Side 1

**UNIVERSITY OF OSLO**

**Faculty of Mathematics and Natural Sciences**

**Exam in MBV4150**

**Day of exam: 24 May 2013**

**Exam hours: 0900 - 1200**

**This examination paper consists of 2 pages.**

**Appendices: Hosokawa et al (2010) and supplementary figures**

**Permitted materials: None**

*Make sure that your copy of this examination paper*

*is complete before answering.*

**English**

The PNAS paper by Hosokawa et al (2010) details a unique symbiotic relationship between the common bedbug and an intracellular bacterium within the genus *Wolbachia*.

1) What do you see to be the most important findings of this work (in your own words - please)?

2) What other types of symbiotic systems presented in the course most strongly resemble that demonstrated in this work? How are they similar? How are they different?

3) Can you identify any weaknesses / flaws in technique, data or logic in the work? If so, what are they?

4) What do you perceive to be the major biological and functional significance of the symbiosis? What does each partner gain from the interaction? Explain the logic behind your answer.

5) What is the logic behind using the *ftsZ* gene sequences for molecular phylogenetic analyses?

6) A second proteobacterial endosymbiont is found in all but the JESC lines of *C. lectularis* (Table S1). What might account for this discrepancy? What role(s) might the second endosymbiont play in the ecology of the insect-bacterium endosymbiosis? How could you test your theories?

6) You suddenly get lucky and are funded to sequence the genome of the *C. lectularis Wolbachia* endosymbiont*.* Based on your current knowledge, what general features do you expect to find for the *Wolbachia* endosymbiont genome when you analyze the data? How might its genome content and organization compare to those of other *Wolbachia* species? How might its genome content and organization compare to those of bacterial symbionts of blood feeding insects?