

Summary of text answers to KEMM15 evaluation HT2016

1. How much did you benefit from the lectures?

It was a good combination of several fields of research.

2. How much did you benefit from the practicals, demonstrations and site visits?

MAX IV and LP3 site visit were fascinating and fruitful to see.

3. What is your opinion about the course material (handouts, PDFs etc.)

"Neutrons" slides were not only focused on neutron scattering, but repeated the crystallization process.

4. For those of you who used the course book by Lattman and Loll, how useful did you find it?

Compact and easy to read.

Since the PDFs of the presentations didn't all contain the full story, the book was helpful when I didn't remember something, or sometimes the explanation in the book was useful to fully understand something.

5. How relevant for your education was the course content?

6. What is your overall impression of the course?

The two parts of the course were well coordinated.

8. How did you find the examination?

Written examination: It was more difficult than expected since we discussed old/possible questions before the exam that were easier.

Practical test: was as expected.

9. What was particularly satisfactory about the course?

It was a good starter's guide for crystallography.

Combination of lectures and exercises, also hands-on at protein crystallography and visit of MAX IV. Getting to know a lot of useful computer programs.

I liked that it was such a small group (which wasn't on purpose), since it made it very personal and the teachers were very approachable!

10. What was particularly unsatisfactory about the course?

Don't know.

That we could only use the cell phone to take pictures of the crystals from the cold room experiments, while the ones from the room temperature were taken with an integrated camera (microscope) and ruler.

Nothing.

A few lectures/lab exercises would have been ordered better in the schedule.

Too early the introduction to Coot and solved questions there!

11. How likely is it that you would recommend the course to a friend or fellow student?

It is a very useful course for anyone who is working with proteins. It shows a lot of tools scientists can use to help solving a problem.

12. Do you have any other comments or suggestions for improvement?

Change the timetable so that the first Coot tutorial is not in Salam's part.

No.

Different teaching approaches could be more interesting. For instance, exercises based on journal reading, problem-based learning could be good try.


No.

Follow-up plan

There were only 7 students on this year's course, an unusually low number. The reasons for this are unknown, but one of them is a general lack of students studying chemistry, in particular the protein science masters program. This we hope for an upswing in the coming years. On the other hand, the low number of students meant that we were able to give each one more attention, which was appreciated.

The response to the course evaluation was 4/7, or 57%. Thus it is appropriate to combine the responses with impressions from interactions with the students during the course. The course was generally appreciated, and the students were engaged and interactive. No major problems were identified apart from the timing of one of the tutorials. This tutorial will be moved to a later time in the schedule. A suggestion for more problem-based learning was made, which will be considered, in particular more use of journal articles. We will also look into better equipment for imaging of cold room crystallisation experiments, but for budget reasons we are unable to have the best cameras in both microscopes.

The student representative was given the opportunity to comment on the evaluation and to contribute to this follow-up plan, but did not take it.



Derek Logan
Course responsible

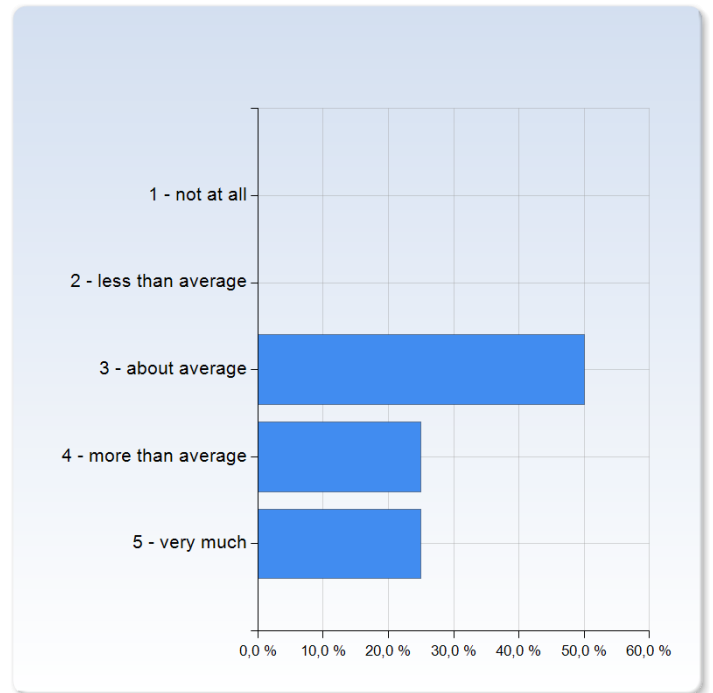
KEMM15, Structural bioinformatics 2016

Answer Count: 4

How much did you benefit from the lectures in

Structural bioinformatics

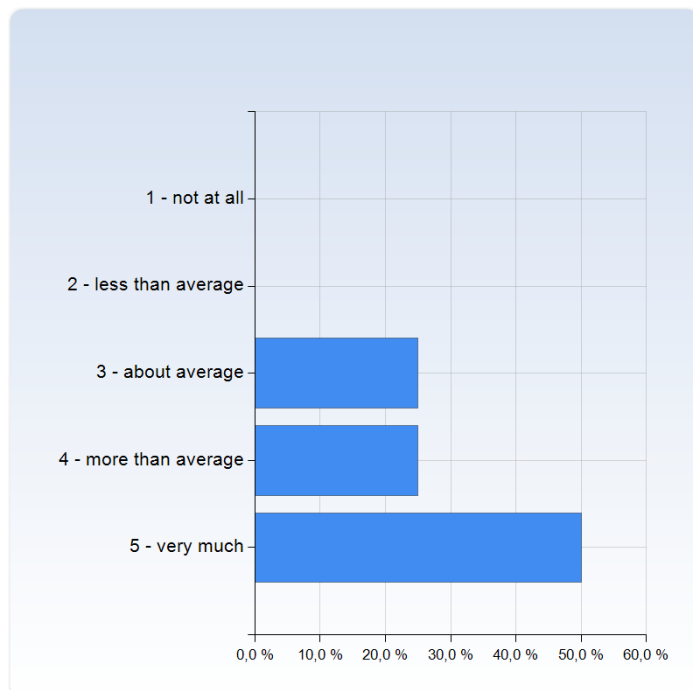
Structural bioinformatics	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	0 (0,0%)
3 - about average	2 (50,0%)
4 - more than average	1 (25,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Structural bioinformatics	3,8	1,0

