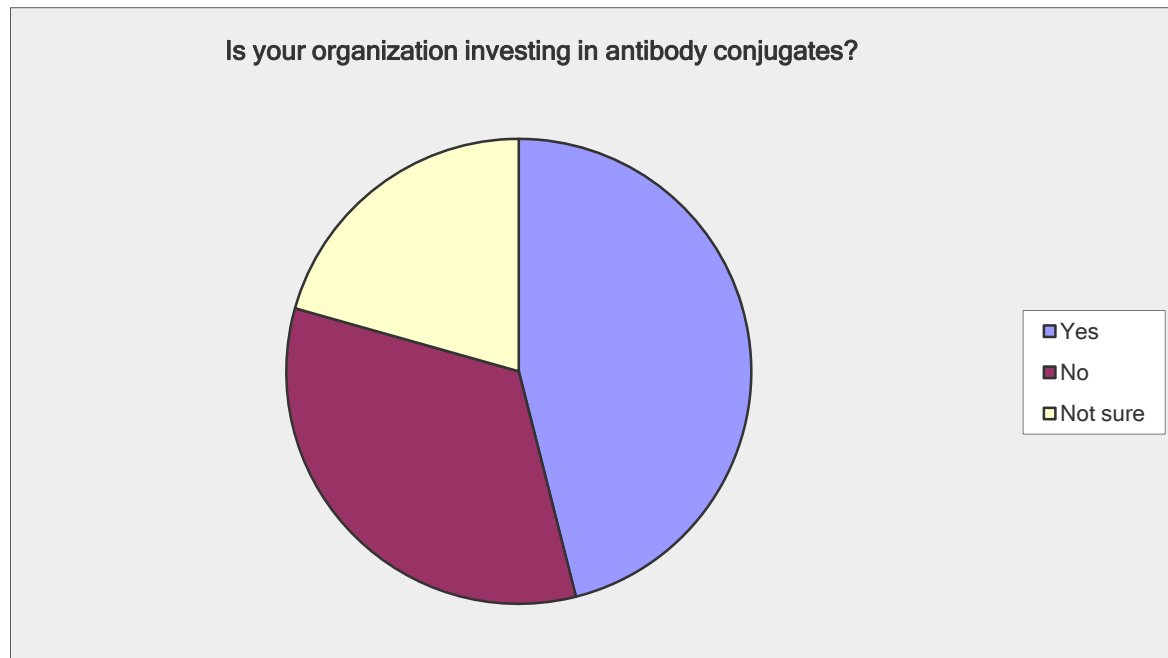
### Other (please specify)

Support of all  
 Clinical trials  
 clinical  
 CRO  
 basic research  
 Law  
 LC/MS method development and optimization  
 INstrument Vendor  
 proteomics  
 glyco conjugates  
 instrument vendor  
 We regularly collaborate with customers in all of these areas.  
 support across the development pipeline  
 CRO, all stage  
 method development  
 Instrument Vendor  
 Regulatory, Quality, Safety  
 all stages  
 authenticity studies



## ASMS 2012 Pharma IG

Is your organization investing in antibody conjugates?		
Answer Options	Response Percent	Response Count
Yes	46.0%	58
No	33.3%	42
Not sure	20.6%	26
<i>answered question</i>		<b>126</b>
<i>skipped question</i>		<b>22</b>

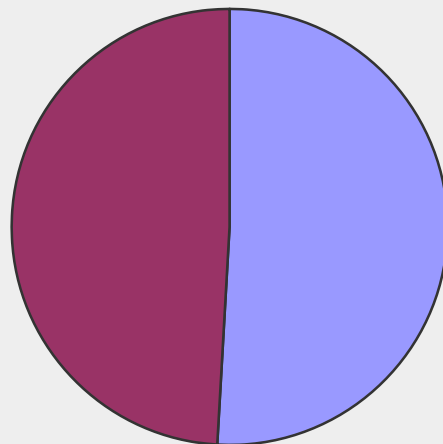


## ASMS 2012 Pharma IG

Is your group currently developing/using mass spectrometry-based methods for the analysis of antibody conjugates?

