Happy snow day ?!

M1D1: in silico cloning, induce protein expression

02/09/2017

I hope these pre-lab discussion notes help you go through the "pretend cloning" exercises in Part 3 of

http://engineerbiology.org/wiki/

20.109(S17):In_silico_cloning_and_induction_of_protein_expression_(Day1)



Today in the lab



- Hand in your homework
- Lab orientation quiz
- Pre-lab discussion

We'll take care of these on M1D2 (Tuesday, 02/14)



 "Clone" FKBP12 protein into pRSETb vector plasmid



 Induce FKBP12 protein expression in BL21(DE3)pLysS E. coli bacteria

Office hours



Noreen Lyell

- M 2-5
- in 16-317



Leslie McClain

- T 9:30-11
- in 56-341c



Maxine Jonas

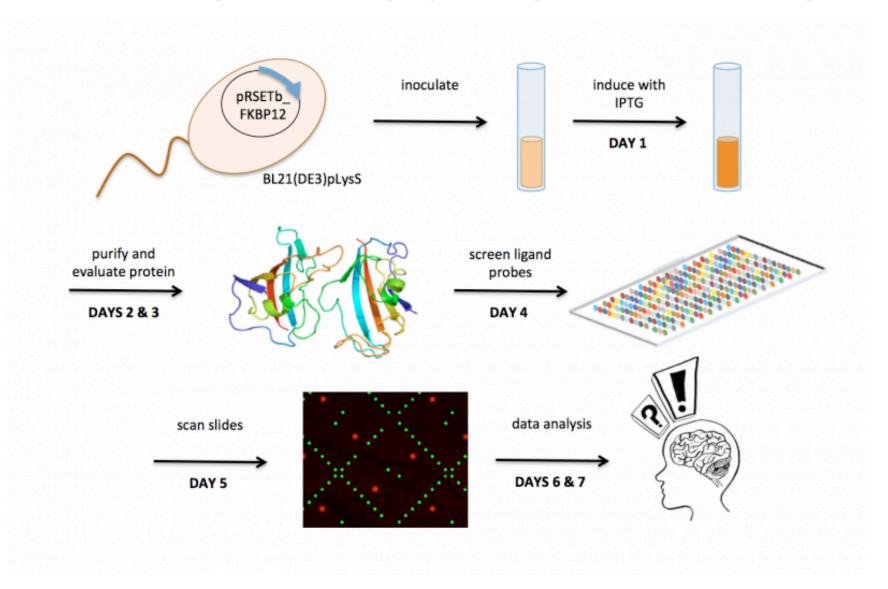
- R 9:30-11
- in 16-239

don't hesitate !

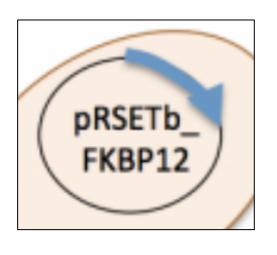
M1 major assignments

- Data summary (15%)
 - in teams, on Stellar
 - draft due 03/10, final revision due 03/27
 - bullet points, .PPTX
- Mini-presentation (5%)
 - individual, video via Gmail
 - due 03/18
- Lab quizzes (extra credit on homework grade)
 - M1D3, M1D5, and M1D7
- Notebook (5% total)
 - one day will be collected and graded by Rob on M1D7
- Blog: http://be20109s17.blogspot.com/ (participation: 5% total)
 - by 04/03

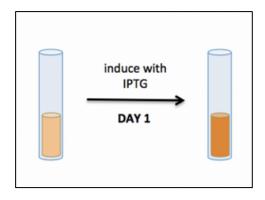
Overview of "M1: High-throughput ligand screening"



Today in lab



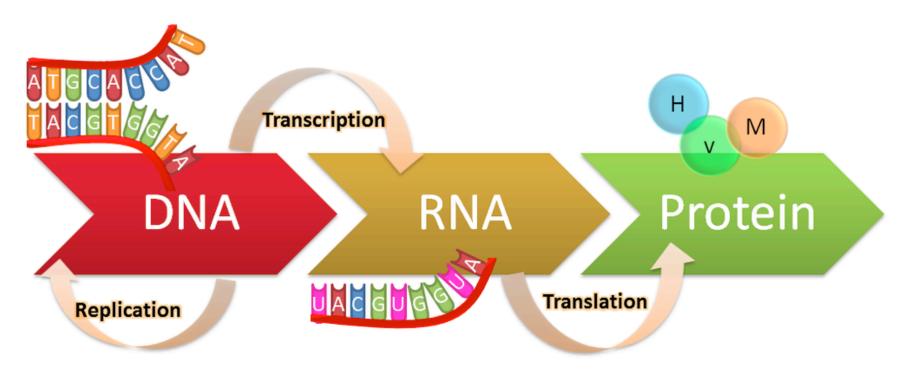
- Reproduce in silico the cloning of pRSETb-FKBP12
 - A Plasmid Editor (APE)
 - PCR amplification of Fkbp12 insert
 - digestion of pRSETb vector by endonucleases
 - ligation



- Induce expression of FKBP12 protein
 - in BL21(DE3)pLysS E. coli cells
 - using IPTG
 - More about these acronyms on M1D2!

