# Top-Down Proteomics Workshop at ASMS 2025

# Software and Data Analysis Strategies for Getting the Most Out of Your Data

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**73rd Annual ASMS Meeting**

**Baltimore, MD**

**June 2, 2025**

**Please access Slido Q&A**

**Code: 5417047**

# Top-Down Proteomics Workshop at ASMS 2025

## Software and Data Analysis Strategies for Getting the Most Out of Your Data

**Xiaowen Liu**
TopPIC

**Boris Krichel**
MASH

**Ken Durbin**
ProSight Suite

**Kyowon Jeong**
FLASH

**Jack Bennett**
precisION

**Mariangela Kosmopoulou**
OmniScape

**Michael Shortreed**
Proteoform Suite

**Please access Slido Q&A**

**Code: 5417047**

# Intro survey

Active poll

48

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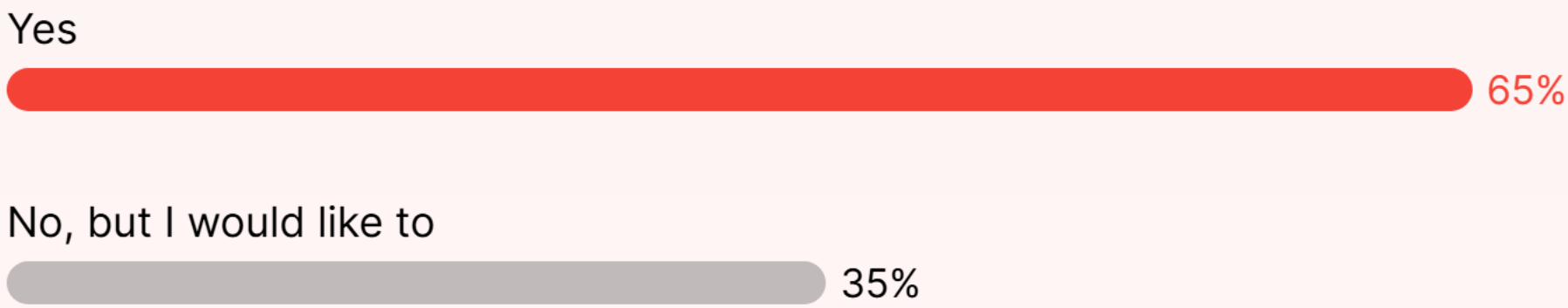
**#5417 047**

**Do you currently use Top-Down (TDP) approach in your research?**



Active poll

47

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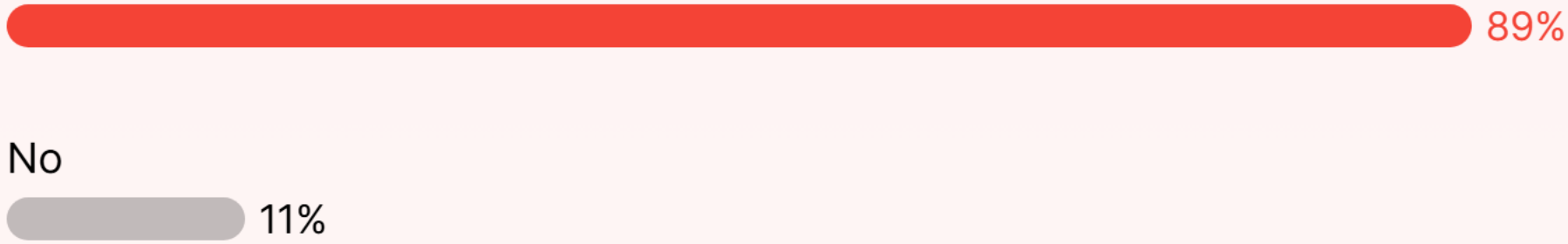
## Is TDP software an obstacle in your work?



