



# DIA / SWATH Market Assessment

December 2014

# Notice

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The information, data and estimates in this report have been obtained from sources believed to be reliable. Every reasonable effort has been made to verify their accuracy. Information contained in this report is very time-sensitive. Please note the publication date.

While all reasonable steps have been taken to ensure the accuracy of the information presented, Biognosys AG cannot accept responsibility for inadvertent errors or omissions. Biognosys AG also takes no responsibility for any incorrect information provided to it by survey participants. The market information contained herein is based on survey results and information obtained from the public domain and therefore is subject to interpretation.

# Introduction

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Data independent acquisition (DIA or SWATH) performed on state of the art high-resolution mass spectrometers enables comprehensive recording of all peptide fragment ion signatures in a single experiment.

DIA is the basis of Biognosys' Hyper Reaction Monitoring (HRM-MS™) - next generation targeted proteomics technology that enables reproducible and precise quantification of 1000s of proteins in a single instrument run.

In this market assessment study we were interested in understanding the perception of the technology by the experts in the mass spectrometry proteomics field. We make the key findings of the study freely accessible to the public in the form of this report.

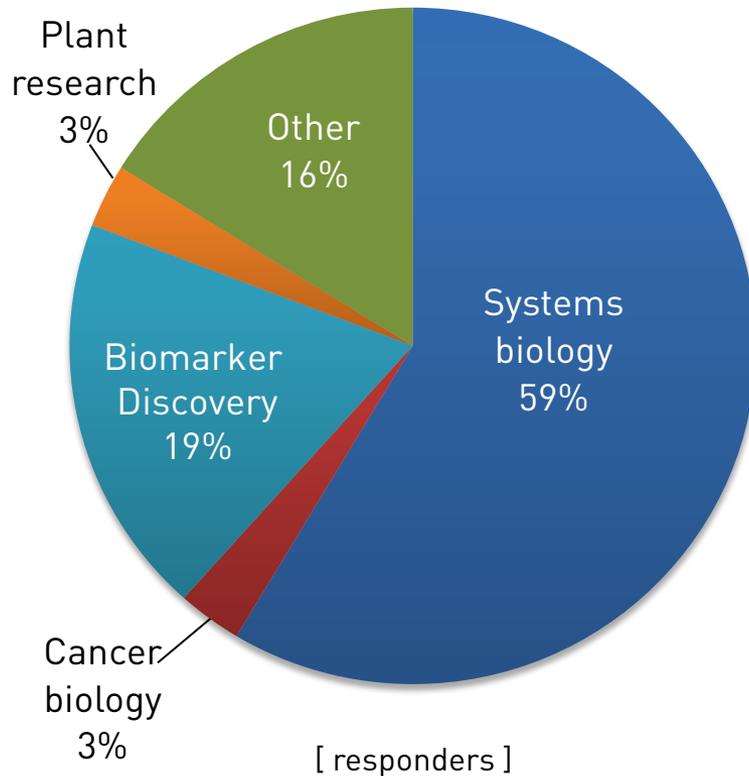
# Summary of approach

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- ◆ The primary goal of this market research project was to assess the users' perception of the DIA / SWATH technology.
- ◆ To gain timely and relevant market data about the use of DIA / SWATH we created an online survey with 11 multiple-choice questions. The survey was distributed to Biognosys' customers and other relevant contacts in October 2014. It was also advertised online on Biognosys' online store webpage during October – November 2014.
- ◆ This document represents the final report of the qualitative findings.

# Participant demographics (field of research)

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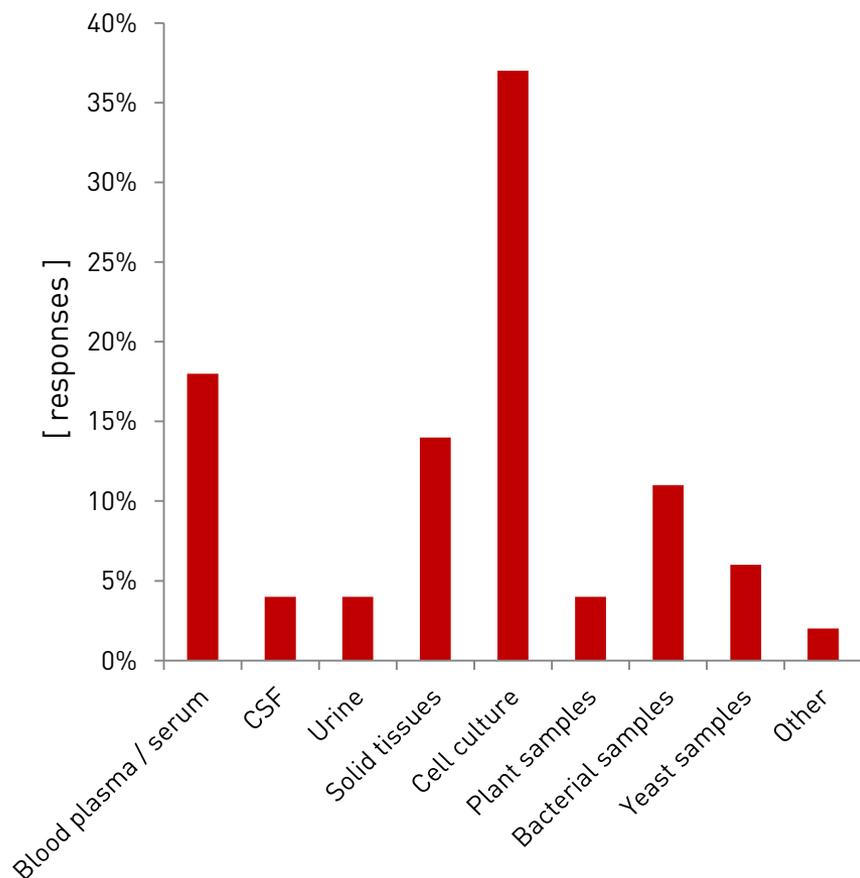
Participants were given a list of categories and asked to categorize their primary field of research.

