#### **Module 2 overview**

#### lecture

- 1. Introduction to the module
- 2. Rational protein design
- 3. Fluorescence and sensors
- 4. Protein expression

## SPRING BREAK

- 5. Review & gene analysis
- 6. Purification and protein analysis
- 7. Binding & affinity measurements
- 8. High throughput engineering

#### lab

- 1. Start-up protein eng.
- 2. Site-directed mutagenesis
- 3. DNA amplification
- 4. Prepare expression system
- 5. Gene analysis & induction
- 6. Characterize expression
- 7. Assay protein behavior
- 8. Data analysis

## Lecture 5: Review & gene analysis

- I. Review of the project
  - A. Project aims and rationale
  - B. Methods, work completed so far
- II. Analysis of mutant genes
  - A. Restriction digests
  - B. DNA sequencing

# Module 2 assignment

Protein engineering research article

- 1. Abstract
- 2. Introduction
- 3. Materials and Methods
- 4. Results
- 5. Discussion
- 6. References
- 7. Figures

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- 2. Introduction

Why are calcium sensors important?

What is protein engineering; how does it relate?

What is inverse pericam?

Why is it useful/interesting to tune pericam?

Why did you choose your mutations?

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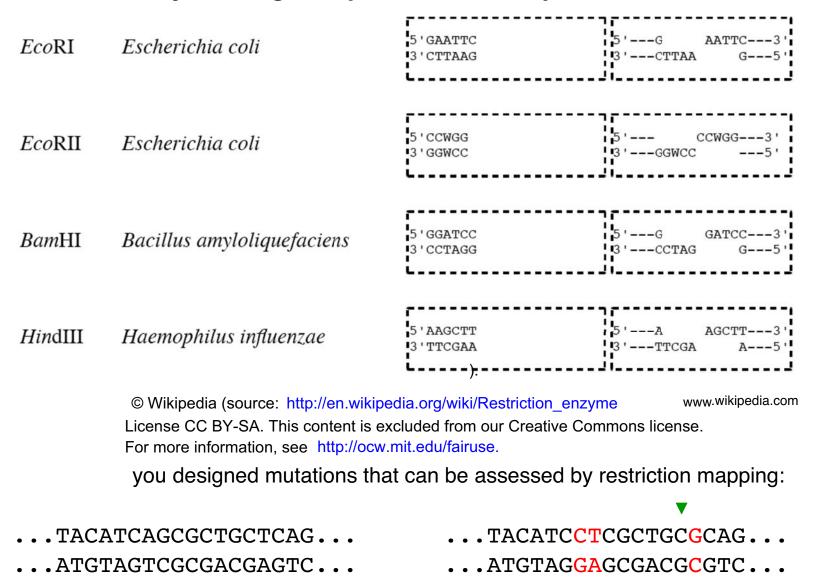
- 3. Materials and Methods
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### Restriction enzymes digest specific DNA sequences

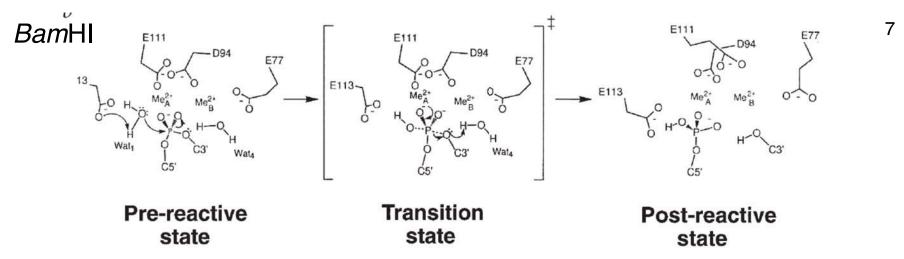
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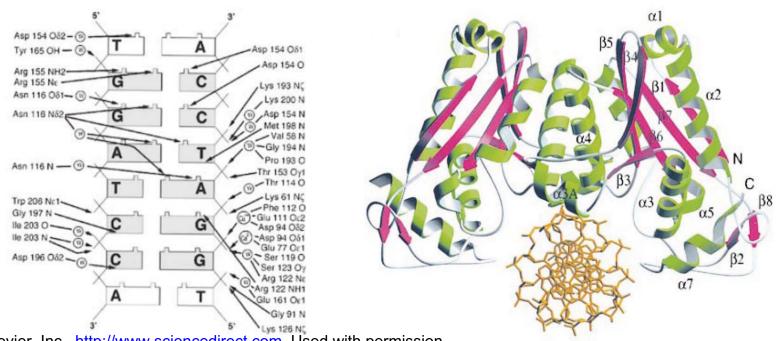
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#### How do restriction endonucleases work?



Reprinted by permission from Macmillan Publishers Ltd: Nature Structural Biology. Source: Viadiu, H., and A. K., Aggarwal. "The Role of Metals in Catalysis by the Restriction Endonuclease Bam HI." *Nature Structural Biology* 5 (1998): 910-916. © 1998.