Answer Options	Response Percent	Response Count
Yes	50.9%	58
No	49.1%	56
<i>answered question</i>		<b>114</b>
<i>skipped question</i>		<b>34</b>

Is your group currently developing/using mass spectrometry-based methods for the analysis of antibody conjugates?



■ Yes  
■ No

## ASMS 2012 Pharma IG

If yes, would you be willing to discuss generic challenges and resolutions during the Pharmaceuticals Interest Group workshop at ASMS 2012?

Answer Options	Response Count
	31
<i>answered question</i>	31
<i>skipped question</i>	117

### Response

#### Text

yes...

Yes

sure, discuss but not present

Yes. As an executive director I could provide a high level overview of challenges and opportunities.

Yes. Biosimilars analysis is critical for the industry

yes

yes

I am still a beginner and not proficient in this field.

Yes. As an executive director of an analytical group, I would discuss this at a more strategic level.

Yes

yes

no

Yes. We would like to discuss our experience and findings about ADCs.

i'm not going to ASMS this year

MS inlet methods - chromatography (SEC, RP, etc.)MS analysis - full conjugate - Drug antibody ratio, site char

We just started with this type of analysis. The main focus is to identify antibody conjugates generated by biotr

Yes

if I am allowed to do so by our company IP Dept

yes

yes

Depends on signed NDAs. Might not be able to discuss much.

yes

No

no, sorry, have not received clearance on this.

Yes

depends on the company's confidence

I would be interested in listening and learning more about the issues

Yes

yes

No, we do not use them

No

## ASMS 2012 Pharma IG

If yes, is mass spectrometry used for... (choose all that apply)		
Answer Options	Response Percent	Response Count
the analysis of intact antibodies	70.0%	49
pharmacokinetic profiling	38.6%	27
antibody stability profiling	45.7%	32
non-specific binding	11.4%	8
free drug	55.7%	39
metabolites	41.4%	29
Other (please specify)	11.4%	8
<i>answered question</i>		<b>70</b>
<i>skipped question</i>		<b>78</b>