X-ray crystallography

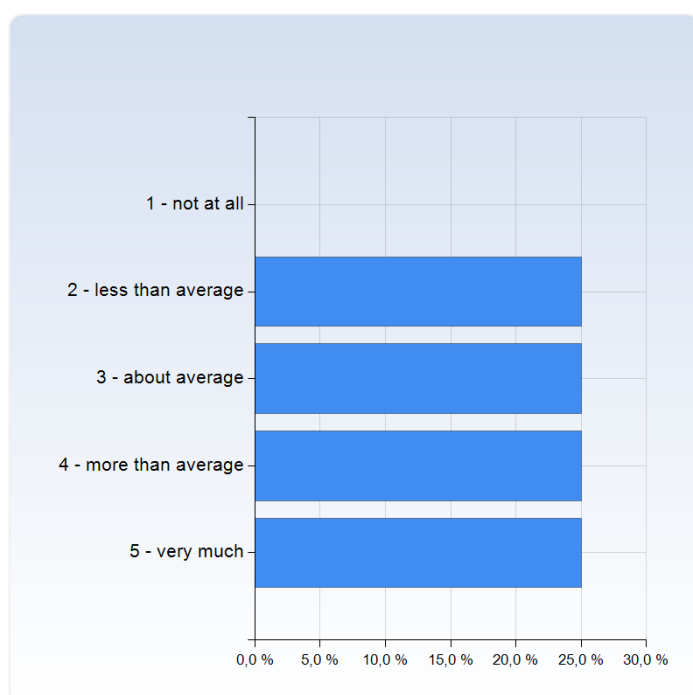
X-ray crystallography	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	0 (0,0%)
3 - about average	1 (25,0%)
4 - more than average	1 (25,0%)
5 - very much	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
X-ray crystallography	4,3	1,0

Protein folding

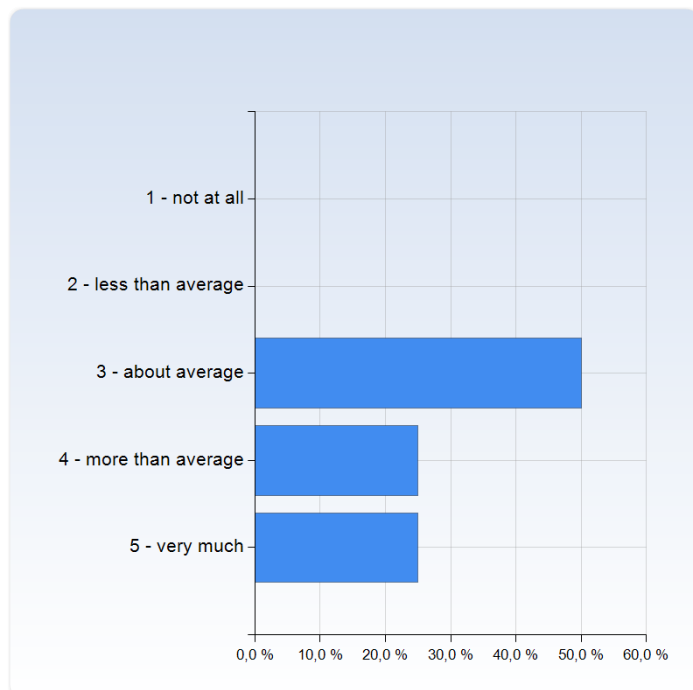
Protein folding	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	1 (25,0%)
4 - more than average	1 (25,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Protein folding	3,5	1,3

Other experimental methods (NMR, neutrons, SAXS)

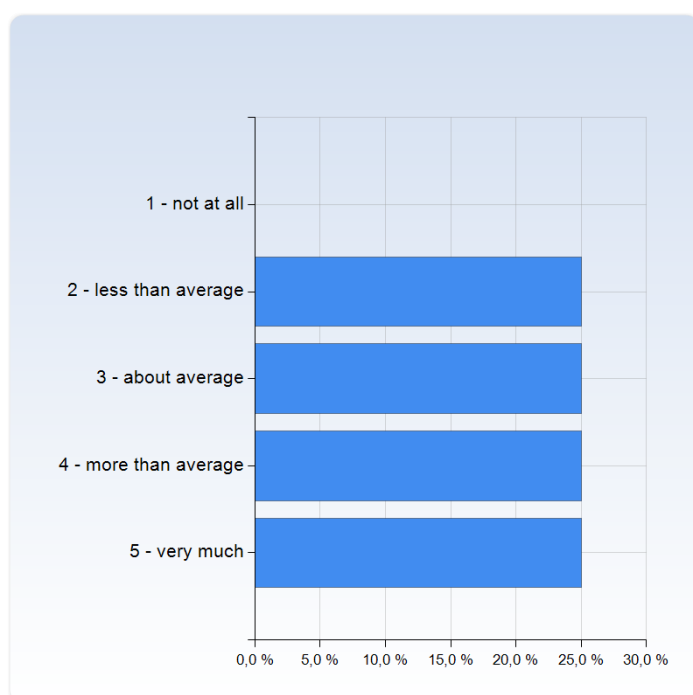
Other experimental methods (NMR, neutrons, SAXS)	Number of Responses
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5 - very much	1 (25,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Other experimental methods (NMR, neutrons, SAXS)	3,8	1,0

Structure-based drug design

Structure-based drug design	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	1 (25,0%)
4 - more than average	1 (25,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)