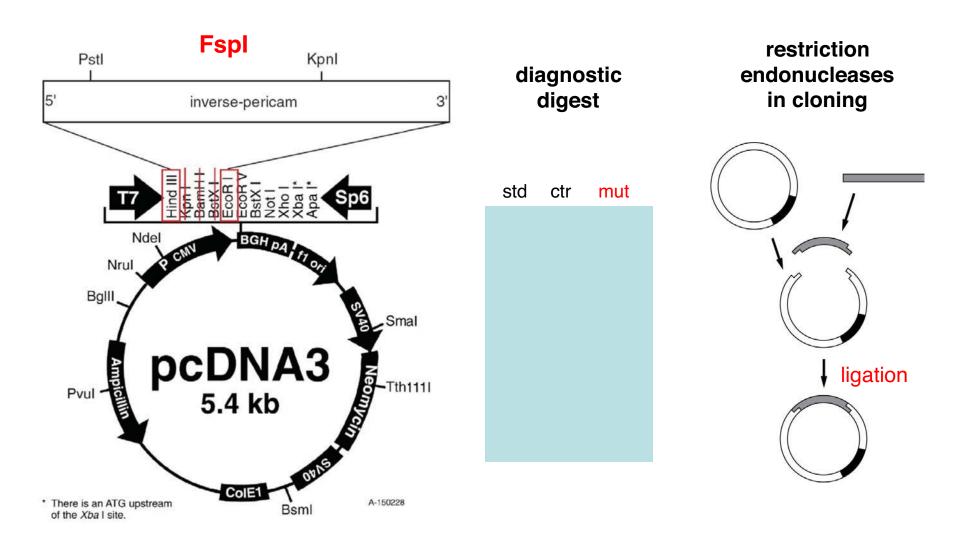


Courtesy of Elsevier, Inc., http://www.sciencedirect.com. Used with permission.

Source: Viadiu, H., and A. K., Aggarwal.

"Structure of BamHI Bound to Nonspecific DNA: A Model for DNA Sliding." *Molecular Cell* 5, no. 5 (2000): 889-895.

Viadiu & Aggarwal (1998, 2000)



Courtesy of Life Technologies. Used with permission.

Genetic polymorphisms can be associated with different distributions of restriction sites—restriction fragment length polymorphisms (**RFLPs**) used for genotyping

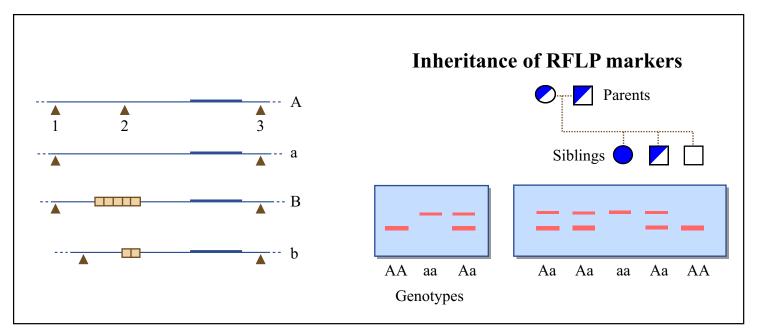


Figure by MIT OpenCourseWare.

Suppose alleles A and B each occur in 50% of the population and segregated independently, what are the chances that a randomly chosen individual displays the AB phenotype?

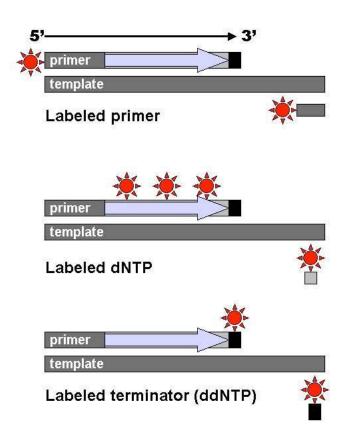
How many biallelic polymorphisms would have to be considered for each genotype to have a 1:1,000,000 chance of occurring, assuming equal prevalence of each?

Reprinted by permission from Macmillan Publishers Ltd: Nature Reviews Genetics. Source: Jobling, M. A., and P. Gill. "Encoded evidence: DNA in Forensic Analysis." *Nature Reviews Genetics* 5, (October 2004): 739-751. © 2004.

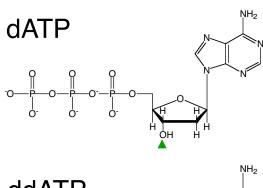
Jobling (2004) Nat. Rev. Genetics

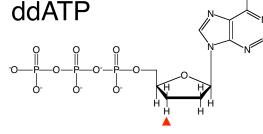
### How does sequencing work?

Perform PCR on template to be sequences; each PCR reaction is terminated by a nucleotide analog that can be incorporated, but not added to. Terminated PCR products must be labeled in some way.

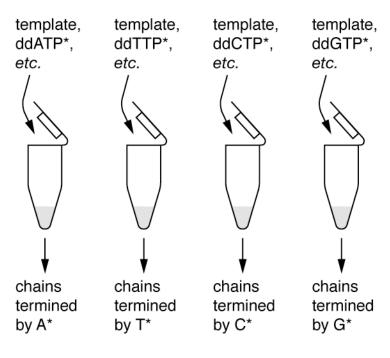


nucleotides linked by phosphodiester bonds

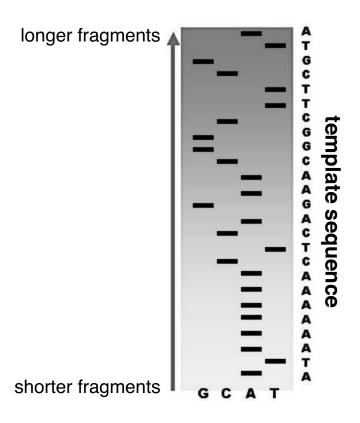




## sequencing with radioactive ddNTPs



run products in four separate lanes on gel, expose X-ray film



Wikipedia (Public domain image)

## "one pot" sequencing more common today:

template, fluorescently tagged ddATP, ddTTP, ddCTP, ddGTP, etc. **TGATTCATC Fluorescence Migration of DNA** detector fragments Laser Sample/ **Buffer** Buffer chains termined by tagged A, T, C, G (all different colors) 40 50 60 70 80 90 SG ACG ATG ATTTAC AC G C ATG TG C TG AAAGTTG G C G G TG C C G C AG TG C G C TC AC C G C 10 20 30 CGATIG A TTIA GC GGC CGCG AATTCGC CC T

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