### Other (please specify) Categories

All of the above

HDX-MS

glyco conjugates

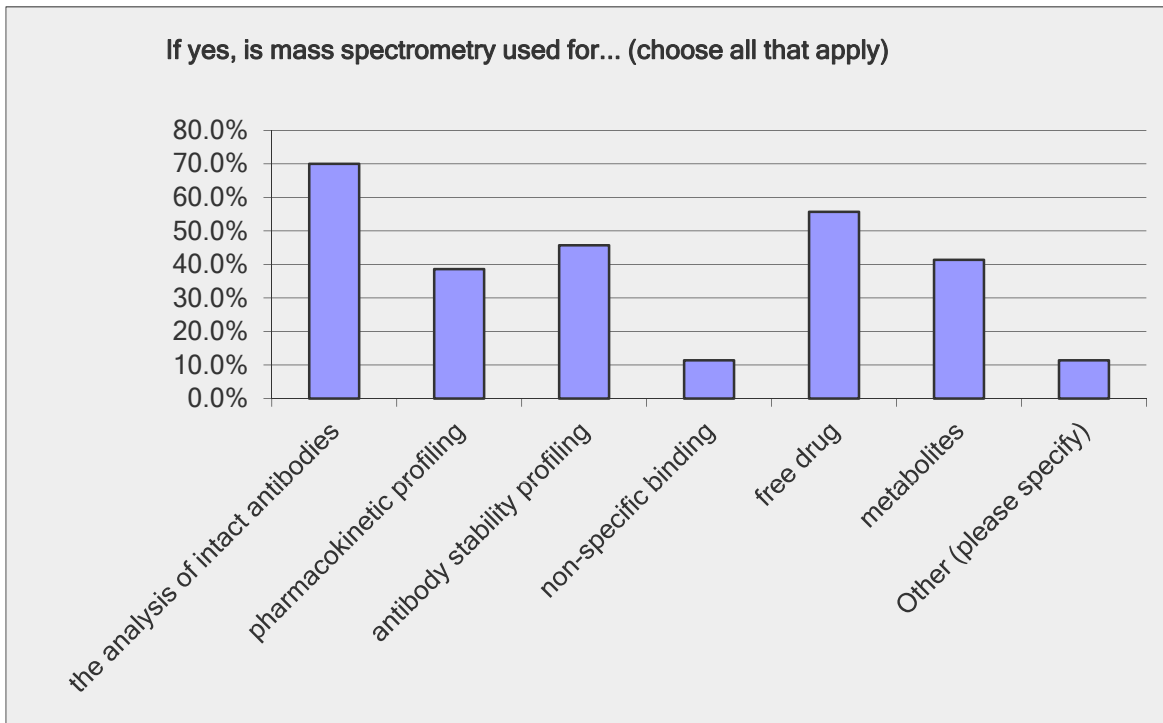
proteomics

small molecule

Warhead characterization, intact conjugated antibodies, process chemistry support of chemical modifica

mass spectral analysis of oligo deamination degradants without separation

conjugation sites



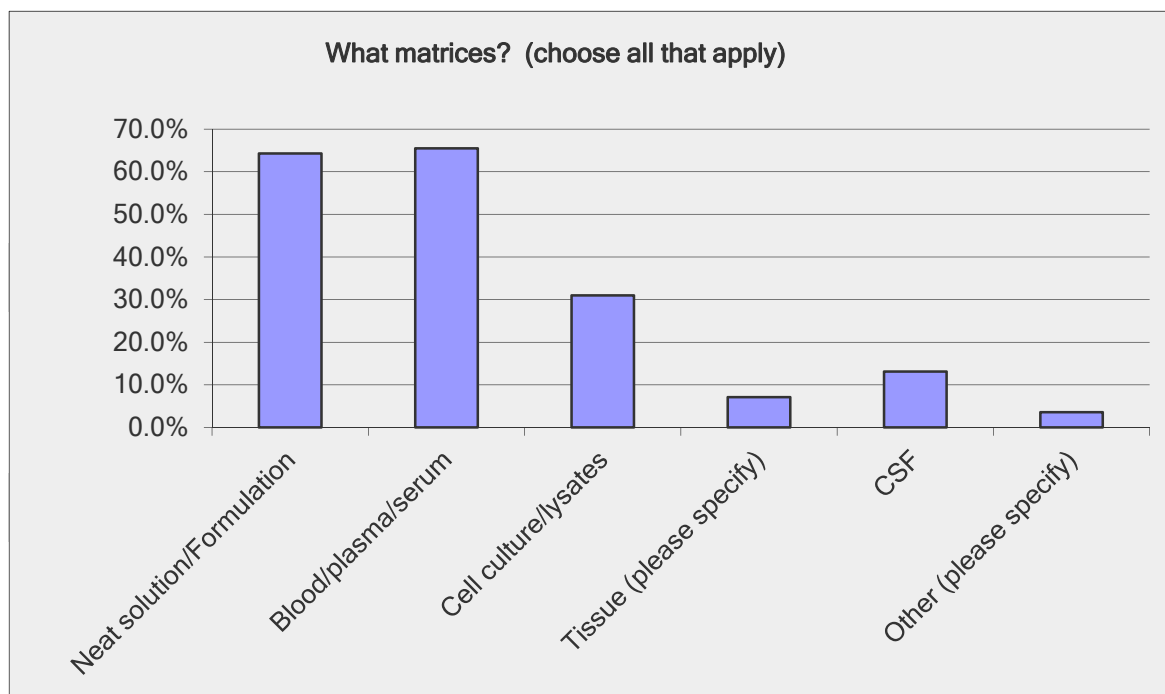


## ASMS 2012 Pharma IG

What matrices? (choose all that apply)

Answer Options	Response Percent	Response Count
Neat solution/Formulation	64.3%	54
Blood/plasma/serum	65.5%	55
Cell culture/lysates	31.0%	26
Tissue (please specify)	7.1%	6
CSF	13.1%	11
Other (please specify)	3.6%	3
<i>answered question</i>		<b>84</b>
<i>skipped question</i>		<b>64</b>

Number	Response Date	Other (please specify)	Categories
1	Mar 1, 2012 5:06 PM	Tissue and urine for signs of adduct formation	
2	Feb 10, 2012 11:53 AM	microarrays and tissues	
3	Feb 6, 2012 8:44 PM	glutathione stability for cysteine conjugates	