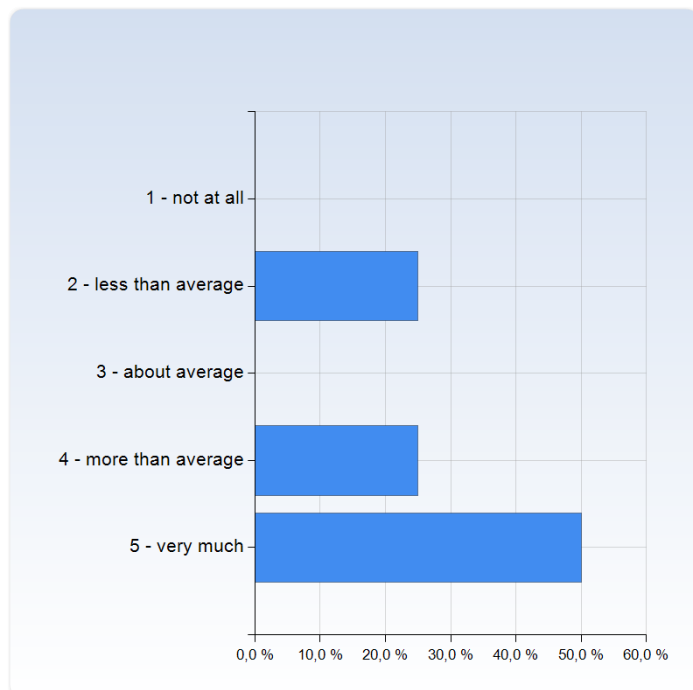


	Mean	Standard Deviation
Structure-based drug design	3,5	1,3

How much did you benefit from the practicals, demonstrations and site visits in

Structural bioinformatics

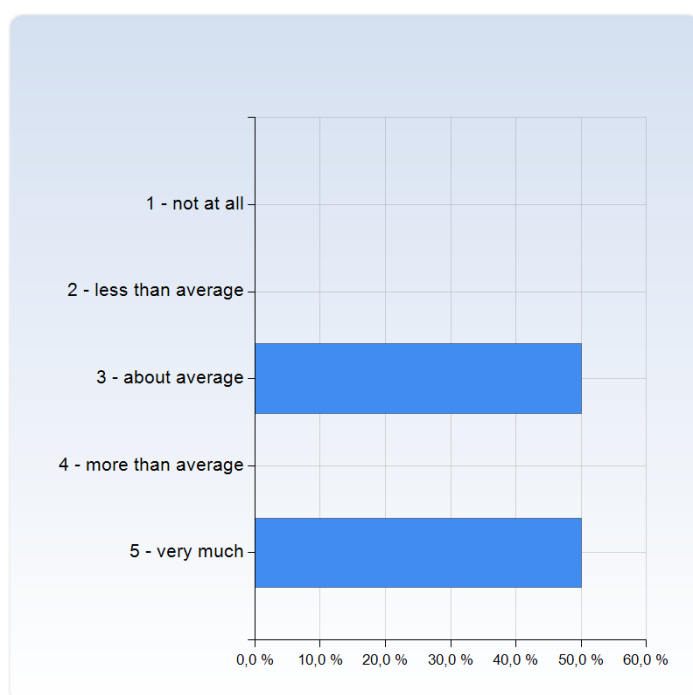
Structural bioinformatics	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	0 (0,0%)
4 - more than average	1 (25,0%)
5 - very much	2 (50,0%)
Total	4 (100,0%)



Structural bioinformatics	Mean	Standard Deviation
	4,0	1,4

X-ray crystallography

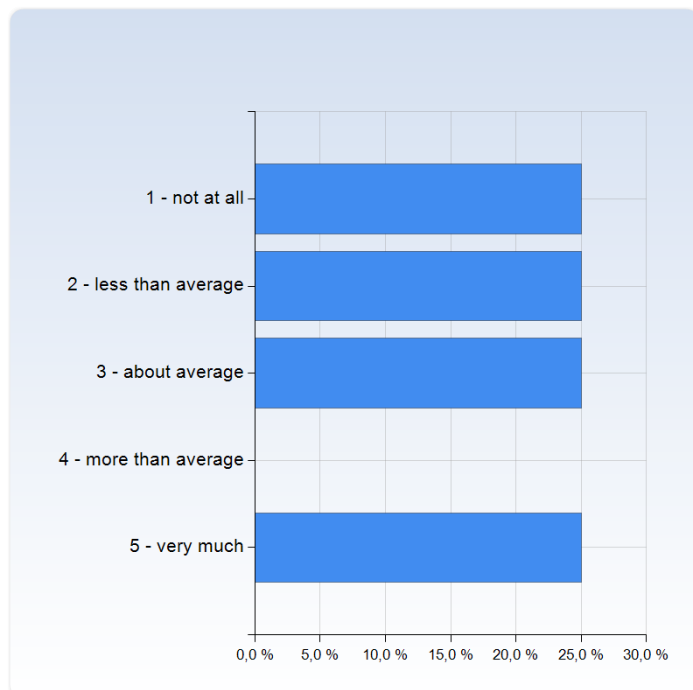
X-ray crystallography	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	0 (0,0%)
3 - about average	2 (50,0%)
4 - more than average	0 (0,0%)
5 - very much	2 (50,0%)
Total	4 (100,0%)



X-ray crystallography	Mean	Standard Deviation
	4,0	1,2

Protein folding

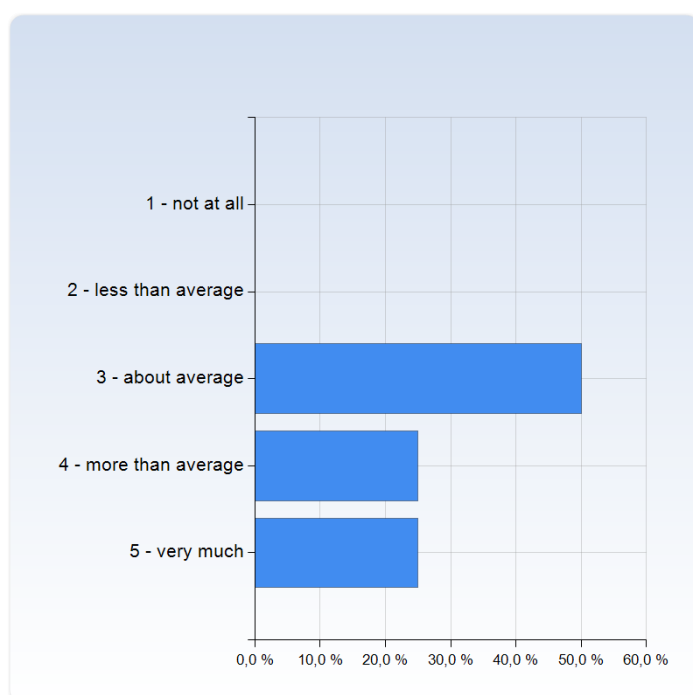
Protein folding	Number of Responses
1 - not at all	1 (25,0%)
2 - less than average	1 (25,0%)
3 - about average	1 (25,0%)
4 - more than average	0 (0,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Protein folding	2,8	1,7

MAX IV site visit

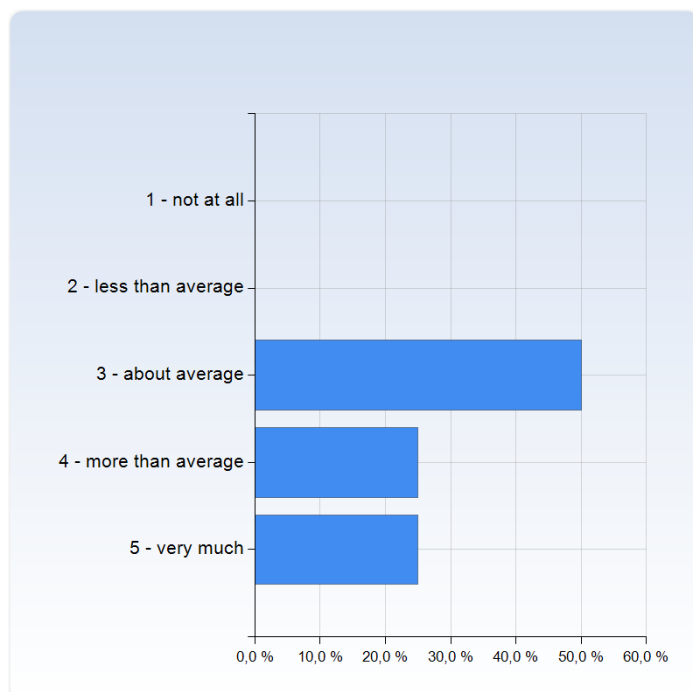
MAX IV site visit	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	0 (0,0%)
3 - about average	2 (50,0%)
4 - more than average	1 (25,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
MAX IV site visit	3,8	1,0