“Other” includes the following responses (free text field):

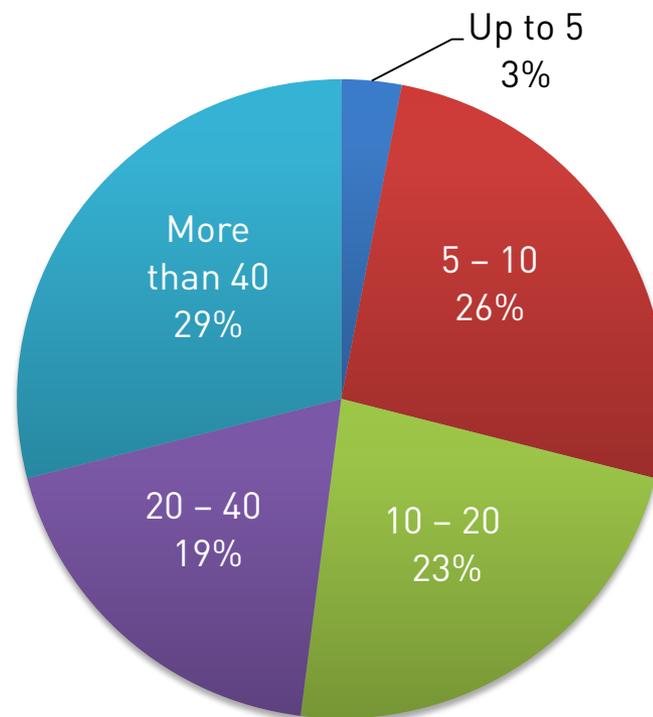
- ◆ General proteomics
- ◆ Proteomics services
- ◆ Structural biology
- ◆ All academic research

# Experimental samples used in DIA / SWATH

## Sample Type



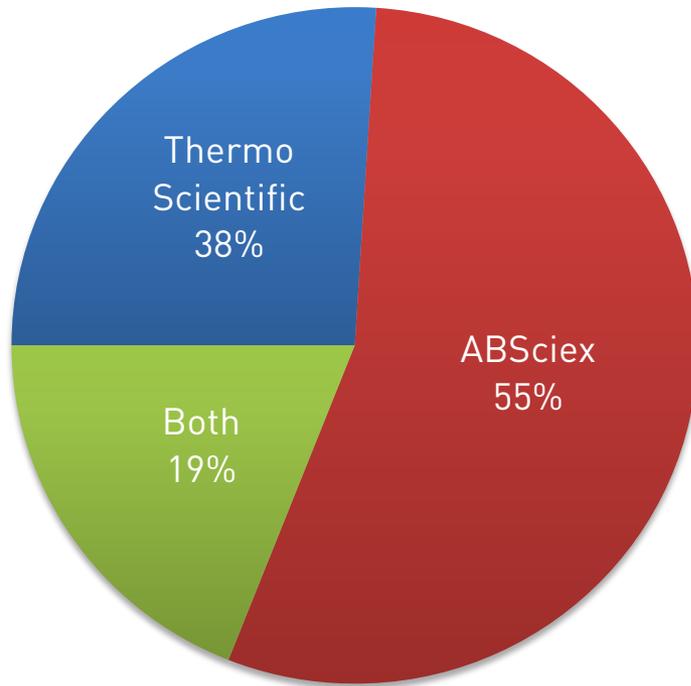
## Number of samples per experiment



[ responders ]

# Instrument vendors in DIA / SWATH

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[ responders ]