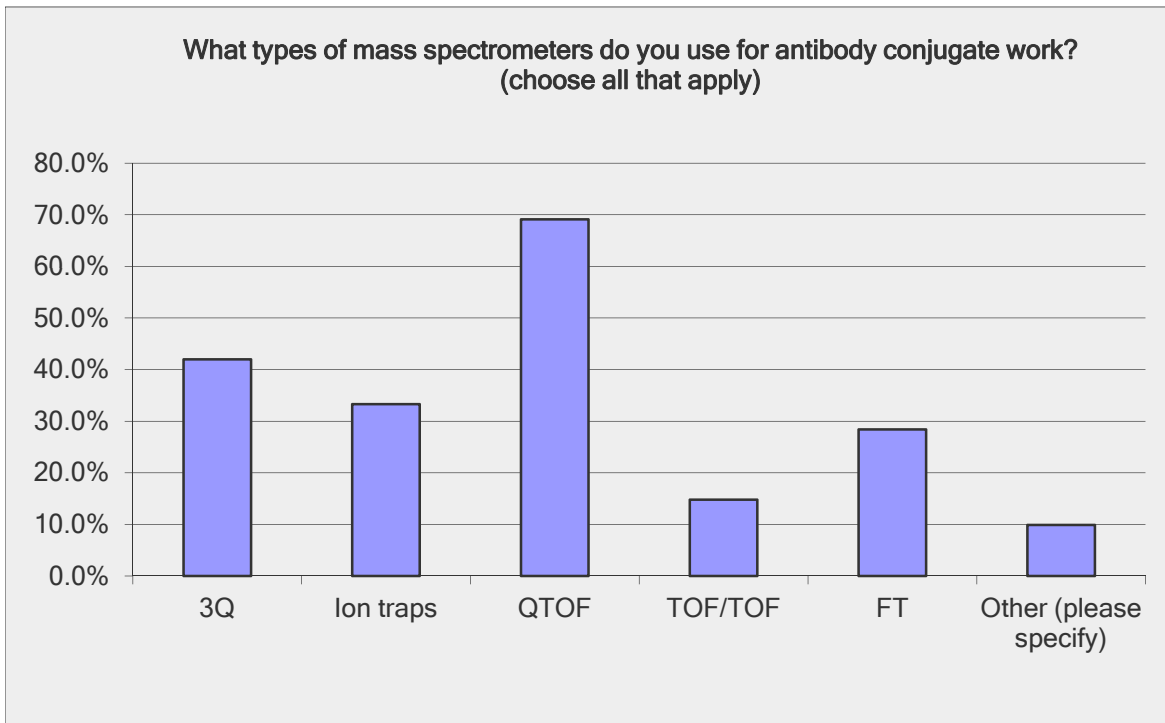
## ASMS 2012 Pharma IG

What types of mass spectrometers do you use for antibody conjugate work? (choose all that apply)

Answer Options	Response Percent	Response Count
3Q	42.0%	34
Ion traps	33.3%	27
QTOF	69.1%	56
TOF/TOF	14.8%	12
FT	28.4%	23
Other (please specify)	9.9%	8
<i>answered question</i>		<b>81</b>
<i>skipped question</i>		<b>67</b>

**Other (please specify) Categories**

orbi  
 Other hybrids  
 GEMMA  
 Not studying antibody conjugates yet  
 tof  
 Orbitrap for FC-Conjugates  
 ortial traps  
 Orbi



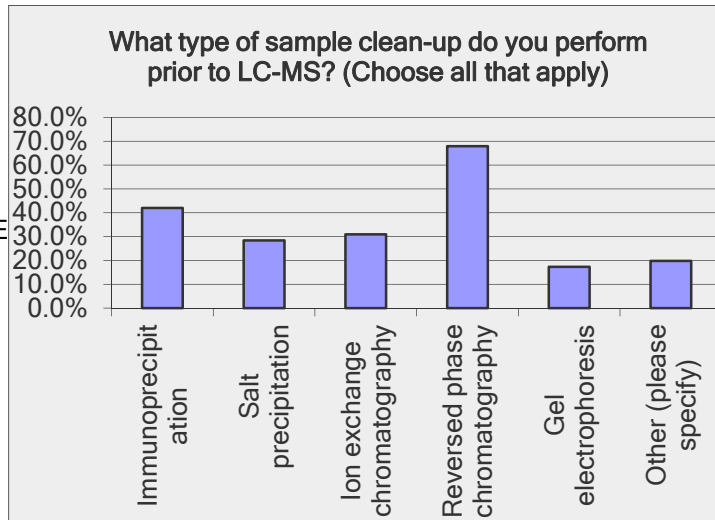
# ASMS 2012 Pharma IG

What type of sample clean-up do you perform prior to LC-MS? (Choose all that apply)