LP3 site visit

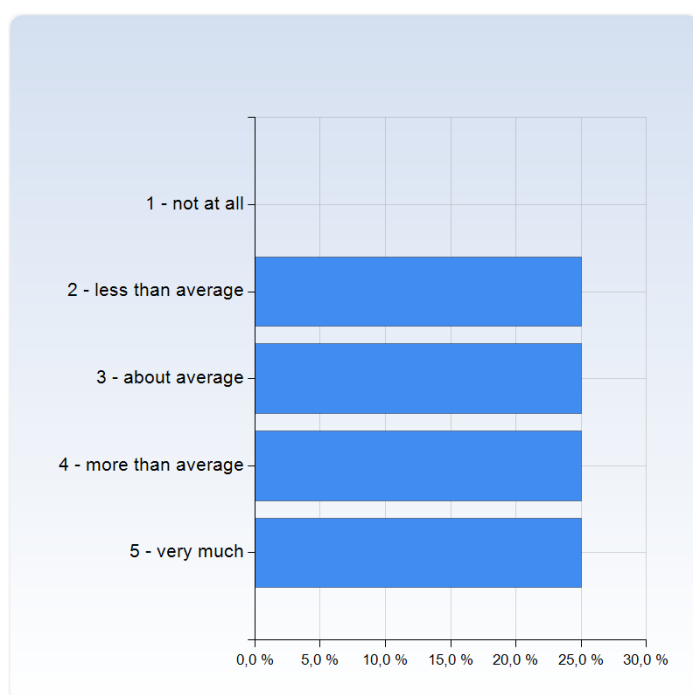
LP3 site visit	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	0 (0,0%)
3 - about average	2 (50,0%)
4 - more than average	1 (25,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
LP3 site visit	3,8	1,0

Structure-based drug design

Structure-based drug design	Number of Responses
1 - not at all	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	1 (25,0%)
4 - more than average	1 (25,0%)
5 - very much	1 (25,0%)
Total	4 (100,0%)

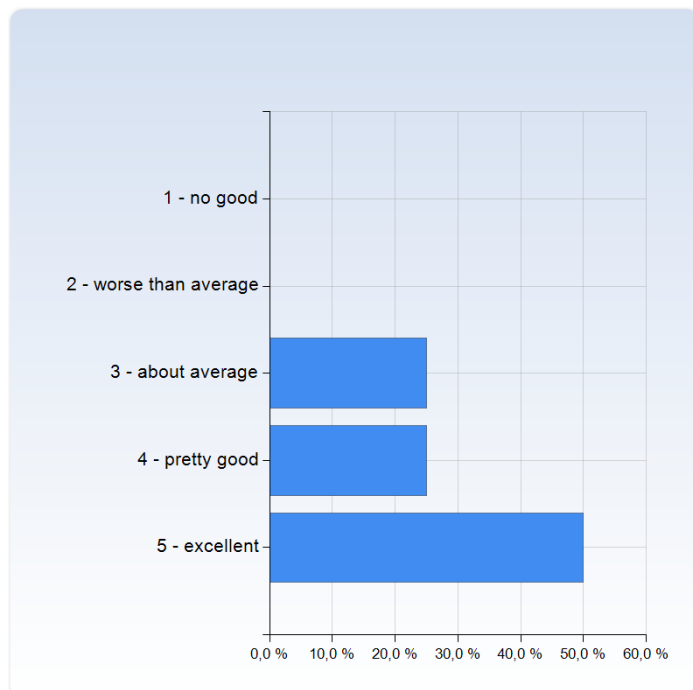


	Mean	Standard Deviation
Structure-based drug design	3,5	1,3

What is your opinion about the course material (handouts, PDFs etc.)

Structural bioinformatics

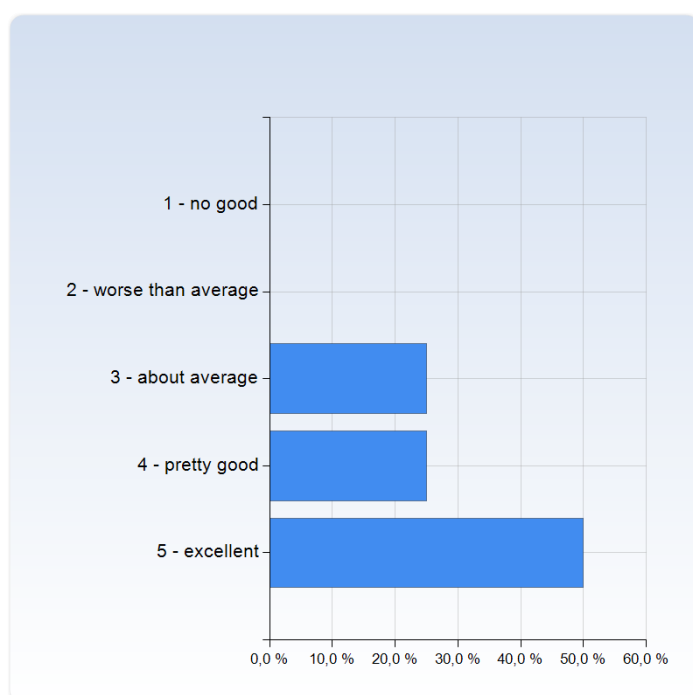
Structural bioinformatics	Number of Responses
1 - no good	0 (0,0%)
2 - worse than average	0 (0,0%)
3 - about average	1 (25,0%)
4 - pretty good	1 (25,0%)
5 - excellent	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Structural bioinformatics	4,3	1,0

