Inquiry-based Learning of Proteomics and Metabolomics

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ABSTRACT: Given the rapid development of data-driven experimental procedures within the life sciences, it is important to equip students with proper skills and knowledge on how to obtain and interpret complex data. While laboratory exercises have for a long time been well established as a teaching method for life sciences, we consider there is room for improvement in how laboratory exercises are conducted. Hence, we designed a laboratory exercise course in which students at the graduate level in the European education system (M.Sc.) are challenged to pose their own biological question and write their own laboratory protocol for a proteomic study to investigate their hypothesis. Here, students are supported in their task with lectures and seminars that take them through the required details on experimental sample preparation, analysis with LC–MS, and proteomic data evaluation of biological function and relevance. According to student interviews, the inquiry-based learning concept we used here provided a deeper understanding of the laboratory protocols they wrote, according to which they eventually performed their own experiments.

KEYWORDS: Analytical chemistry, Molecular biology, Mass spectrometry, Proteins/Peptides, Multidisciplinary, Laboratory instruction, Graduate education, Inquiry-based learning, Hands-on learning

INTRODUCTION

Many courses in chemistry use laboratory exercises to strengthen the learning process of the students. Given its costly hourly rate compared to a lecture, this activity sometimes comes under siege due to decreasing teaching budgets. However, laboratory exercises are still regarded as a tool of the trade, encompassing the craftsmanship that every chemist in training should learn. Hence, teaching based on laboratory exercises is tentatively the ultimate student-active learning method and has even found its way into teaching humanities and social science. Why are laboratory exercises useful? According to John Dewey, “doing is learning”—yet, Dewey also stressed experience, that involves both doing and undergoing.1,2 Hence, learning is not limited to the reception of data, in turn, compared to theoretical conceptual constructs. Further, undergoing, i.e., the transformation of experiences (learning) requires doing (action). Ultimately, this stresses an interactional and situational view of meaning.3 Here, we provide an approach for teaching proteomics at the level of a European Master’s degree program, based on Dewey’s learning-by-doing philosophy. We also utilize the concept of Wickman’s practical epistemologies analysis,4 where meaning-making is analyzed by dividing a learning event into “stand fast”, “encounter”, “relation”, and “gap”. We decided to design a course where the gap-filling events according to Wickman’s practical epistemology are shuffled, compared to the traditional lecture-then-lab-session course. The design of laboratory exercises in the educational system is usually streamlined and focused on showing a physical or chemical phenomenon, and it often includes proof-of-concept experiments. However, an inability to associate the laboratory exercise with real-life applications promotes a “get it over with” attitude. Therefore, the advantages of more advanced and student-active laboratory exercises are regarded not only to provide a broader learning outcome but also to increase the student’s motivation to actively participate in the learning process. Hence, we consider an inquiry-based learning strategy to be useful for teaching proteomics, in particular, if the goal with the laboratory exercise is not only for the students to understand the importance of theoretical knowledge but also to understand how this knowledge and practical use fits into a wider, real-life context.

The laboratory exercise as a teaching method can even in its traditional meaning fall into the categories of inquiry-based learning and student-active participation. However, certain pitfalls do exist. While the traditional laboratory exercise is a method considered useful for teaching chemistry, students often raise the issue of mismatches between content covered in lectures and the work done in laboratory exercises. It is not uncommon that laboratory exercises will have to take place...
before the material has been covered in lectures due to logistic reasons when the class has, for example, over 100 students enrolled. Further, some students are prone to consider laboratory exercises just another checkbox to tick among the mandatory requirements in the class along the journey to the final destination: the written final examination. With this in mind, a possible survival strategy to pass the class with minimal effort is to focus as much as possible on the final examination, while laboratory exercises can be tackled simply by following the "recipe" and the horde of fellow students during the exercise. This phenomenon has been referred to as "cookbook-style" laboratory exercises,\(^4\) where much focus is spent in the laboratory to get the right output, but the understanding of "who" and "what" often must stand back for the "how". As such, a knowledge gap arises during a laboratory exercise when students miss connecting how they are conducting the experiment according to the instruction protocol with the reasons for why these steps are there in the first place. Hence, while laboratory exercises are often well intended and provide students with critical practical skills, the message is easily lost in translation. This observation sheds light on a problem not motivated by the students design their own laboratory protocols.\(^5\) These notions have been previously observed, and strategies to make laboratory exercises more student-active to facilitate learning have been made, most importantly by letting the students design their own laboratory protocols.\(^4,12\)