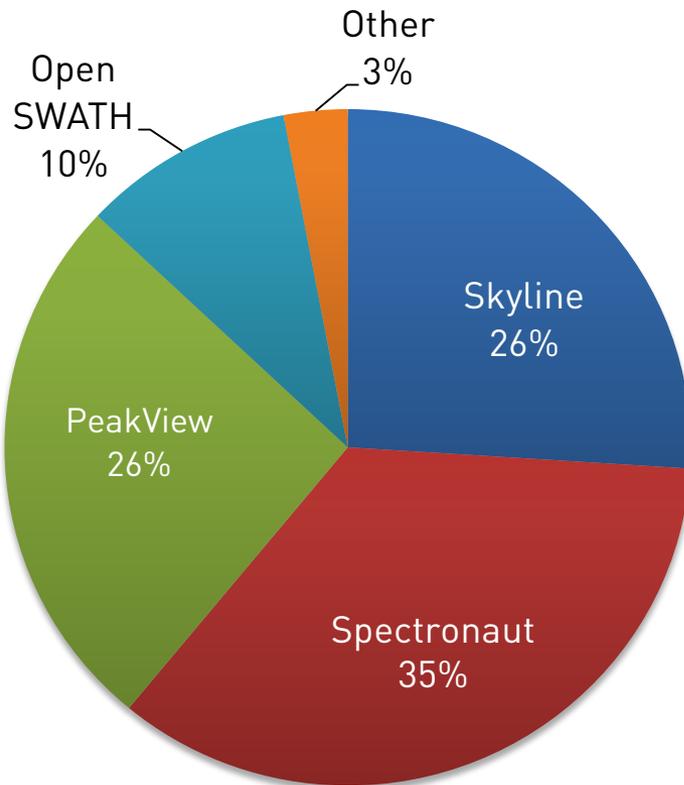
Participants had to select vendors of the instruments they use for DIA/SWATH from a list of vendors that provide mass spectrometers for proteomics applications.

Multiple vendors could be selected.

No vendor other than Thermo Scientific and AB Sciex has been chosen.

# Software for DIA / SWATH data analysis

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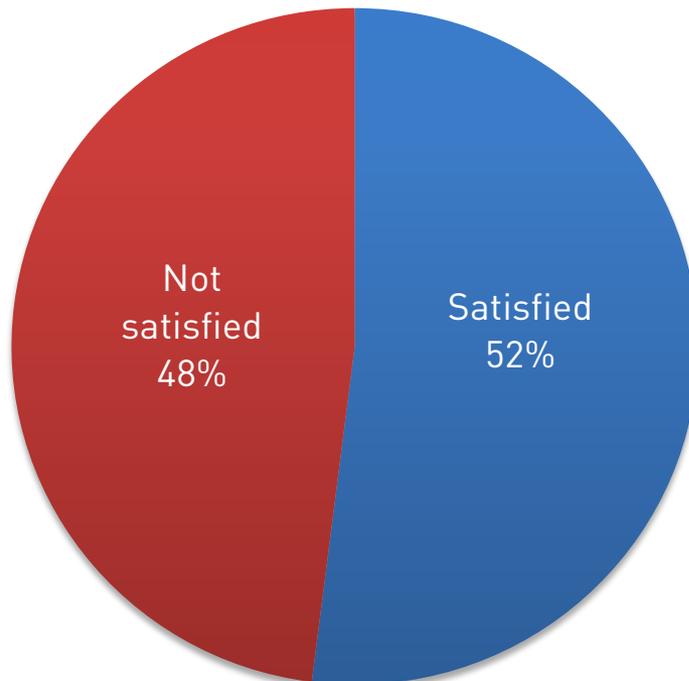
[ responders ]

Participants were asked to select the software they predominantly use from a list of software products that can potentially be utilized for signal processing and data analysis of DIA / SWATH data.

Only one software product could be selected.

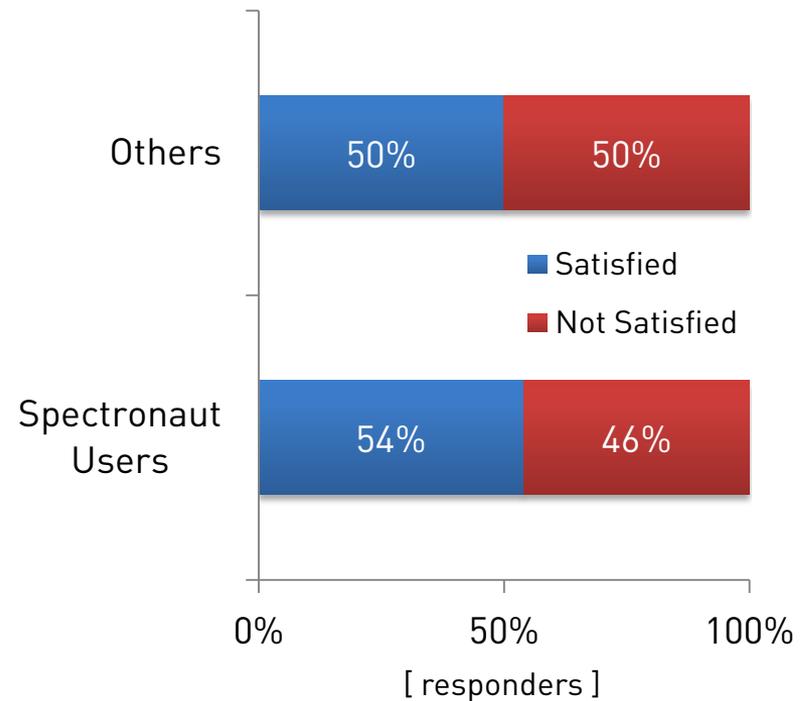
# Satisfaction with available consumables for DIA / SWATH