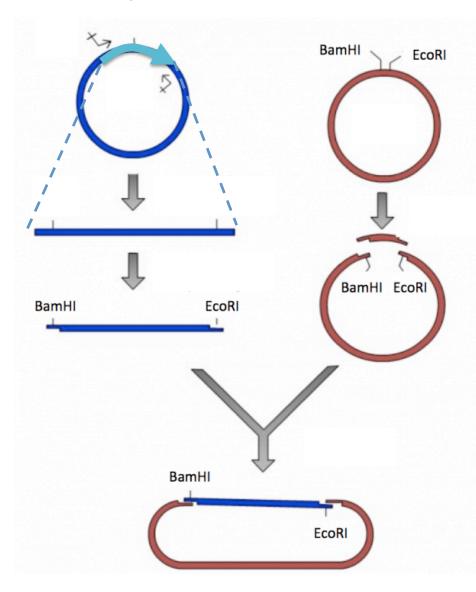
The central dogma

- To study interactions of FKBP12 protein,
 - first make FKBP12 protein
 - by having the Fkbp12 gene transcribed and translated



insert fragment *Fkbp12*

vector backbone pRSETb



How is DNA engineered?

- amplification
 - PCR:



polymerase chain reaction

- Kary Mullis 1993
- primers

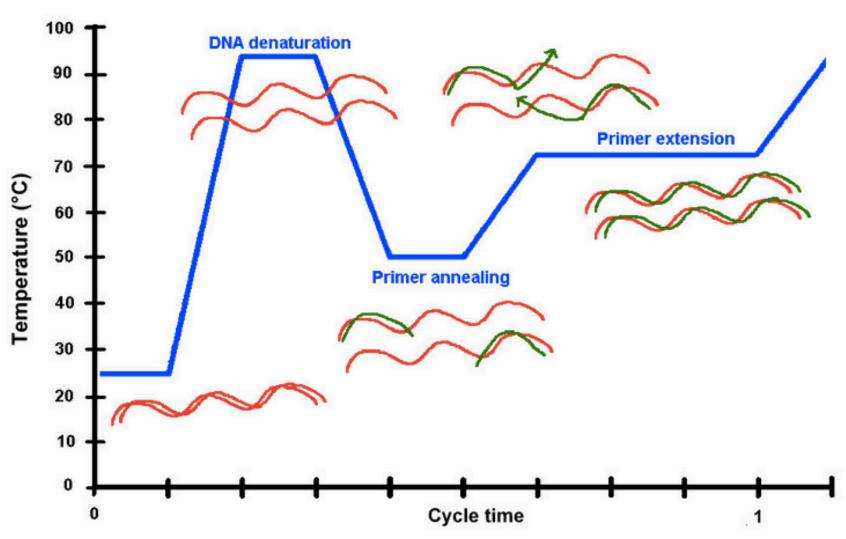
complementary to the beginning and to the end of your gene of interest

- digestion
 - restriction enzymes

also called "endonucleases"

ligation

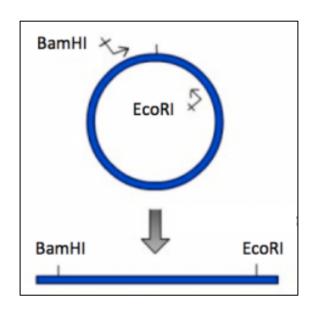
Polymerase chain reaction (PCR): 1 cycle



Using PCR to generate FKBP12 *gene* flanked by restriction enzyme recognition sites

3 major steps in each cycle:

- Melt
 - − 95 °C
 - break hydrogen bonds
- Anneal
 - $T_m(primer) = half is annealed$
 - $-T_{anneal} \sim T_{m}(primer) 5^{\circ}C$
- Extend
 - 72 °C (for Taq)
 - 1 min / 1000 bp

