Study material.
This study guide covers material for the second exam: "Methods in molecular biology and the mechanics of replicating, repairing and copying genetic information." This material comes from lectures 7-12 on the syllabus, Sept. 27 through Oct. 20. This material lends itself to definitions and objective questions more than to the sort of problems you saw on the first exam. I particularly like a style of question in which you are asked to identify which of two similar statements is correct and which is bogus. I recommend that you look at the questions at the end of chapters 9-11, 13, 14, 16, 17 and 21 of Hartwell and review the old exams. You are encouraged to consult reliable online sources in addition to the text (the sources on the NCBI books site are reliable).

Be able to define, discuss, and explain the following:
- clone
- (cloning) host
- cloning vector
- transformation
- conjugation
- transduction
- F
- F'
- Hfr
- temperate bacteriophage
- C0t
- cosmid
- cDNA
- Southern
- Northern
- SNP
- microsatellite
- polymorphism
- CAPs
- anticipation
- illegitimate recombination
- site-specific recombination
- homologous recombination
- prophage
- provirus
- lysogen
- consensus sequence
- RNA polymerases I, II & III
- EMSA
- footprinting
- dideoxynucleotide
- recA
- attenuation
- rho factor
- sigma factor
- core polymerase
- operon
- operator
- helix-turn-helix motif
- recognition helix
- CTD
- core promoter
- enhancer
- recBCD
- general transcription factors
- preinitiation complex
- zinc finger
- topoisomerase II
- base excision repair
- nucleotide excision repair
- Holliday junction
- mismatch repair
- AP endonuclease
- radiation hybrid
- YAC
- BAC
- pseudogenes
- LINES
- SINES
- LTR
- transposase
- satellite DNA
- L1
- Alu
- retrotransposons
- retroviruslike transposable elements
- target site duplications
- Terminal inverted repeats.

Review questions.
Be sure that you understand the yeast two-hybrid assay for protein-protein interactions, both as a technique and as an illustration of principles behind transcriptional activation (see lecture 12).

1. Transcription of a class II gene (a gene transcribed by RNA polymerase II) starts at a G 30 bp downstream of the first T in the TATA box. A deletion of 10 bp between the G and the TATA box would result in transcription starting where?

2. You have a cloned and sequenced a gene from the East Mongolian rabbit, a species without a known genetic map of any kind. How might you generate a map and place this gene on the map of the East Mongolian rabbit genome without performing any pedigree analyses and without using a microscope. What tools or resources would you need, and how would you proceed? This is a general question about map construction in non-model mammalian genomes.