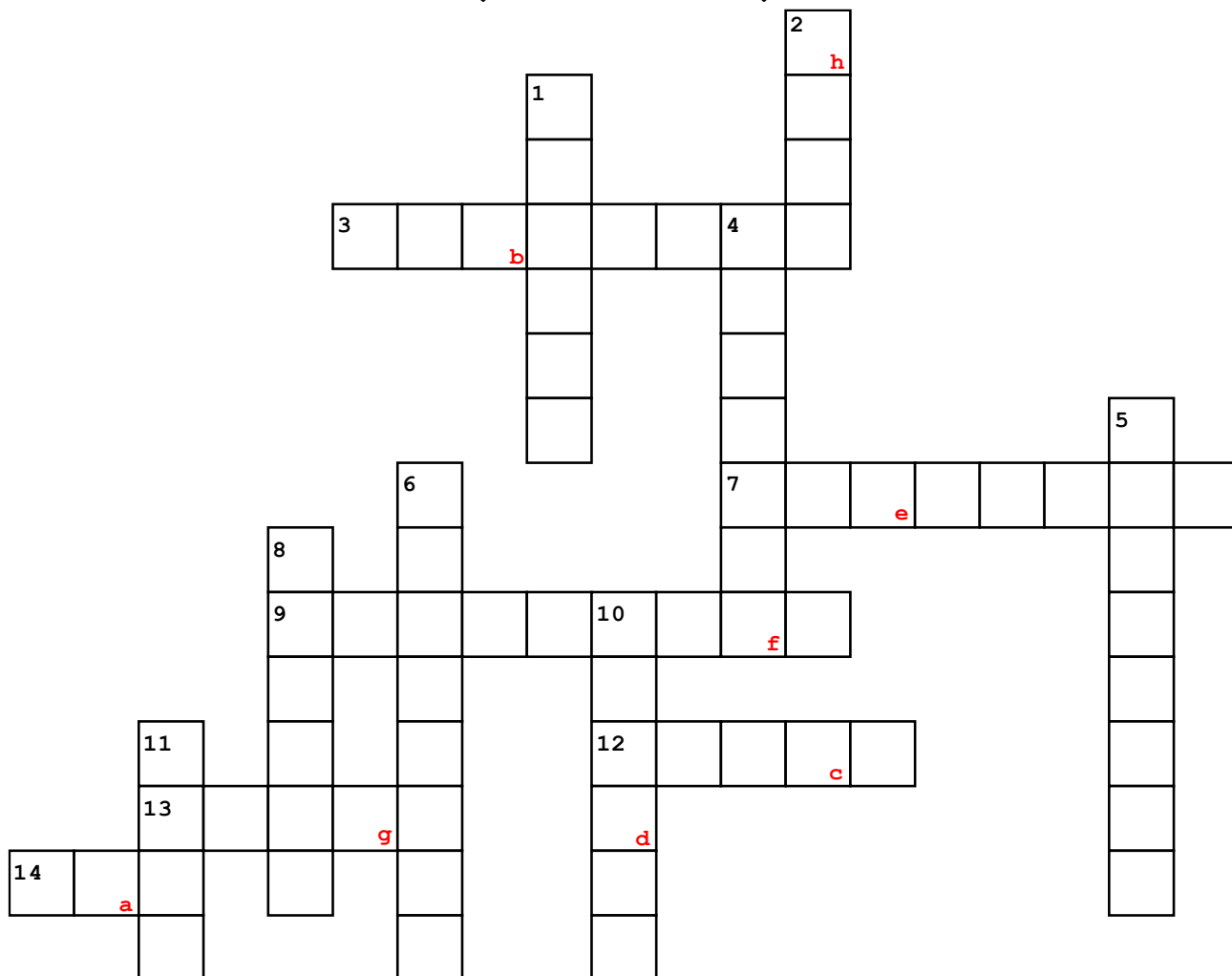


ProteoBench self-guided cross-worded tour (HUPO 2025)



Across

3. Which tool has the datapoint with the best performance in terms of quantification error for the DIA quantification module on diaPASEF data?

7. If a user wants to submit a custom tsv, which PSI standard needs to be used to denote the precursor?

9. The All-Ion-Fragmentation DIA benchmarking module was archived because of a problem with differential peptide ____ between the conditions

12. What species is not present in the ground-truth samples used for the single cell precursor ion benchmark module, that is present in all other three-species benchmark modules present in ProteoBench?

13. For DIA, FragPipe uses ____ as a quantification engine, therefore the input format to submit FragPipe results to the DIA benchmarking modules has the same format as what other software tool?

14. In the DDA Precursor Quantification module (QExactive), two clusters of MaxQuant points are evident. The difference between these two clusters is the enabling of ____ (acronym)

Down

1. Aided by the limited datapoints made public for this module, the module benchmarking DDA precursor ion quantification for Astral data is a prime showcase of how a higher number of quantified precursors will usually lead to a ____ quantification error.

2. Referring to clue 1, a datapoint coming from the software tool ____ falls outside of this almost perfect correlation

4. In April, GitHub user @MatthewThe proposed a module to benchmark the identification of ____ peptides in DDA

5. Currently only available on the DDA Precursor quantification module on QExactive data, an additional report with quality control statistics for submitted workflow results can be generated with ____

6. Which result file should be uploaded to submit a MaxQuant datapoint (ignore the extension) for the current LFQ benchmarking modules?

8. Which workflow, named after a cute animal, is the only tool publicly benchmarked in the DDA peptidome quantification module?

10. AlphaDIA version 1.____.1 shows a clear benchmarking improvement over previous versions in the Astral DIA Quantification module (write number in full)

11. Public submission of a QuantMS workflow result needs three parameter files to be uploaded to collect the required parameters. Two of these are required, whereas the third is optional. What metadata file is optional?

What appears when you successfully make a public ProteoBench submission?

a	b	c	d	e	f	g	h
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