To circumvent the disconnect between material covered in lectures and laboratory exercises, we decided to create a problem-solving-oriented course to teach mass-spectrometry-based proteomics at the advanced level (European Master’s program level) at Uppsala University. The goal of the course was for the students to learn advanced mass spectrometry (MS) and separation techniques used for proteomic and metabolomics analysis. Here, we describe this inquiry-based laboratory course that we designed, where emphasis has been placed on training students to conduct a project similar to bottom-up proteomics studies actually conducted in research laboratories. We also describe the demonstration module that we created to showcase mass spectrometry imaging (MSI). Lectures and seminars were planned along the course to provide the students with important skills and knowledge so that they could plan and accordingly conduct their research study.

Proteomics is the subject of studying the protein content and abundance in a biological specimen, derived from genomics that considers the expression of genes. In detail, the proteome may be assessed by extraction of proteins from tissues, followed by a bottom-up approach where proteins are digested into smaller peptides and, in turn, separated with liquid chromatography (LC) and identified through computational matching of fragments obtained with MS. In contrast to the bottom-up approach, a top-down method does not rely on protein digestion, but rather the intact proteins are fragmented by MS alone. Bottom-up proteomic studies have become important in translational drug research to assess effects of drug treatments but also to identify biomarkers associated with certain diseases. Searching for biomarkers used to be a targeted approach using molecular biology methods. However, development during the past two decades has placed LC−MS as the gold standard for proteomics; this technology provides an opportunity for untargeted, data-driven research.\(^13−15\) Even though proteomics is a constantly developing field, it has become a routine procedure in biological sample analysis, not only for research purposes but also for quality control. Recent studies have addressed the lack of teaching proteomics and have facilitated coursework to fill this gap.\(^16,19\) This interdisciplinary field, combining molecular biology with analytical chemistry and bioinformatics, may seem challenging to teach at the grade level. Yet, we consider that the skill-set of chemists or other majors related to life sciences should envelop emerging technologies into their education, either to prepare them well for graduate studies or for careers in industry.
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basis for examination:
In the course curriculum at Uppsala University, the course
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Figure 2.
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understanding of proteomics within a 5-week time frame,
order to provide the students with comprehensive skills and
strategies and processes of proteomics experimental design. In
students per year.
and the course has run since 2023 with enrollment of
Master’s program in Biopharmaceuticals at Uppsala University,
2023, the course became mandatory within the two-year
groups consisting of 3
lectures (Figure 1). The laboratory project was typically done in
the main project task during the first seminar at the beginning of
students were prepared to compose the laboratory protocol.
They were assigned with drafting the protocol and were given
assistance during seminars to ensure that their chosen methods
match available equipment. Next, the students conducted the
study. Thereafter, a lecture was given on data analysis, followed
by a seminar where the students are led through an R-script for
data analysis. Here, the students were able to analyze their data
for up- and downregulation with the R-package limma. Further,
this seminar also showed how pathway analysis is done with
online databases such as Panther and the Reactome. After the
data analysis, the students wrote a project report that described
the method they used and a short interpretation of the biological
findings obtained with the pathway analysis. Next, the students
presented their results during a final seminar at the end of the
course. Here, other student groups asked questions of the
presenting group. Later in the course, after the proteomics
module but before the final written exam, a demonstration
laboratory exercise was used for the instruction of MSI, where a
short paper written individually by the students was used for
assessment.

■ LEARNING OBJECTIVES
In the course curriculum at Uppsala University, the course
“Proteomics for drug design” has the following objectives as
basis for examination:
- Identify, explain, and motivate the use of mass
spectrometry as a tool for development of biological
drugs in preclinical and clinical phase.
- Identify, explain, and motivate the choice of analytical
separation techniques coupled to mass spectrometry as a
function of sample type.
- Design strategies for identification of target proteins and
lead compounds for drug development with proteomics
methods.
- Use basic sample preparation and analysis techniques for
proteomics studies.
- Apply bioinformatics methods for analysis of qualitative
and quantitative data from proteomics studies and
account for background, methods, and results in a
scientific report.

