

The second exam will be Tuesday, Nov. 1, 2005

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	C ₀ t	cosmid
cDNA	Southern	Northern
Western	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.