X-ray crystallography & SAXS

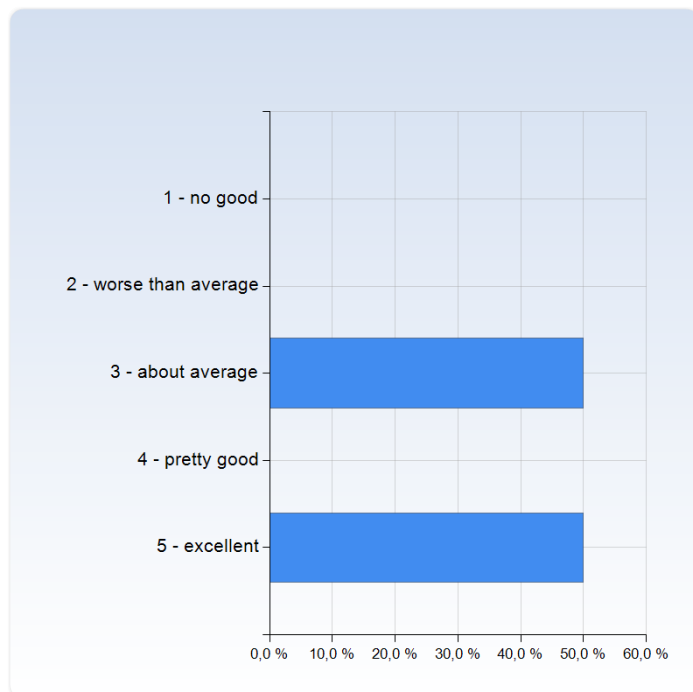
X-ray crystallography & SAXS	Number of Responses
1 - no good	0 (0,0%)
2 - worse than average	0 (0,0%)
3 - about average	1 (25,0%)
4 - pretty good	1 (25,0%)
5 - excellent	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
X-ray crystallography & SAXS	4,3	1,0

Protein folding

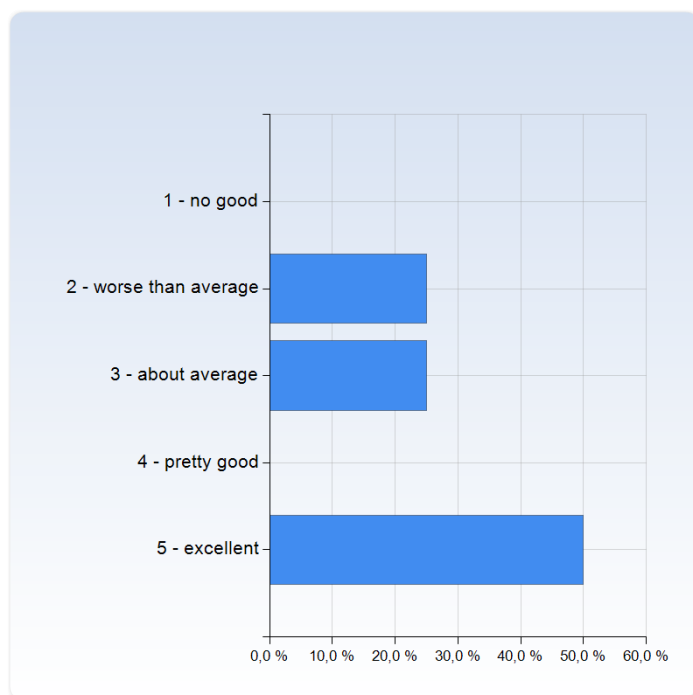
Protein folding	Number of Responses
1 - no good	0 (0,0%)
2 - worse than average	0 (0,0%)
3 - about average	2 (50,0%)
4 - pretty good	0 (0,0%)
5 - excellent	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Protein folding	4,0	1,2

NMR

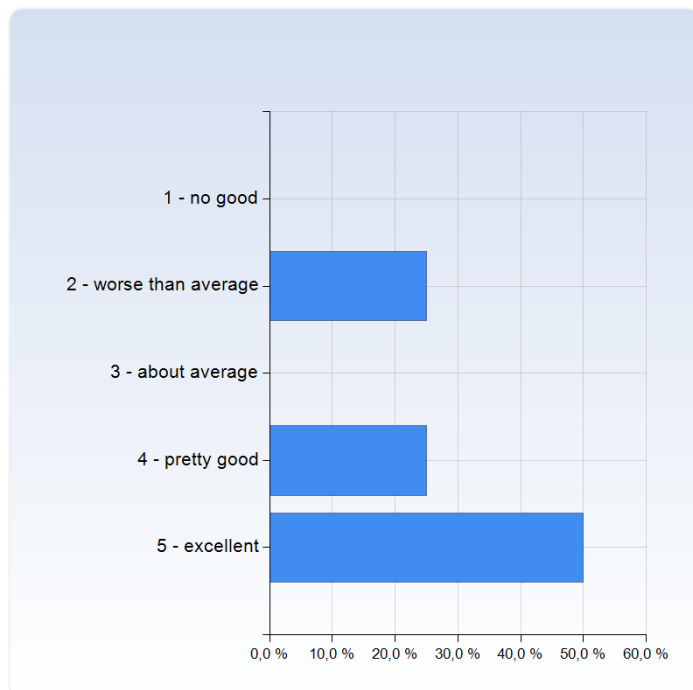
NMR	Number of Responses
1 - no good	0 (0,0%)
2 - worse than average	1 (25,0%)
3 - about average	1 (25,0%)
4 - pretty good	0 (0,0%)
5 - excellent	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
NMR	3,8	1,5

Neutrons

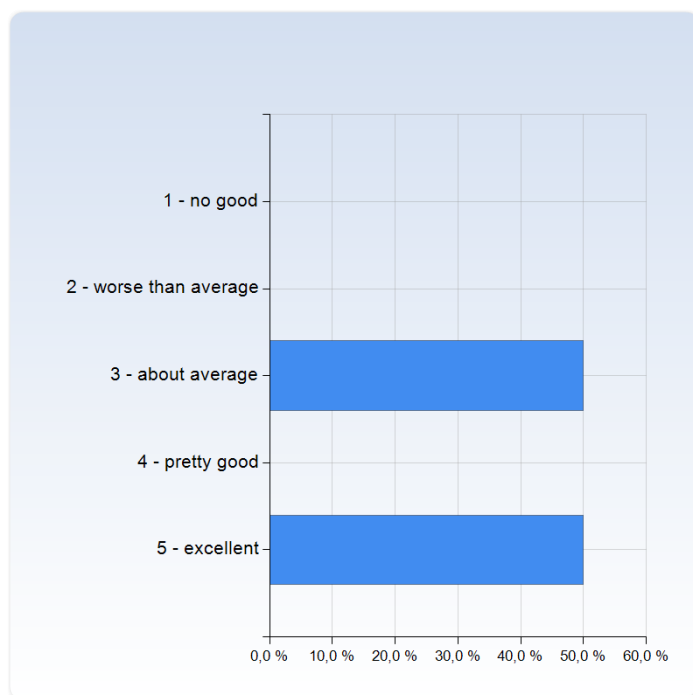
Neutrons	Number of Responses
1 - no good	0 (0,0%)
2 - worse than average	1 (25,0%)
3 - about average	0 (0,0%)
4 - pretty good	1 (25,0%)
5 - excellent	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Neutrons	4,0	1,4