■ COURSE STRUCTURE, CONTENT, AND
IMPLEMENTATION
This is a new course that we designed to focus on experimental
laboratory skills for proteomics and had 2–6 students per class
in the first years the course was running, starting in 2020. In
2023, the course became mandatory within the two-year
Master’s program in Biopharmaceuticals at Uppsala University,
and the course has run since 2023 with enrollment of ~30
students per year.
Our main goal of the course was to show students the
strategies and processes of proteomics experimental design. In
order to provide the students with comprehensive skills and
understanding of proteomics within a 5-week time frame,
laboratory exercises were integrated well with guidance from
lectures (Figure 1). The laboratory project was typically done in
groups consisting of 3–4 students. Students were introduced to
the main project task during the first seminar at the beginning of
the course. As the course progressed, each lecture assisted the
students in planning different steps of the experimental protocol.
Here, lectures focused on each step in a proteomics workflow
guide the students with detailed explanations of sample
preparation, LC, MS, and data analysis. While the seminars
and laboratory exercises were mandatory, the lectures were not.
However, we noted that most students would attend the lectures
equally well as the mandatory sessions. The bottom-up
proteomics workflows taught include examples of the most
common steps in a proteomics experiment. After the first set of
lectures that cover sample preparation and LC and MS, the
students were prepared to compose the laboratory protocol.

Task
Students were asked to plan and perform a study of how a
particular drug affects the proteome of a specific cell line. The
students got a list of available drugs from which they could
choose for treatment of cultured cells. The students were then
given an opportunity to evaluate the feasibility of the experiment
and hypothesize about the tentative result at the stage of task
formulation. Their options were to treat a HEK 293 cell line
overexpressing a melanocortin receptor with one of the
following molecules: DMSO, ACTH, α-MSH, or γ-MSH.
Lectures were aiming to step-by-step provide the students
with concepts and knowledge that are critical for the
experimental planning. Figure 2 shows a schematic overview
of the laboratory exercise workflow.
We consider that this approach allowed the students to
practically implement the gained theoretical knowledge. There-
fore, every lecture was well anchored in the process of designing
the experimental protocol. Even though the students eventually
chose the most suitable method, they had to critically evaluate all
methods discussed in the lectures. During the first weeks of
lectures, the students could directly apply their knowledge to
write and submit a draft of the experimental protocol to the
teaching assistant, who provided feedback on it. Further, for the
seminars of the course where the protocol is discussed, the
students were given four articles to read. These articles and the
seminars guide the students toward techniques that are feasible
to use within our laboratory. Additionally, the students were
informed of what type of mass spectrometer is available, so they
were not able to choose to conduct experiments on
instrumentation that we do not have. In summary, the role of
the teaching assistant in this step of the seminars was to point out
any changes that are necessary to make the protocol compatible with available materials and equipment.

Briefly, the bottom-up laboratory exercise included the following parts: working with a cell line and introducing the treatment, protein digestion and enrichment, nanoLC−MS analysis, and data analysis. A detailed description is given below.

Biological Sample Preparation

The first step in a bottom-up proteomics workflow is to obtain biological samples and maximize the output in terms of qualitative and quantitative information. In the bottom-up proteomics experiment, we introduced students to work with cell lines. This first part of the laboratory exercise was held in parallel with lectures about types of biological samples, the 3Rs (reduction, refinement, replacement), aseptic techniques, and planning the amounts of biological material needed for the study. Further, in order to successfully analyze the samples, the students were taught to plan for sufficient amounts of biological material, have a low risk of sample contamination, estimate the sample to sample variation, assess the sample complexity, and use mass spectrometry-compatible chemicals.

Various sample preparation methods exist, where the choice is based on the aim of the study, type of sample, and sample amount (essentially to ensure the sample concentration is higher than the limit of detection); in our course, we emphasized methods suitable for bottom-up proteomics using mass spectrometry analysis. Biological sample collection, in our case treated and nontreated cells, was followed by mild lysis and sample cleanup, concentration, and enzyme digestion. Filter aided sample preparation (FASP) is a procedure where the sample is washed and digested on a molecular weight cutoff filter; it is a routinely used method in our laboratory which gives the most informative results in combination with our nanoLC system (nanoACQUITY, Waters). Students were guided to use this method as their sample preparation, based on provided literature and lectures. They had to plan the following steps: cell lysis, sample cleanup, protein reduction, and alkylation and digestion of the material on the filter; see Figure 2.

The goal of these preparation steps was to end up with concentrated tryptic digest of their sample. A Bradford assay was used to measure the protein concentration after the lysis step.