Answer Options	Response Percent	Response Count
Immunoprecipitation	42.0%	34
Salt precipitation	28.4%	23
Ion exchange chromatography	30.9%	25
Reversed phase chromatography	67.9%	55
Gel electrophoresis	17.3%	14
Other (please specify)	19.8%	16
<i>answered question</i>		<b>81</b>
<i>skipped question</i>		<b>67</b>

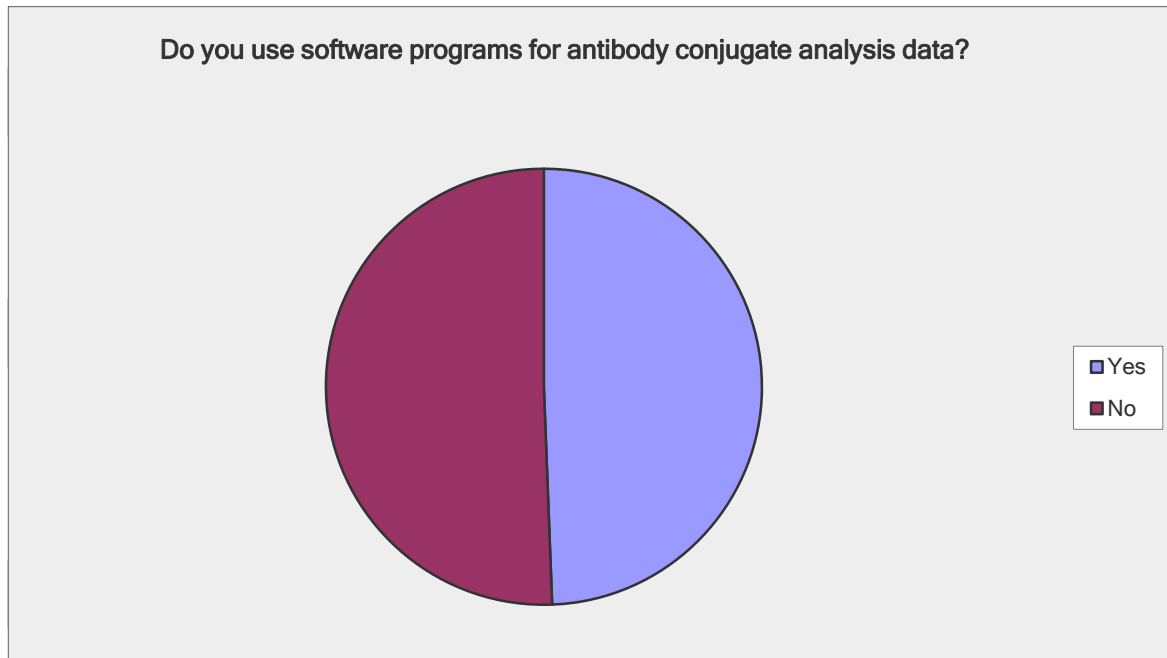
**Other  
(please  
specify)**

- SPE
- none
- protein precipitation
- SPE and Buffer exchange
- DBS
- SPE of digests
- Dialysis
- protein precipitation, liq-liq extraction, SPE
- dialysis
- none
- Solid phase microextraction
- SEC
- Turbulent Flow Chromatography
- Surfactant removal
- PGC cartridge
- DBS



# ASMS 2012 Pharma IG

Do you use software programs for antibody conjugate analysis data?		
Answer Options	Response Percent	Response Count
Yes	49.4%	42
No	50.6%	43
<i>answered question</i>		<b>85</b>
<i>skipped question</i>		<b>63</b>



## ASMS 2012 Pharma IG

If yes, please state for what application (mass deconvolution, quantitation, etc.)