## General satisfaction



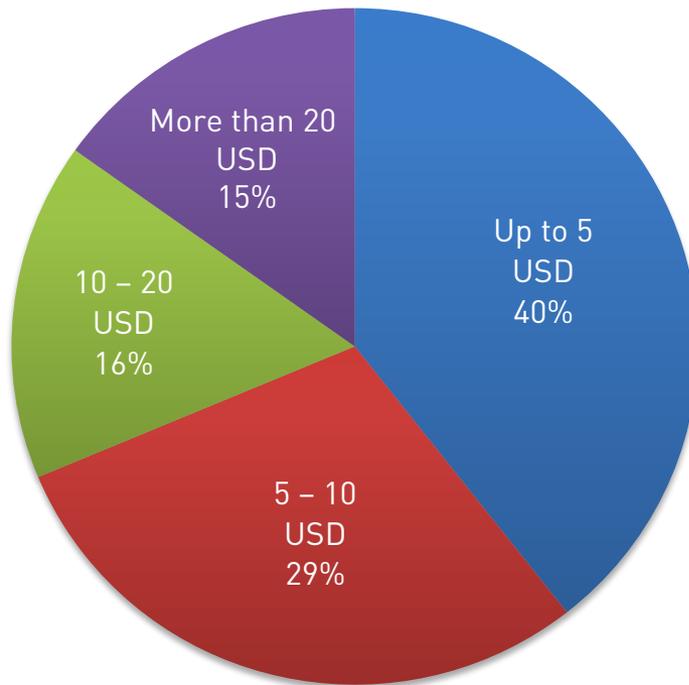
[ responders ]

## Depending on the software used\*



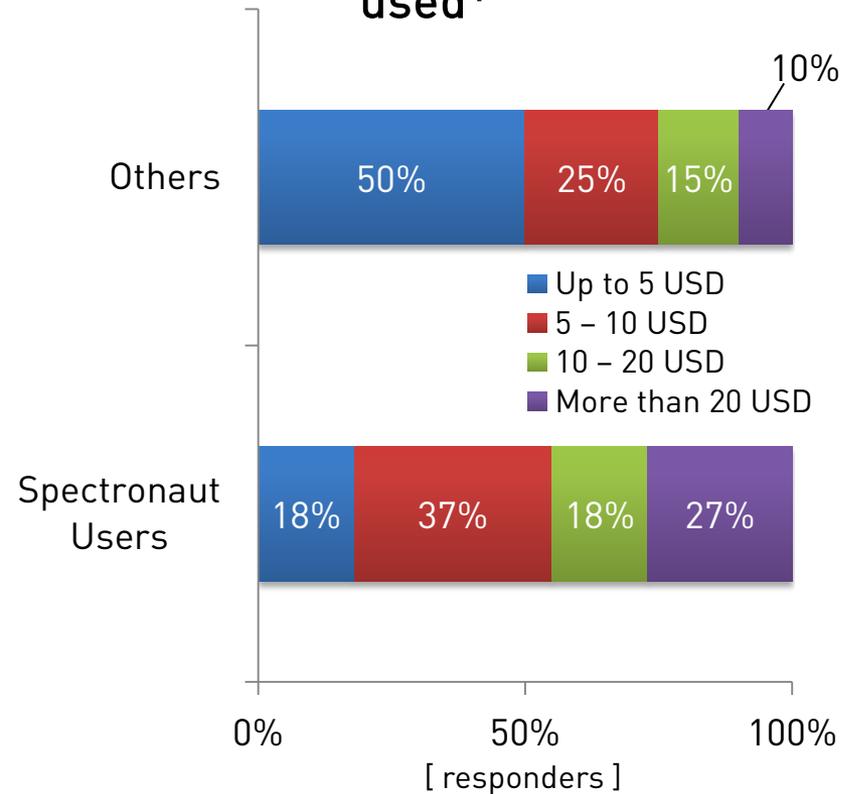
# Perceived optimal cost of consumables per sample