Structure-based drug design

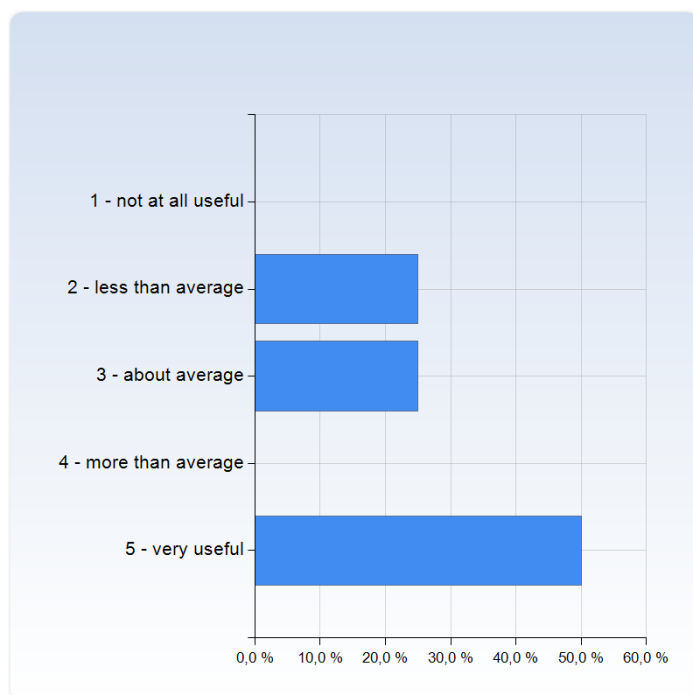
Structure-based drug design	Number of Responses
1 - no good	0 (0,0%)
2 - worse than average	0 (0,0%)
3 - about average	2 (50,0%)
4 - pretty good	0 (0,0%)
5 - excellent	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Structure-based drug design	4,0	1,2

For those of you who used the course book by Lattman and Loll, how useful did you find it?

For those of you who used the course book by Lattman and Loll, how useful did you find it?	Number of Responses
1 - not at all useful	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	1 (25,0%)
4 - more than average	0 (0,0%)
5 - very useful	2 (50,0%)
Total	4 (100,0%)

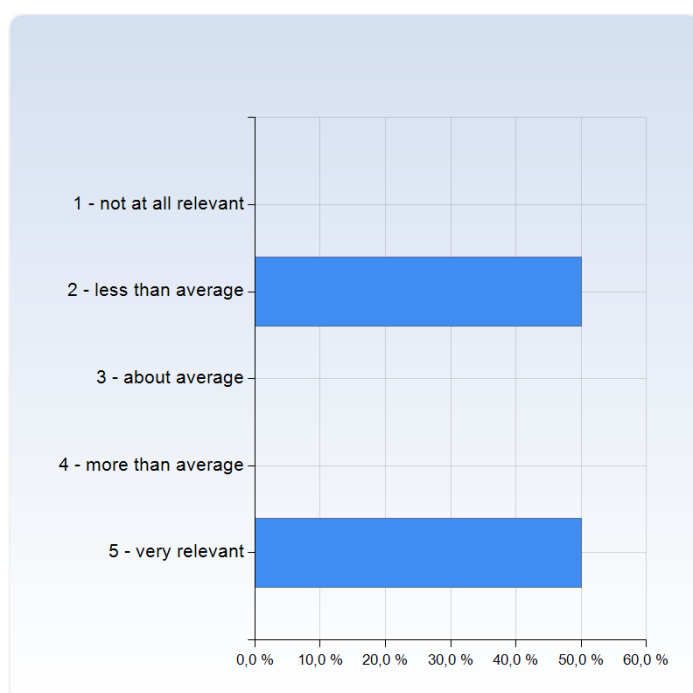


For those of you who used the course book by Lattman and Loll, how useful did you find it?	Mean	Standard Deviation
	3,8	1,5

How relevant for your education was the course content?

Structural bioinformatics

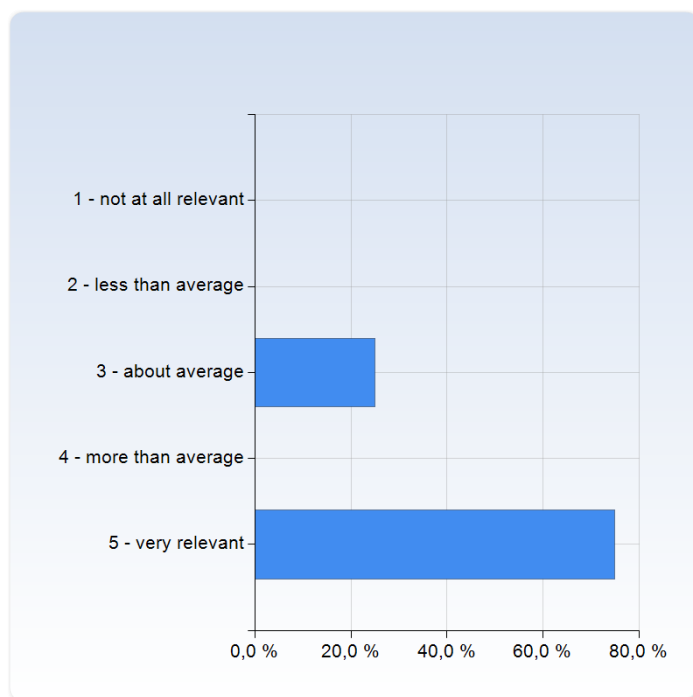
Structural bioinformatics	Number of Responses
1 - not at all relevant	0 (0,0%)
2 - less than average	2 (50,0%)
3 - about average	0 (0,0%)
4 - more than average	0 (0,0%)
5 - very relevant	2 (50,0%)
Total	4 (100,0%)