LC−MS

After achieving an understanding of biological sample preparation, the students next need to be prepared for instrumental methods. The students have, in previous lectures, been introduced to protein separation. However, in this part of the course, the lectures covered separation techniques, with a focus on LC−MS. We took into account that the students did not have any practical experience with MS. Hence, MS was thoroughly explained: from general principles and types of instruments to different acquisition methods and strategies. In the experimental protocol, the students had to define the conditions for separation with LC and parameters for the MS-acquisition method. This was an untargeted, exploratory study, so data-independent acquisition (DIA) was employed, where all ions are fragmented in the MS/MS stage. Students were also introduced to MassLynx software (instrumental settings; to make the students aware of the system conditions) and the instrumentation setup.

Data Analysis

Hereafter, the students were taught how database searching with protein identification and quantitation for bottom-up samples is conducted. Unfortunately, search software is quite specific for each vendor, and it is hard to provide full coverage. However, we conveyed the analysis parameters that influence the trustworthiness of the result such as false discovery rates and multiple test correction. Such advanced data analysis requires at least basic programming skills. For this reason, our students were asked to complete a beginner level course, “Learn R” on the Codecademy platform (www.codecademy.com). This is a voluntary module that we do not assess in the course. The students are not expected to write their own code in this course; rather, they are provided with a working R-script that is covered line by line in a seminar. However, the student groups are typically very heterogeneous, in terms of programming knowl-
edge. Hence, to facilitate a better understanding of the data analysis script in the data analysis seminar, we recommend those students who are not so familiar with R to go through this self-learning module.

Biological Interpretation
Finally, the students explored and interacted with the generated data using the web-based interface of the Reactome (www.reactome.org). Here, the students uploaded their data set with log-transformed relative protein abundance and assessed the tentative enrichment of biological pathways. Using the Reactome can provide the student directly with detailed information about the proteins involved in specific pathways while also providing a holistic overview of the complex mesh of reactions encompassed within a biological sample. The Reactome web-interface allows for both Over Representation Analysis (ORA) and Gene Set Enrichment Analysis (GSEA) that the students could explore their data with (Figure 3).

Contingency Plan
If any experiments failed for a student group, we let the students use data from another group or similar proteomics data that we had available. This allowed the students to learn about data analysis, even if their experiments did not work.

■ METABOLOMICS MODULE
Next, toward the end of our course when the proteomics module is completed but before the final written exam, we also incorporated a module to teach MSI that lasts for 2 days. The first day includes a 4 h lecture which covers the basics and connects the module with the previously taught topics, especially MS. The second day is a full day of computational work mainly performed by the students. MSI is a technique used to directly map a wide range of molecules such as lipids, neurotransmitters, amino acids, and metabolic intermediates. MSI has recently emerged as a valuable technique in drug design and development owing to its potential to provide localization information with relatively high lateral resolution (μm level). Although the applicability of the technique in untargeted proteomics is somewhat limited at the moment, MSI offers a great capacity for metabolomics and lipidomics studies. Therefore, we found it beneficial for the students to get acquainted with an alternative application of MS and its capabilities and limitations. In turn, this module was expected to enhance their understanding of the technique in general and its applicability in real-life scientific questions.

The design and implementation of the module was based on the didactic triangle (the “who”: students and teacher; the “what”: the subject; the “how”: the teaching methods) and the constructive alignment between the intended learning outcomes, the teaching and learning activities and the assessment (Figure 4). The teaching and learning activities as well as the assessment approaches were selected to be aligned with the intended learning outcomes. A constructivism approach focusing on research-based and research-tutored teaching was considered to be the direction of choice. Constructive teaching aims at engaging the students in a deeper learning approach by presenting the new knowledge in association with what the students already know. That way, the students “build up” knowledge and skills and benefit for their whole studies. This approach required the teacher to provide time for the students to acquire and process knowledge, cooperate in groups, and formulate their ideas. It also required the instructor to evaluate what is important for deep understanding of the material. Inquiry-based teaching, allowing the students to be participants in research, has also been shown to improve understanding, especially in pharmaceutical studies. Formative assessment in the form of small regular assignments in the classroom improve students’ perceptions of the topic. A harmonious combination of lecture (research-led approach) with laboratory exercises (research-oriented and research-based approach)
appeared as a challenge for the teaching of this module. The existing lab premises specialized for this technique cannot accommodate this number of students simultaneously. Therefore, a fused approach was followed, with virtual lab, class assessment techniques and group work. During Day 1 of the MSI module, a traditional lecture was mixed with videos, group work, and small exercises. In the beginning of the lecture, the students were asked to help the instructor draw a mass spectrum on the blackboard based on what they had already learned during the course. This way, the students understood the connection between the metabolomics module and what they had already learned in the previous proteomics module, which enabled the comprehension of novel concepts that were presented later. Day 1 was divided into a theoretical part, i.e., explaining the technique (research-led) and into a second part where specific applications (published original articles) were discussed, focusing on MSI applications in neuropeptide research. Between the two parts, the students were asked to work in groups or individually (free choice) to complete a small exercise within 5 min. That way, the teacher evaluated whether the fundamental concept behind the technique was clear.