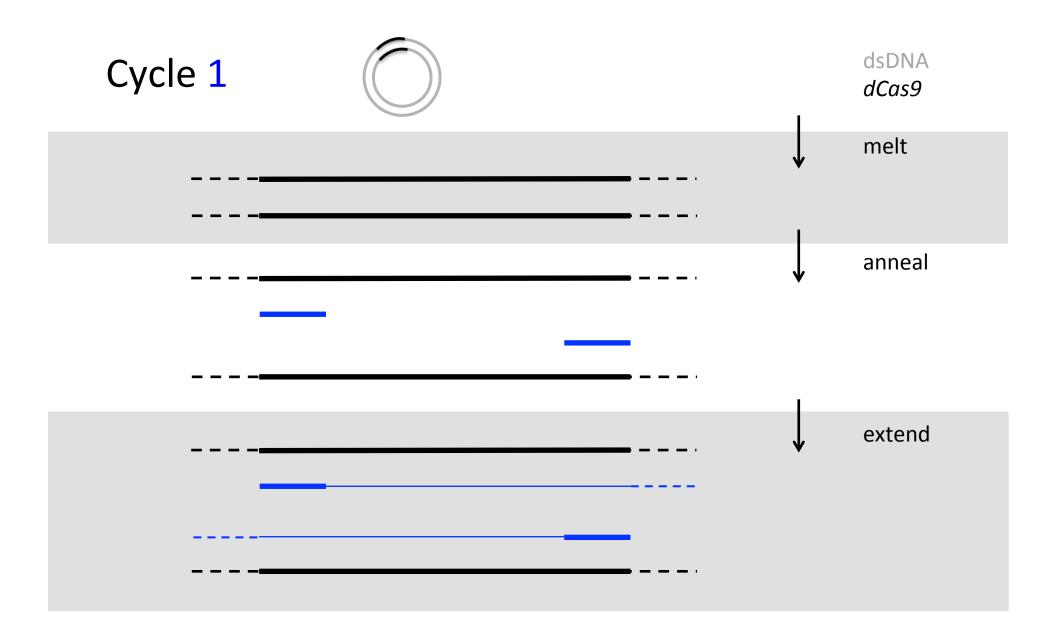


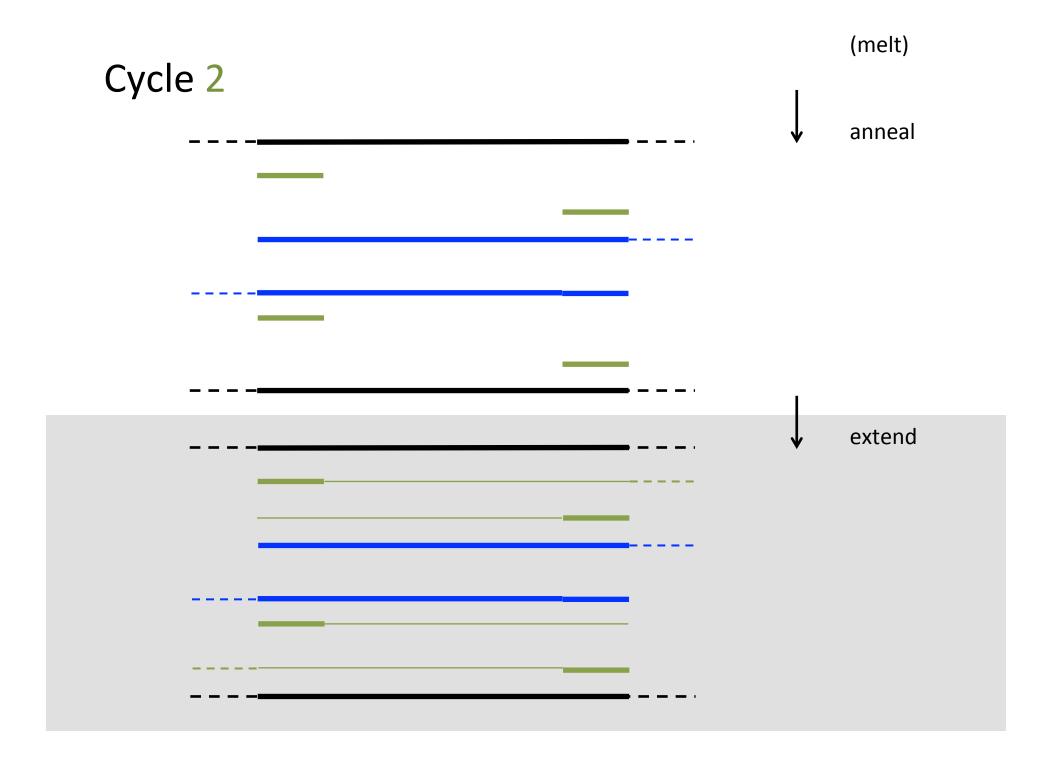
♦ Primers

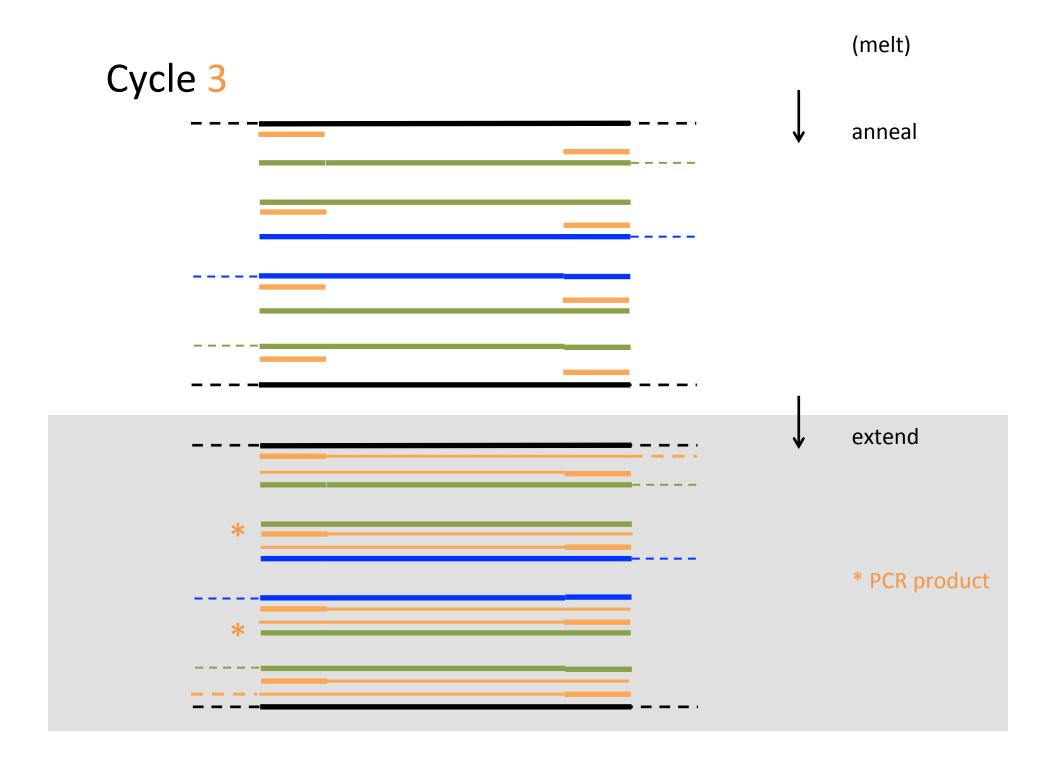
- specificity
- option to add base pairs, e.g. endonuclease recognition sequence

Make sure you understand and can reproduce yourself the next 3 slides :

How many PCR cycles until only your amplicon?

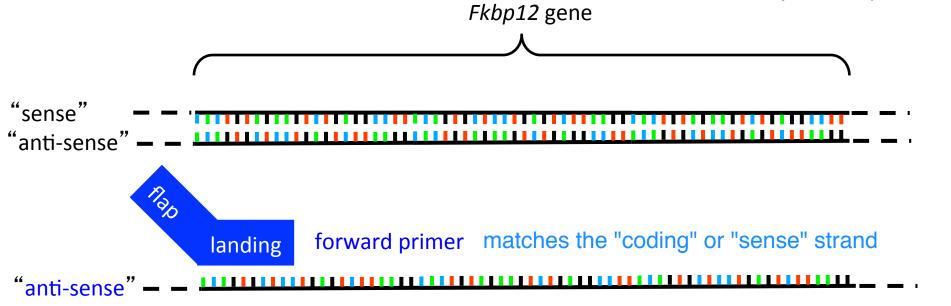






How do you design primers?