## General perception



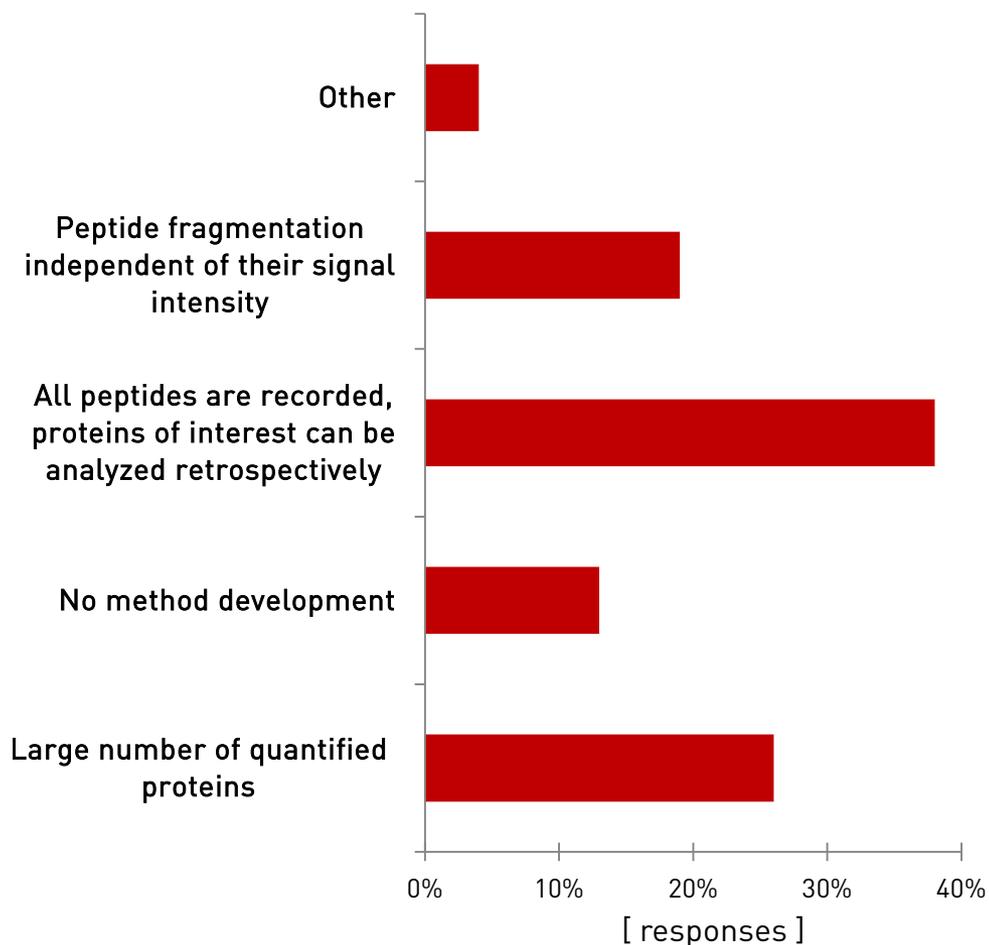
[ responders ]

## Depending on the software used\*



# Perceived advantages of DIA / SWATH

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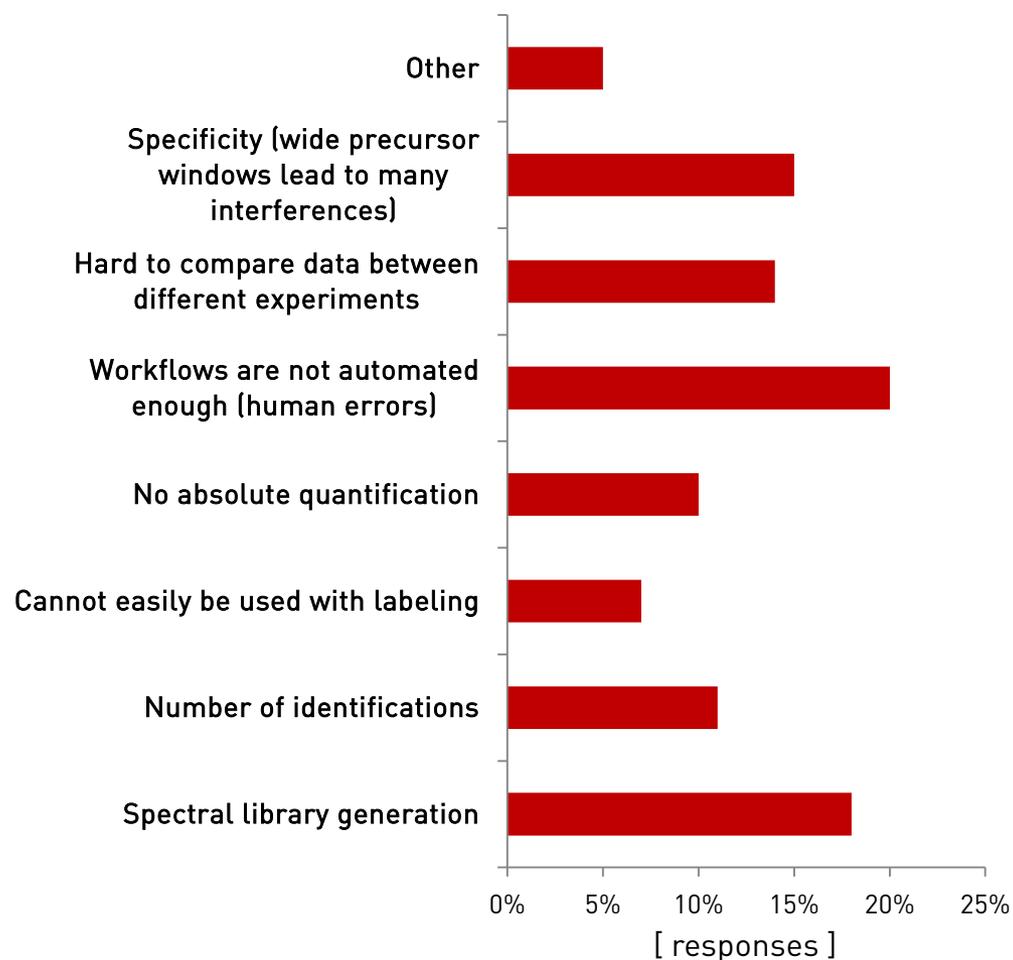
Participants were given a list of features, several of which could be selected.