Structural bioinformatics	Mean	Standard Deviation
	3,5	1,7

X-ray crystallography

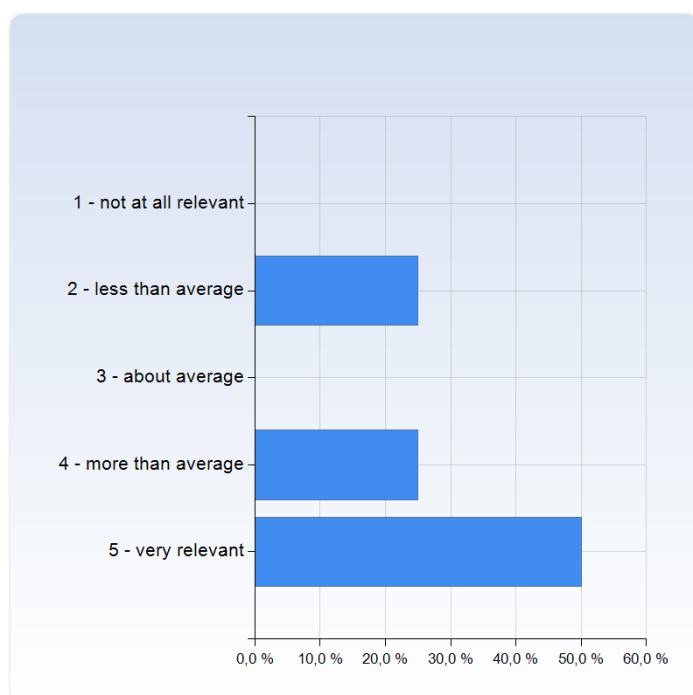
X-ray crystallography	Number of Responses
1 - not at all relevant	0 (0,0%)
2 - less than average	0 (0,0%)
3 - about average	1 (25,0%)
4 - more than average	0 (0,0%)
5 - very relevant	3 (75,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
X-ray crystallography	4,5	1,0

Protein folding

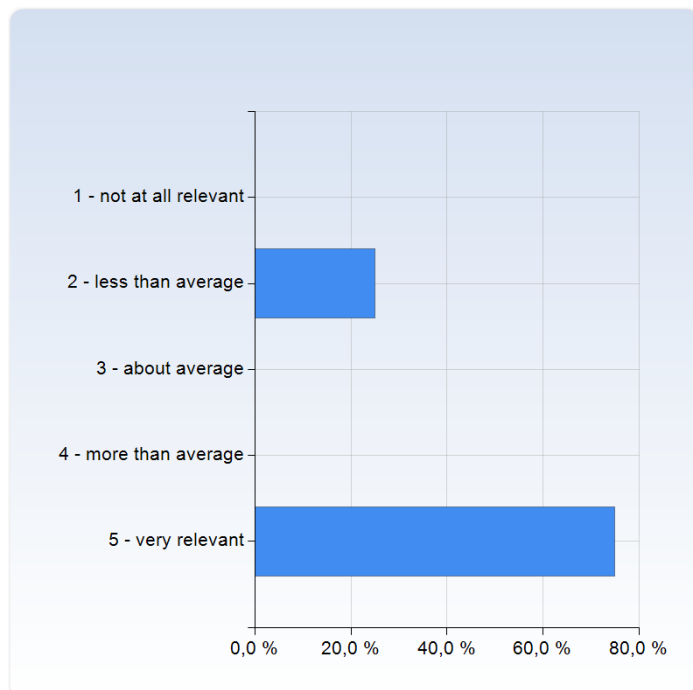
Protein folding	Number of Responses
1 - not at all relevant	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	0 (0,0%)
4 - more than average	1 (25,0%)
5 - very relevant	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Protein folding	4,0	1,4

Other experimental methods (NMR, neutrons, SAXS)

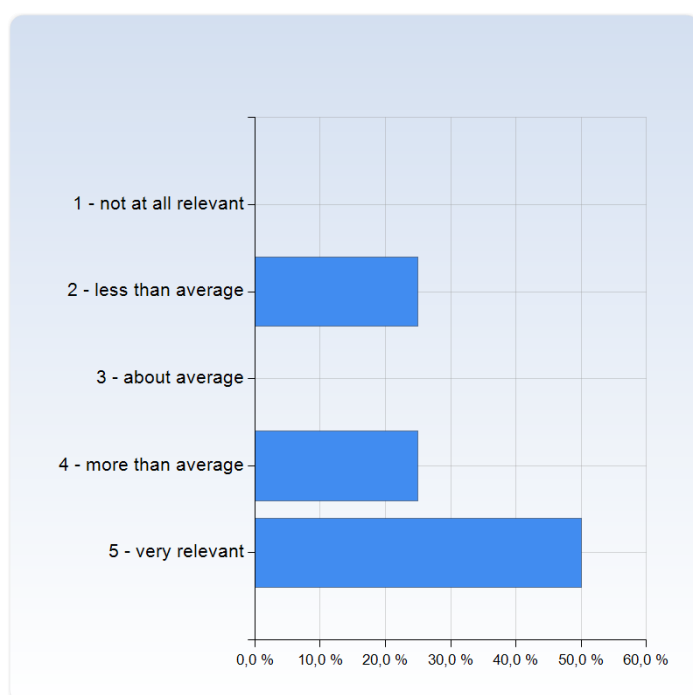
Other experimental methods (NMR, neutrons, SAXS)	Number of Responses
1 - not at all relevant	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	0 (0,0%)
4 - more than average	0 (0,0%)
5 - very relevant	3 (75,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Other experimental methods (NMR, neutrons, SAXS)	4,3	1,5

Structure-based drug design

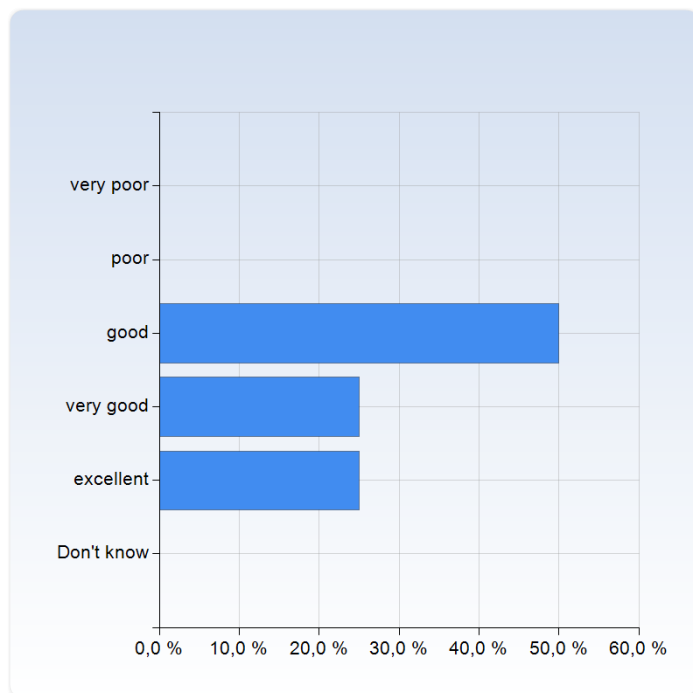
Structure-based drug design	Number of Responses
1 - not at all relevant	0 (0,0%)
2 - less than average	1 (25,0%)
3 - about average	0 (0,0%)
4 - more than average	1 (25,0%)
5 - very relevant	2 (50,0%)
Total	4 (100,0%)



	Mean	Standard Deviation
Structure-based drug design	4,0	1,4

What is your overall impression of the course?