In the beginning of Day 2, the teacher asked the students to discuss in groups or think by themselves and come up with words that had the most impact on them from Day 1. The students were given two min, and after that the teacher wrote the words on a word document, presented to all on the classroom projector, in the order of mentioning. The students and the teacher tried to make a story out of these words that could help someone outside the field to understand what the technique is about. With this approach, the students refreshed their memory, and the teacher evaluated what was perceived sufficiently and what needed further explanation. Next, the teacher was remotely connected to a processing computer located in the MSI lab and displayed MSI data analysis (commercially available software with a limited number of available licenses in the lab) on the classroom screen. When this demonstration was completed, the students, under the teacher’s instructions, used an online and freely available tool (metaboanalyst.ca) to analyze data extracted from the previous analysis. The students were asked to identify the neurotransmitters/metabolites and the brain regions affected significantly by two independent factors; age and drug administration. This was done with guidance from the teacher, leading the students through this task. For this teaching activity, a published MSI study was used, where a derivatization approach was applied to increase the sensitivity toward catecholamines and other biogenic amines, poorly ionized with conventional MSI. As an assignment to assess the learning outcome, the students were asked to answer a few questions related to the metabolomics module.

### EVALUATION OF STUDENT RESPONSES

During the first and last session of the course, questionnaires were conducted using the Mentimeter web application (www.mentimeter.com) to gather information on student self-assessment of knowledge in the course topics, and preferences in teaching styles. Students responded at the beginning (n = 22) and the end of the course (n = 30) to the question “I know a lot about...” and then individually graded the keywords “Aseptic techniques”, “Cell culture”, “Chromatography”, “Mass spectrometry”, “Programming”, and “Proteomics” with scores 1–5, where a higher number indicated a stronger knowledge. Similarly, the students responded to the question “Do you learn better with...?” and then individually graded the alternatives “Demo experiments”, “Hands on practice”, “Recording of lab instruction videos” with scores 1–5, where a higher number indicated a stronger preference. The histograms are normalized within each group by their total population count and show the fraction of respondents to each score (1–5). A Student self-assessment of knowledgeability within key concepts related to the course outline. B Student self-assessment of various instruction methods for learning chemical methods. C Student self-assessment of expected learning outcome for handed out lab protocols compared to writing it themselves.
“Recorded lab instruction videos”, and also the alternatives “Handed out lab protocols” and “Writing your own lab manual”. Figure 5 shows the student self-assessment of learning outcome, where the distribution of most answers shows a trend to shift to the right. This reflects an increase of knowledge in most of fields, in particular for proteomics. From the teacher’s perspective, results from the evaluation of submitted laboratory reports and the written exam in the course support this level of learning outcomes, where in the final written exam 14 students passed with distinction, 13 students passed, and 5 students failed (the Swedish Higher Education System only has three grades: fail, pass, pass with distinction). We want to emphasize that in the Swedish Higher Education System, only individual assessments are allowed to be used to set grades. Hence, the group work on protocol preparations and final reports and presentations are only marked pass/fail and must be completed to obtained a final grade. The scores given by student self-assessment on effectiveness and motivation induced by various teaching methods showed that to write their own laboratory protocol and conducting the experiments hands-on was regarded as valuable to the students, observed in the histogram of “Handed out lab protocols” and “Writing your own lab manual”. In contrast, demonstration experiments were considered to not be as instructive. Further, “hands on practice” was regarded as the most instructive method of learning by the students.

The written course evaluation that was conducted in addition to the onsite clicker rating with Mentimeter, showed that the course promoted student-active learning; it was evaluated as an important part of the course, which made the subject more comprehensible. In particular, designing their own laboratory protocol was considered helpful for achieving the learning objectives.

“Getting this type of hands-on experience is very unusual, please keep this format for the course, I am very positive about it.”

“It was useful for us to write our own protocols.”

