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## Summary for KEMM15 HT 2017

**Course responsible:** Derek Logan

**Other teachers:** Ingemar André, Salam Al-Karadaghi, Susanna Horsefield, Kristofer Modig (Biophysical Chemistry), Esko Oksanen (ESS), Marjolein Thunnissen (MAX IV), Bo Svensson (SARomics Biostructures), Björn Walse (SARomics Biostructures)

**Number of students:** 11

**Results:** 2 U, 2 G, 7 VG.

### Evaluation

#### I. Summary of the evaluation

Total number of responses: 5 (43%)

*Short summary of the results:*

KEMM15 consists of two main parts, Structural Bioinformatics followed by Experimental Techniques. The main complaints were

- 1) a lack of structure or “thread” in the Structural Bioinformatics section
- 2) poorly-prepared course assistants in the Structural Bioinformatics section
- 3) the density of information in the experimental methods section

On the other hand, the students were generally satisfied with the Experimental Methods section, in particular with site visits to Lund Protein Production Facility and MAX IV. This is in line with all previous years.

The students also rated the quality of the course handouts lower than in previous years.

#### II. Teachers' comments

Despite repeated reminders to participate in the survey, and finally an e-mail sent out after the end of the course, only 5 replied (45%). This makes it rather difficult to draw any conclusions from the responses. On the whole, the students appear to be somewhat less satisfied than in previous years. This is in contrast to the impression I got of a positive group of students with engagement who enjoyed the course and generally did well in the



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examinations. The comments on quality of course handouts are difficult to understand, as they are essentially the same as in previous years. Both these points demonstrate the problems of interpreting satisfaction from a small number of responses, which may not be representative.

### **III. Suggestions for changes to the upcoming course**

We will make a particular effort to strengthen the Structural Bioinformatics section and to make sure that the course assistants are well-trained before the course. We will consider the relative lengths of each part of the course to maintain an even pace. The length of time between theoretical lectures and practicals in the experimental methods part may be increased so that the students have time to assimilate the information.

A further change to the schedule will be that the final week on Structural Biology in Drug Design will not be given by external guest lecturers, but rather by course teachers, which will hopefully result in an experience of greater continuity.

2018-08-30, summary prepared by Derek Logan



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## **Appendix: Some representative comments**

- The practicals were very useful but I didn't know what to do in some of the practicals in Structural Bioinformatics. Not enough instructions were given.
- Structural bioinformatics: Maybe give the course assistant at least some information on what we are doing.
- It was too early for me to start with the x-ray crystallography tutorials directly, I needed more time to understand it well enough to actually benefit from it.
- Maybe proof-read the compendium at least once before. [Comment: it has been proof-read many times, but one can always miss something.]
- All of the PDF's uploaded at liveatlund did have a very good quality overall.
- The first part could maybe somehow be compressed/given less time. Since the crystallography-part demands more of you and you would benefit to have more time for that part.
- Very good exam.
- I would've loved to see more on protein folding, as it is the topic that interests me the most, but it's a personal opinion and I considered it "about average" because I didn't see too many new things, but that's normal taking into account we are all different students from different studies.
- Structural bioinformatics: Did not get the connection between the lectures, what we did on the tutorials or the project until after everything was done. Complete absence of a red thread.
- I did not have enough background to grasp the x-ray crystallography during the lectures. Pieces did not fall into place until like 3 weeks after the lectures.
- The structure-based drug design lectures were very interesting but could maybe be excluded from the actual exam.

### What was best about the course?

- Seeing all the process of X-ray crystallography data processing, from scattering to structure, with tutorials was the absolutely best thing. Although it was tedious and tiring most of the times, it proved to be amazingly helpful to understand the whole thing better and made me even more interested in the technique.
- The practicals when everything from the theory started making sense
- X-ray crystallography
- I really appreciated the visit to MAX IV.
- Structural bioinformatics part



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What was unsatisfactory?

- The fact that most tutorials could only be done at the university computers. Wasn't especially unsatisfactory, but it was the worst thing if I had to choose something.
- Crystallography part