“Other” includes the following responses (free text field):

- ◆ Data matrix completeness
- ◆ Reproducibility
- ◆ More accurate and reproducible quantitation

Interestingly, responders that see an advantage in “No method development” and “Large number of quantified proteins” are more satisfied with available consumables (80% and 74%, resp.).

# Perceived limitations of DIA / SWATH



Participants were given a list of features, several of which could be selected.

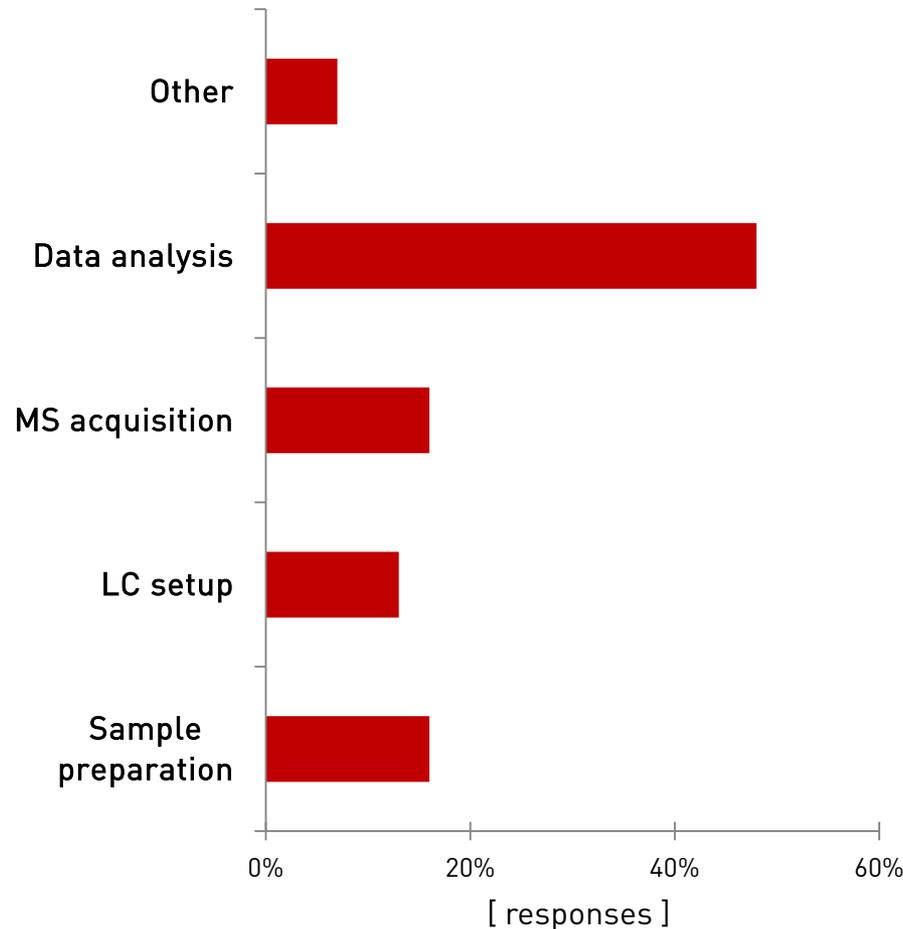
“Other” includes the following responses (free text field):

- ◆ Data analysis complexity
- ◆ Reproducibility
- ◆ Relatively low sensitivity

Interestingly, responders that see limitations in “Workflows...” and “Spectral library generation” are less satisfied with available consumables (67% and 62%, resp.).