Answer Options	Response Count
	34
<i>answered question</i>	<b>34</b>
<i>skipped question</i>	<b>114</b>

### Response

#### Text

mass deconvolution, quantitation  
 mass deconvolution, peptide mapping  
 quantitation  
 Bruker BioTools, for intact mass deconvolution, and peptide mapping (with modifications specified)  
 mass deconvolution and peptide ID  
 Mass deconvolutionPeptide maps analysis  
 Various  
 Mass decon  
 Mass hunterProteome discoverer  
 mass deconvolution, PTM identification, de novo sequencing, identification of truncations (metabolites) of the  
 BioAnalyst  
 MassLynx, Biopharmalynx  
 Mass deconvolutionquantitation  
 deconvolution  
 Deconvolution, characterization  
 mass deconvolution  
 Intact MS deconvolutionquantitation  
 Deconvoltution  
 biopharmalynx  
 MaxEnt, Protein Deconvolution (new from thermo)  
 BioPharmaLynx 1.3 from Waters but also various software available from academia.  
 Mass deconvolution  
 a unified software for both spectral deconvolution and relative quantitation  
 ProMass, ThermoFisher  
 deconvolution  
 decon  
 deconvolution, peptide mass mapping  
 maxent (through Bruker compas) for deconvolution. Excel for quantitation.  
 Mass deconvolutionDrug distribution prediction  
 Masslynx  
 deconvolution, quantitation  
 all  
 mass deconvolution  
 Quantitation

## ASMS 2012 Pharma IG

What challenges would you like this workshop to address about antibody drug conjugates and mass spectrometry?

Answer Options	Response Count
	42
<i>answered question</i>	<b>42</b>
<i>skipped question</i>	<b>106</b>

### Response Text

Quantitative analysis of conjugation levels  
 accuracy for quantitation; matrix effect; the efficiency of trypsin digestion.  
 Balance of Qual / Quant and specific approaches for each separately and together  
 Characterization (peptide mapping).  
 sample prep and analytical tips on what works well; compatibility of sample prep and analysis re: intact Ab vs  
 Conversion efficiency to release loaded drugs from mAb's and compensation by stable label IS (released peptide sample cleanup/sensitivity  
 Regulatory expectations for characterization and quantification of adduct variants in drug product/drug substances  
 New and novel techniques to elucidate interactions  
 characterization and quantitation and extraction from complex biological matrices.  
 Antibodies with large protein conjugates.  
 Identification of biotransformation products of antibody drug conjugates in plasma from animals and human.  
 Regulatory requirements/expectations for characterization, PK  
 binding sites, affinity, screening,  
 What needs to be quantified: Free drug? Total Ab? Total drug (bound+ free)? AB-Drug conjugates only?  
 Define the challenges, describe successful approaches to quantitation, discuss emerging/potential approaches  
 getting good spectra, maldi, esi techniques  
 Resolution, sensitivity  
 instrument resolution needed, software features to help process this type of data  
 analytical methods to describe specificity  
 1) platform development to understand ADC stability in vivo 2) ADC catabolism 3) ADC characterization for metabolite analysis, Quantitation of conjugate species  
 specific site of conjugation reaction on protein  
 Inlet approaches - SEC/RP Optimal site characterization approaches (top-down/bottom-up/middle...etc.) MS  
 Discussion of different top-down and bottom-up approaches to narrow down the site of conjugation or metabolite  
 Assay sensitivity.  
 a mathematically correct and defensible model for full mass spectral profile mode data on these complex mixtures  
 2D chromatography, Gel ADC samples and PK profiling,  
 Software  
 The challenges of developing SOPs, methods and validations to meet the regulatory requirements from the FDA  
 Interested in knowing approaches being used out there.  
 how do they differentiate from other drugs (mAb, small molecule) in terms of successfully passing through clinical trials  
 Stability issue; Internal standard  
 I am here to learn  
 In-source artifacts like oxidation or dehydration.  
 Sample workup such as immunocapture; can these conjugates be detected after digestion by MS?  
 sensitivity, resolution and software analysis  
 I think the largest issue is the stability of the linker that conjugates the toxic payload and how to design it to allow a  
 transition from research based experiments to routine (GMP/GMP like) experiments.