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Summary of course evaluation for KEMM25 Structural Biochemistry HT 2021

Course responsible: Derek Logan

Other teachers: Ingemar André, Susanna Horsefield, Salam Al-Karadaghi, Kristofer Modig, Esko Oksanen (ESS), Ipsita Banerjee, Niels Meijer (course assistants), Maria Gourdon (LP3), Oskar Berntsson, Ana Gonzalez (MAX IV)

Number of students: 15, of whom one was a PhD student.

Grades: 1 student U, 6 students G, 8 students VG. Average grade: 63%.

Utvärdering

I. Summary of the course evaluation

Total no. of responses: 8 (53%)

Brief summary of the evaluation: The students who responded were in general very happy with the course. Suggestions for improvement were very constructive.

5/8 students said that the course fitted well with their study interests, and none replied that it was a bad fit. 7/8 said that the balance of course elements should be maintained but 2 said that we could have more labs. There was a wide spread in the time students said they spent on the course, but most spent between 30-40h per week.

The students appreciated that lectures recorded during the height of the coronavirus pandemic were still available to view. The site visits to the BioMAX beamline, the electron microscope at nCHREM and the crystallisation facility at Lund Protein Production Platform were, as usual, greatly appreciated.

II. Comments of the teaching team

We found the students this year to be enthusiastic and easy to maintain a dialogue with. They generally performed well in the exam and in the practical exercises.

III. Evaluation of changes since the last course

In 2020 an external expert lecturer was employed to teach cryoEM, with mixed success. DL took over the cryoEM module this year and tried to run it as a “flipped classroom”. The module was appreciated but we got the comment that



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the group discussions should have been more structured by giving the students tasks to encourage them to prepare more formally.

IV. Suggestions for changes to the next course

The course will be substantially restructured in preparation for autumn 2022, when it will have the new course code KEMM35. The material on homology modelling will be replaced with more up-to-date material on e.g. AlphaFold. We will as far as possible try to create “red threads” that run through the course and link together the different experimental and simulation methods presented. The cryoEM module will be extended further, possibly including a data processing tutorial. We will investigate how many of the computer-based tutorials can be run using resources at LUNARC.

2022-04-20, summary made by Derek Logan, course responsible.