# Perceived limitations of DIA workflows

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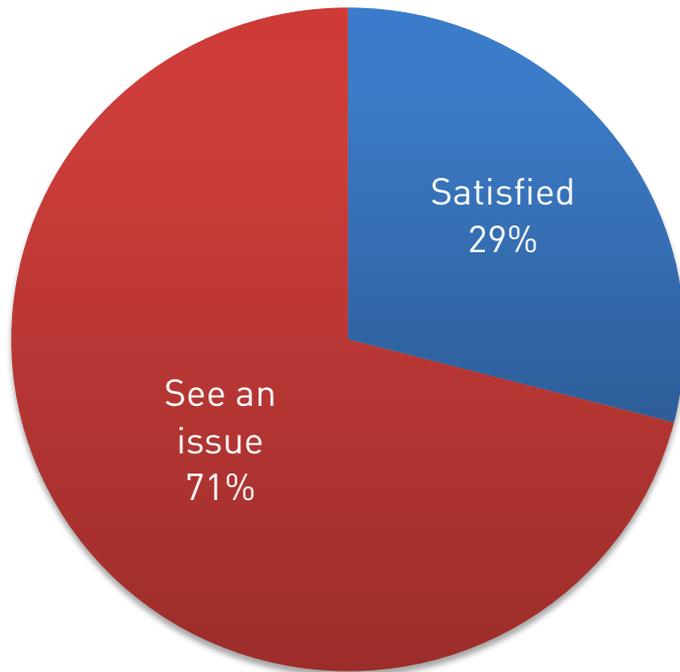


Participants were given a list of features, several of which could be selected.

- ◆ Data analysis is perceived as a major issue in DIA *(for further segmentation see next page)*
- ◆ Sample preparation represents a limitation in large-scale experiments only *(more than 10 samples at once)*

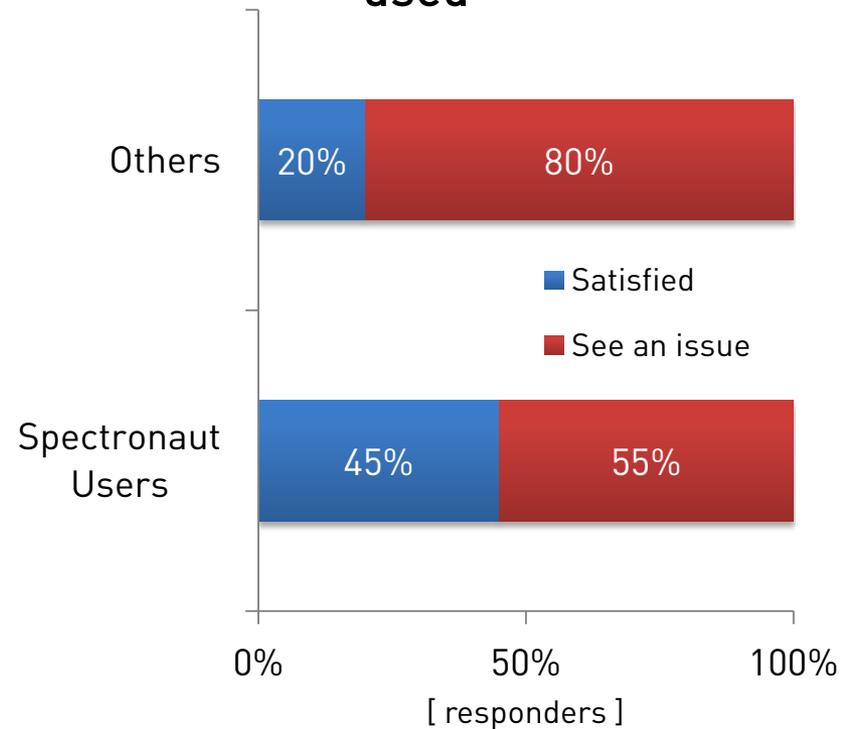
# Satisfaction with data analysis in DIA / SWATH