“I liked that we saw the MS in person and worked with it.”

“Writing my own lab manual helped me learn better about the process and the reasons behind every step, keep this!”

Suggestions on improvements are also given:

“We need more explanations and seminars to discuss about the tools and methods like R, reactome, panther...”

### Discussion

It is challenging to cover a constantly developing field such as proteomics for students. In the case of more static subjects, such as general chemistry or thermodynamics, the teaching program can be well-defined, where most often laboratory exercises are built on providing an already made protocol to the students showing straightforward experiments. Therefore, these particular laboratory exercises are focused on obtaining measurements to get a result, plotting the graphs, and writing a report. However, while this provides the students with a fixed set of skills, the ability to perform or design similar experiments is not necessarily achieved. Since our course concept provides a skill set of planning experimental work in general, the students are better prepared for learning a developing field, which also can be applicable in other courses.

Adaptive experimental design is a critical skill set for proteomics, which is a research subject that is still rapidly changing. Therefore, teaching strategies invoking student-active learning should focus on teaching students to remain current with the progress of the area. In particular, they should become aware of the need to adapt their methodological reasoning in accordance with rapidly emerging technologies. Furthermore, we regard the student-active participation with protocol preparation as immensely important for the purpose of strengthening experimental planning skills. As an example, with a prepared protocol, the students would be told to conduct solid phase extraction using a C18 resin to prepare a sample for mass spectrometry analysis. In contrast, if the students are tasked with preparing their own laboratory protocol and instructed that sample cleanup must be performed prior to analysis with mass spectrometry, the students would learn that there is a wide variety of resins available for this process. Hence, the students will have achieved a deeper understanding of the reason for each step and will be better equipped to design future experiments by themselves.

Introducing students to the large project in the beginning of the course can be overwhelming, but balancing the homework and supervision helps to facilitate efficient learning. This way, each explained concept from a lecture falls into the place of project progression. Further, designing a protocol under teacher supervision provides a dialogue during which the student may obtain further feedback and maintain subject focus. Hence, the course plan was based on students’ previous knowledge in the proteomics field and the need to facilitate their successful completion of the course project. We factored in aspects of the pharmaceutical study program and its learning focus by making the project centered around molecules acting as drugs and their tentative effect on model cell lines and providing reiteration of basic concepts of separation and mass spectrometry.

With a multitude of omics and data-driven tools quickly expanding in the life sciences, it is important to equip students with the knowledge and usefulness of their capabilities. Sample preparation for proteomics analysis with LC−MS is not more complex than most other molecular biology projects. Compared to many laboratory exercises taught within general chemistry where, e.g., a handful of synthesized products are weighed and characterized for purity or the enthalpy of a reaction is estimated, the data generated from a proteomics experiment are vast and its interpretation complex. The curriculum is aimed at last-year students within the Master’s program in Biopharmaceuticals and pharmacists, and the level of teaching material could not be more apt. We note that this was the first time ever these fourth-year students were exposed to work with mammalian cell cultures and the associated aseptic techniques on laminar airflow benches.

While it is recognized that many institutions cannot afford to dedicate an LC−MS setup for graduate teaching, we emphasize that the outcome of the exercise should more consider the workflow and interpretation of the biological meaning the results provide, rather than turning the students into fully fledged mass spectrometrists (which would require far more time). Many measurements within omics are done in core facilities, and proteomics is no exception to this rule. Further, open access to proteomics data is available through the PRIDE repository (https://www.ebi.ac.uk/pride/). Hence, creating a curriculum solely focusing on proteomics data analysis is possible, even if teaching sample preparation and LC−MS analysis in the laboratory is not feasible.

Regarding the potential improvement of the course, handling large groups in the lab is a challenge. In the first iterations of the course (before it became a mandatory course in the Master’s program in Biopharmaceuticals) it was very easy having only up
to 6 students enrolled. The current number of 30 students is where we need to be at a minimum in terms of student enrollment to make the course economically feasible given the teacher time invested. However, expanding the student count beyond 30 would make the hands-on experience hard to follow through and necessitate cuts of lab time and losing the original idea of the course.

■ CONCLUSION

We consider that student-active participation is beneficial for the education process, in particular to align the understanding of the learning outcome of the course and laboratory exercises between teachers and students. Our course was designed with focus on the laboratory exercises with active student involvement in the teaching and learning process and was met with positive feedback from the students taking the class and appears to have facilitated a positive impact on learning proteomics.

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