Active poll

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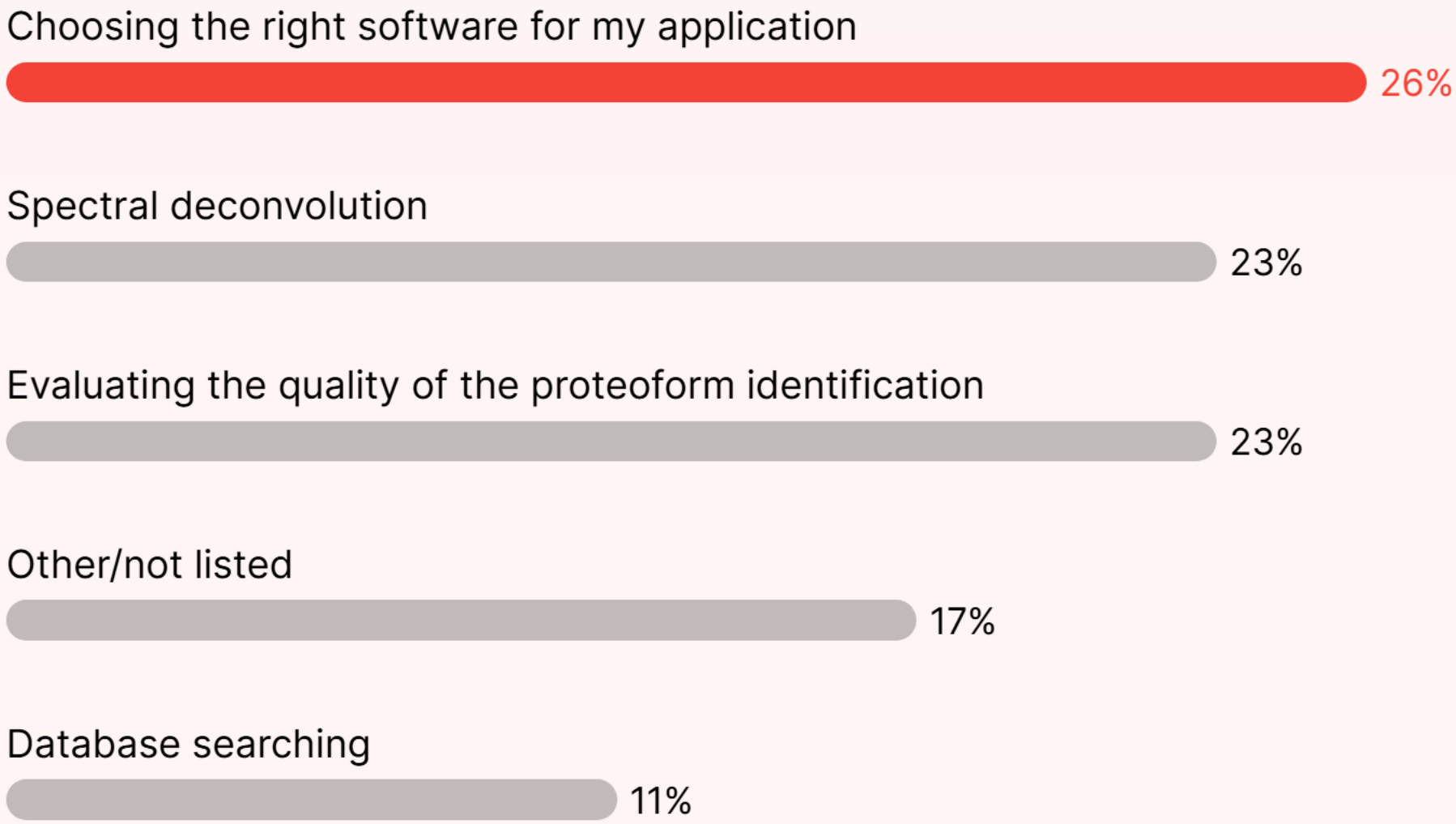
**What is the largest obstacle you encounter with TDP software?**