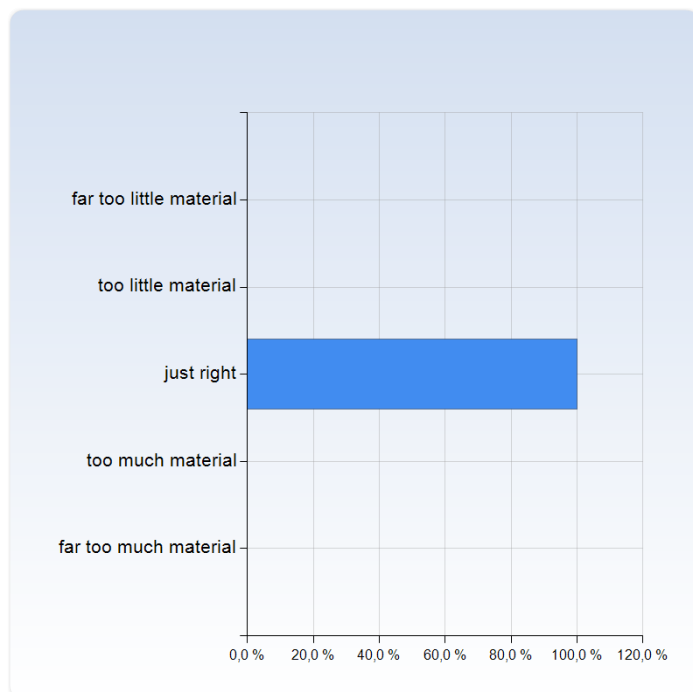
What is your overall impression of the course?	Number of Responses
very poor	0 (0,0%)
poor	0 (0,0%)
good	2 (50,0%)
very good	1 (25,0%)
excellent	1 (25,0%)
Don't know	0 (0,0%)
Total	4 (100,0%)



What is your overall impression of the course?	Mean	Standard Deviation
	3,8	1,0

How did you find the amount of material in relation to the length of the course (15hp)

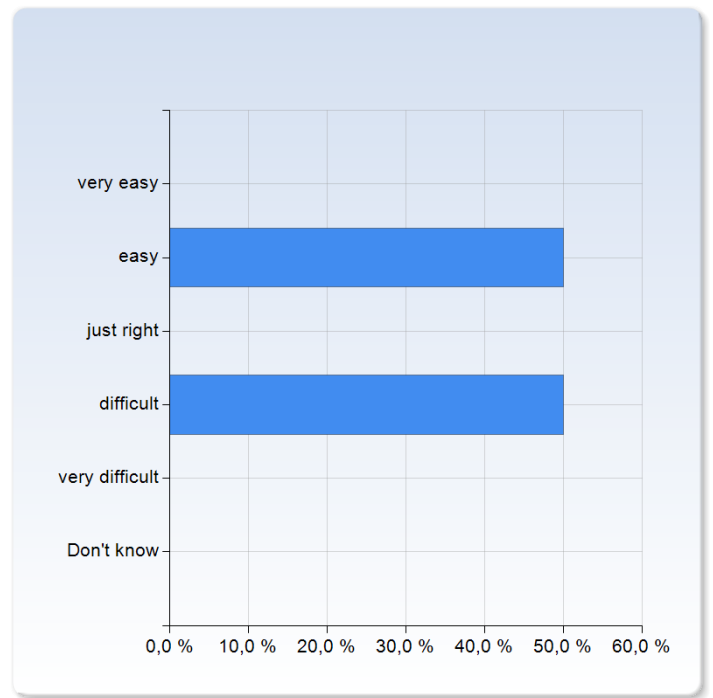
How did you find the amount of material in relation to the length of the course (15hp)	Number of Responses
far too little material	0 (0,0%)
too little material	0 (0,0%)
just right	4 (100,0%)
too much material	0 (0,0%)
far too much material	0 (0,0%)
Total	4 (100,0%)



How did you find the amount of material in relation to the length of the course (15hp)	Mean	Standard Deviation
	3,0	0,0

How did you find the examination?

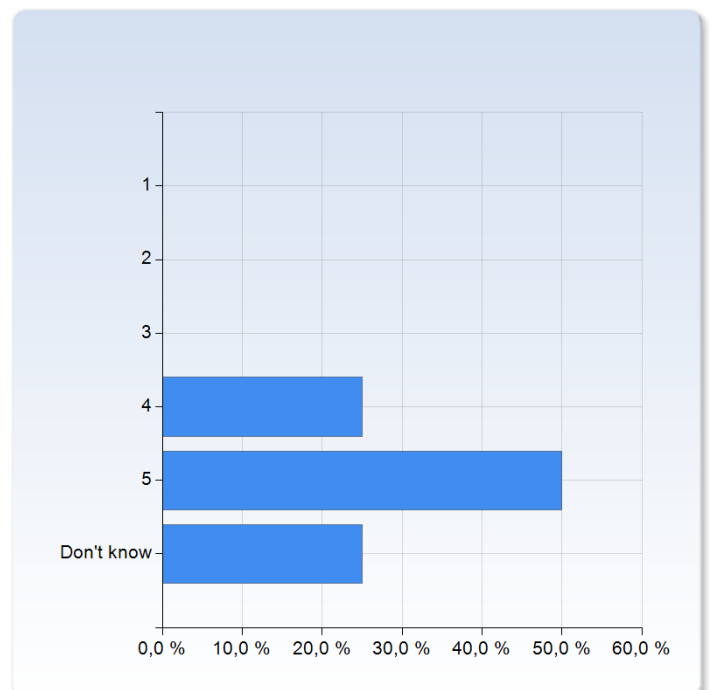
How did you find the examination?	Number of Responses
very easy	0 (0,0%)
easy	2 (50,0%)
just right	0 (0,0%)
difficult	2 (50,0%)
very difficult	0 (0,0%)
Don't know	0 (0,0%)
Total	4 (100,0%)



How did you find the examination?	Mean	Standard Deviation
How did you find the examination?	3,0	1,2

How likely is it that you would recommend the course to a friend or fellow student?

How likely is it that you would recommend the course to a friend or fellow student?	Number of Responses
1	0 (0,0%)
2	0 (0,0%)
3	0 (0,0%)
4	1 (25,0%)
5	2 (50,0%)
Don't know	1 (25,0%)
Total	4 (100,0%)



How likely is it that you would recommend the course to a friend or fellow student?	Mean	Standard Deviation
How likely is it that you would recommend the course to a friend or fellow student?	4,7	0,6