## General satisfaction



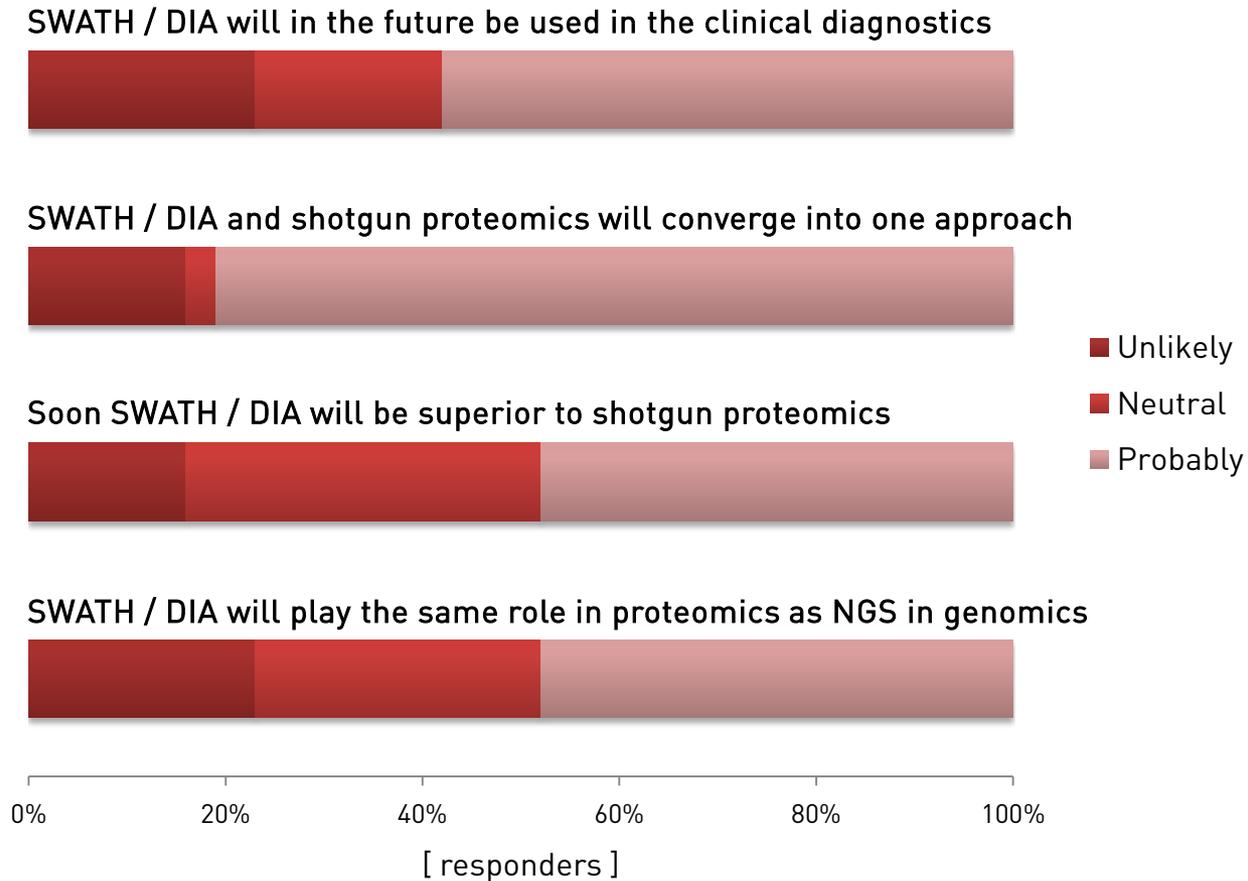
[ responders ]

## Depending on the software used\*



# Future perspectives of DIA / SWATH

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# Responders' comments

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*“There is still a need to improve the dynamic range of the instrumentation/detection - 5.5 orders is about the best on the new generation, but for serum proteomics without upstream fractionation (increasing sample numbers significantly) large scale high sample numbers analyses will not be routine.”* – **Scientist, Biomarker Discovery, AB Sciex user**

*“I think DIA is the wave of the future [...] and will eclipse shotgun techniques. The big limitation has been data processing and Spectronaut does a very good job of filling that void.”* – **Scientists, Systems Biology, Thermo Scientific user**

*“Our current issues: 1. interference, partly countered by using smaller SWATH windows and/or improved mass spectrometers in the future, but perhaps further software algorithms can help with deconvolution; 2. sensitivity, low abundant peptides yield low quality fragment groups that don't really look like a gaussian peak. Probably only solved by using less complex samples/or improved mass spectrometers; 3. And last but not least, keep up the great work on Spectronaut !!”* – **Scientists, Systems Biology, AB Sciex user**

*“More tutorials on how to get started on data analysis. Examples on library spectral generation. Examples on analysis of samples.”* – **Scientists, Systems Biology, Thermo Scientific user**

# Key Findings

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- ◆ Systems Biology is the main application field for DIA / SWATH technology followed by Biomarker Discovery research
- ◆ Cell culture samples are the most commonly used sample type in DIA / SWATH applications
- ◆ Users see the main advantage of DIA / SWATH in the ability to record all peptide ion signals enabling retrospective analysis of proteins of interest
- ◆ Workflow automation and spectral library generation are perceived as main limitations of the current DIA / SWATH workflows
- ◆ Data analysis represents a major issue in DIA / SWATH applications, especially for non-Spectronaut users
- ◆ Limited informational material is available on how to analyze DIA / SWATH data on real examples
- ◆ DIA / SWATH is believed to eclipse shotgun proteomics in the future or to converge with it into one approach

# Contact details

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