Active poll

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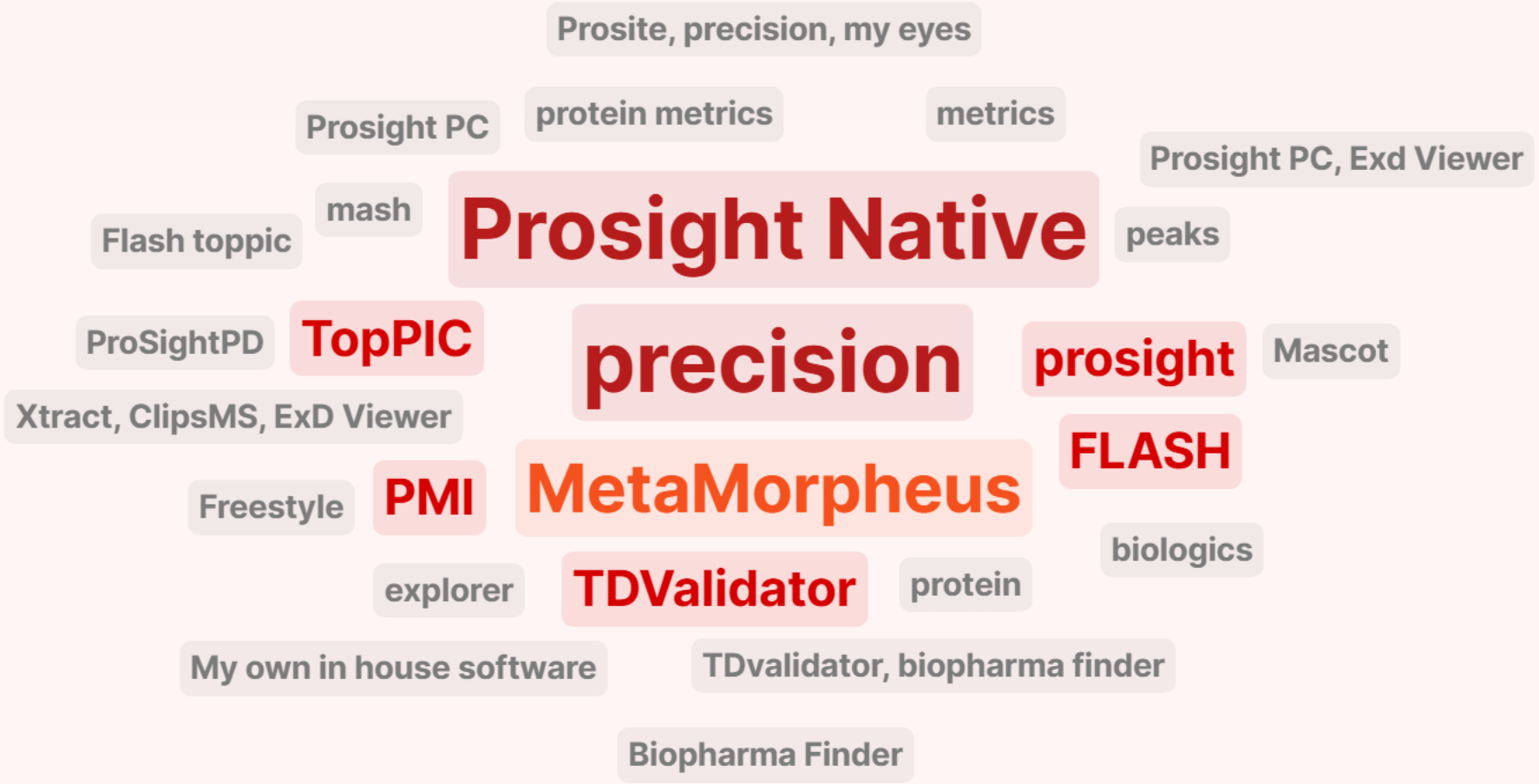
## What software do you use?



Active poll

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**What would you like TDP software to be able to do but currently can't?**

Internal fragments are a problem

Better validation (Retention/Migration Times, deconvolution, etc.) and classification.

Give me reliable monisotopic masses for both precursors and fragments; I often get masses that are clearly 1-2 Da or even more off, especially for larger masses! And there's no good way to minimize false positives while not making huge concessions for false negatives!

Untargeted analysis of top down proteomics

Manually inspect annotations; Integrated data visualization

Active poll

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**What would you like TDP software to be able to do but currently can't?**

Correct for monoisotopic mis assignment instead of assigning as hydrogen atom exchange

Identify ligand binding sites and variable modifications

Data interpretation and visualization

Get reliable label-free quantification

Accurate deconvolution

Be more user friendly !!!! Always very complicated

Active poll

16

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## What would you like TDP software to be able to do but currently can't?

Be more user friendly !!!! Always very complicated

database searching and mapping like bottom up proteomics

Assign more peaks based on empirical observations of fragmentation propensity in tdms rather than adopting bottom up approaches

Glyco

Label raw mass spectra, be more reliable in fragment assignment and protein ID

Automatic fragment peak annotation

Active poll

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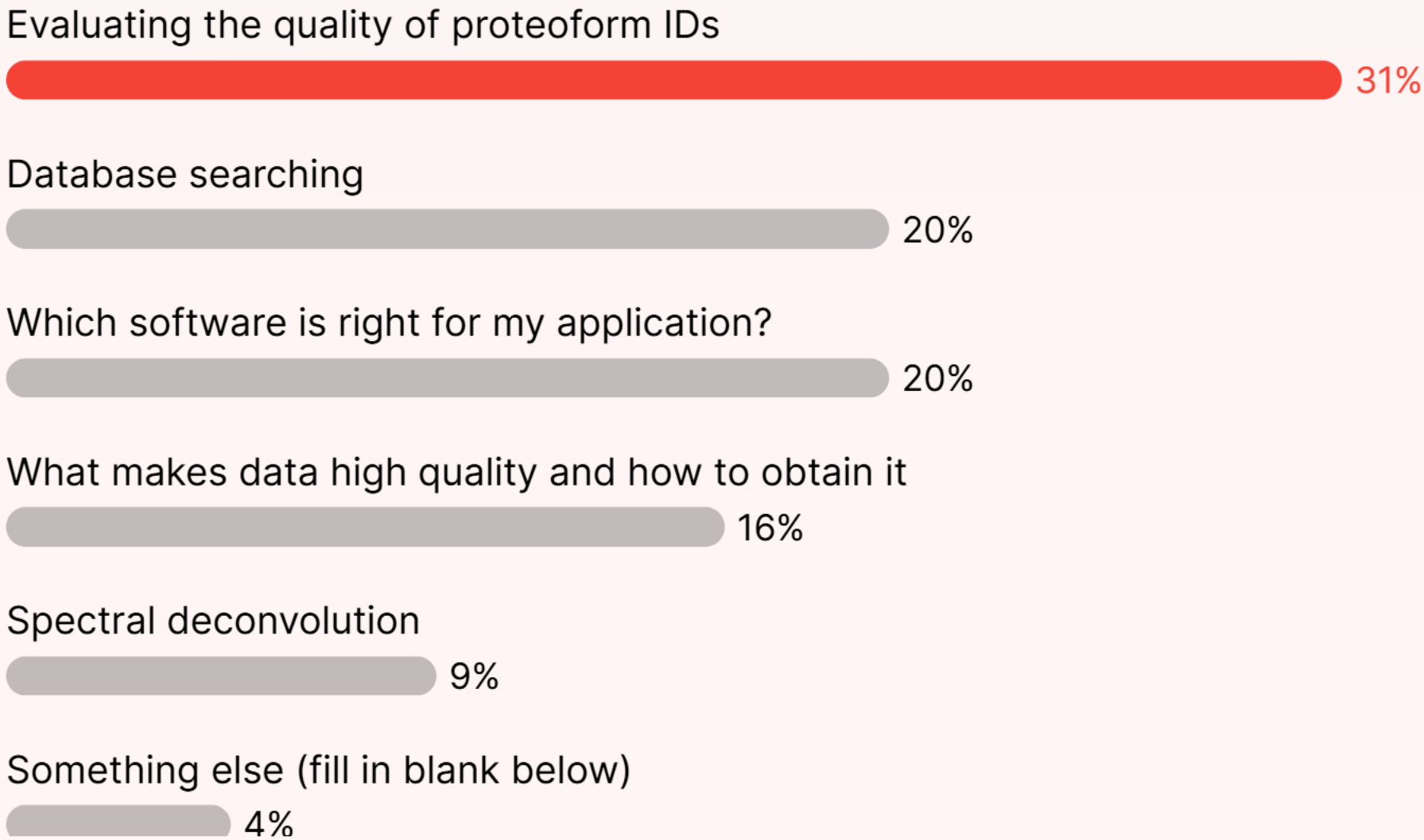
**What topic are you most interested in discussing in this workshop?**



Active poll

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**Do you have any suggestions for the topic of the next TDP workshop?**

When we have BUP and TDP data of one sample how can we relate them together to find specific PTMs shared between them??

How to obtain high-quality proteoform identification in complex TDP datasets

End-to-End validation of identification quality

Proteoform quantitation for function and mechanism

Sample preparation and separation of intact proteins

What are the best softwares for database searching and relative

Active poll

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**Do you have any suggestions for the topic of the next TDP workshop?**

Proteoform quantitation for function and mechanism

Sample preparation and separation of intact proteins

What are the best softwares for database searching and relative quantitation?

Analysing complex samples natively

No

Lc-ms tips

# Audience Q&A

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Q&A

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Anonymous 3

How can we analyze modifications other than PTM in different tools? for identification and quantification

Anonymous 2

Do the softwares analyze protein information including adducts or metal complex in the MS1 and/or MS2 data?

Latest question

Anonymous 2

How do you normalize ???

Q&A

Popular 8

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Anonymous 1

Which software suites have support for ion mobility?

Anonymous 1

How do you approach proteoform quantification

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Latest question

Anonymous 2

How do you normalize ???

Q&A

Popular 8

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Anonymous 0

What does each developer think their software is most well suited for?

Anonymous 0

Can you please specify the difference between Top-Down MS and Top-Down Proteomics? And which Tool is suitable for TD MS and TDP?

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Latest question

Anonymous 2

How do you normalize ???

Q&A

Popular 8

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Anonymous 0

Can you please specify the difference between Top-Down MS and Top-Down Proteomics? And which Tool is suitable for TD MS and TDP?

Anonymous 0

Can I quantitatively analyze proteins with and without glycosylation using intact or top down method?

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Latest question

Anonymous 2

How do you normalize ???

**Thank you for participating in this work**

**See you in the Top-Down Proteomics Workshop at ASMS 2026**