always list primers' sequence 5' to 3' (even for the reverse primer, hence the terminology "reverse-complement")





reverse primer is the reverse-complement of the "non-coding" or "anti-sense" strand

landing

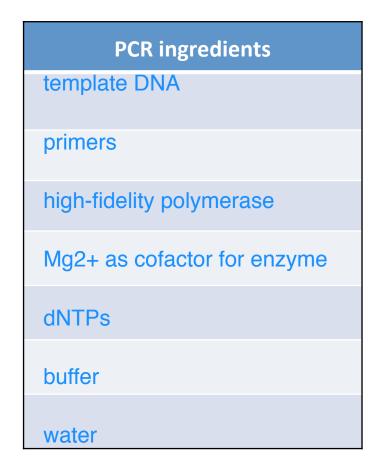
Primer design guidelines

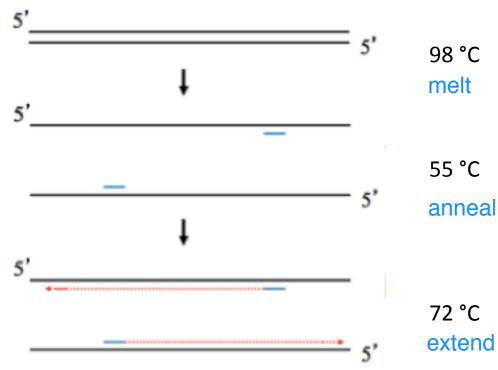


- Length
 - 17-28 base pairs
 - _ long enough for specificity, short enough to anneal at T_anneal
- GC content
 - **-** 40-60%
 - GC clamp at ends
- T_m(primer)
 - $< 65 \,^{\circ}\text{C}$

- Specificity
 - is primer complementary to other loci of the plasmid?
- Secondary structure
 - hairpins
 - complementation
- Repetitive sequence
 - di-nucleotides < 4
 - runs < 4 bp</p>

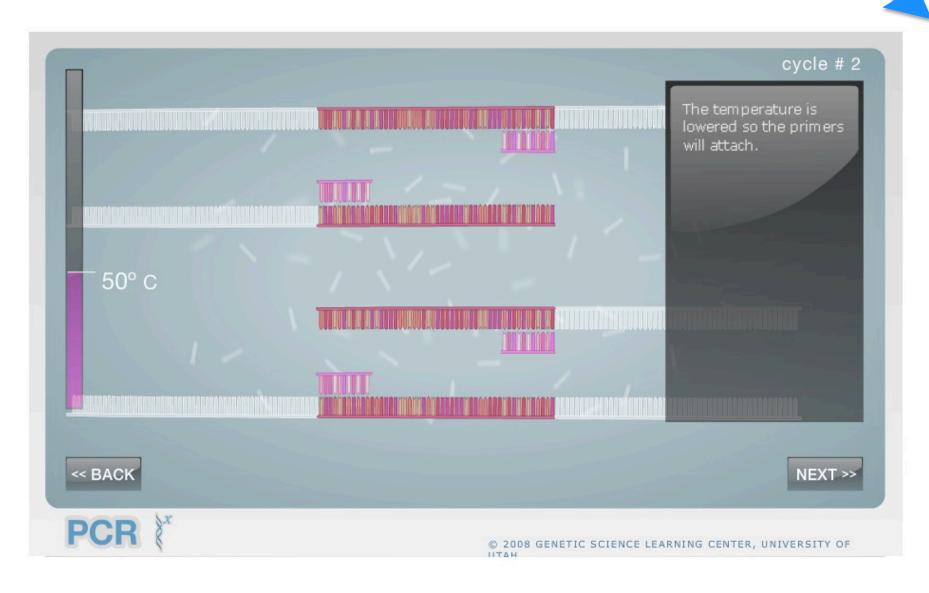
PCR ingredients and cycling conditions



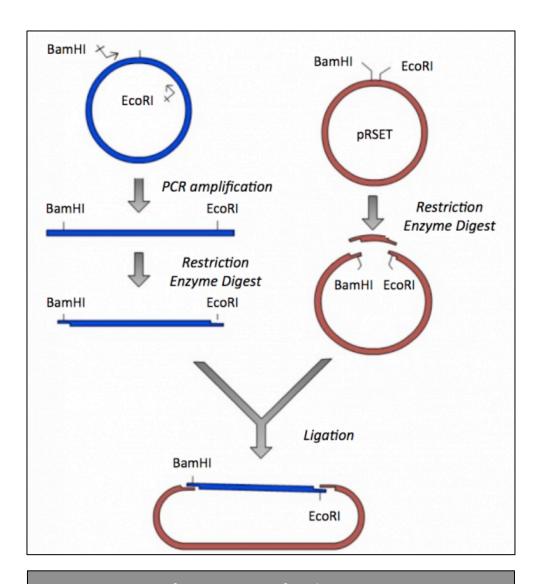


25 cycles

Leslie's favorite PCR animation



pRSETb-FKBP12 was constructed by ligation

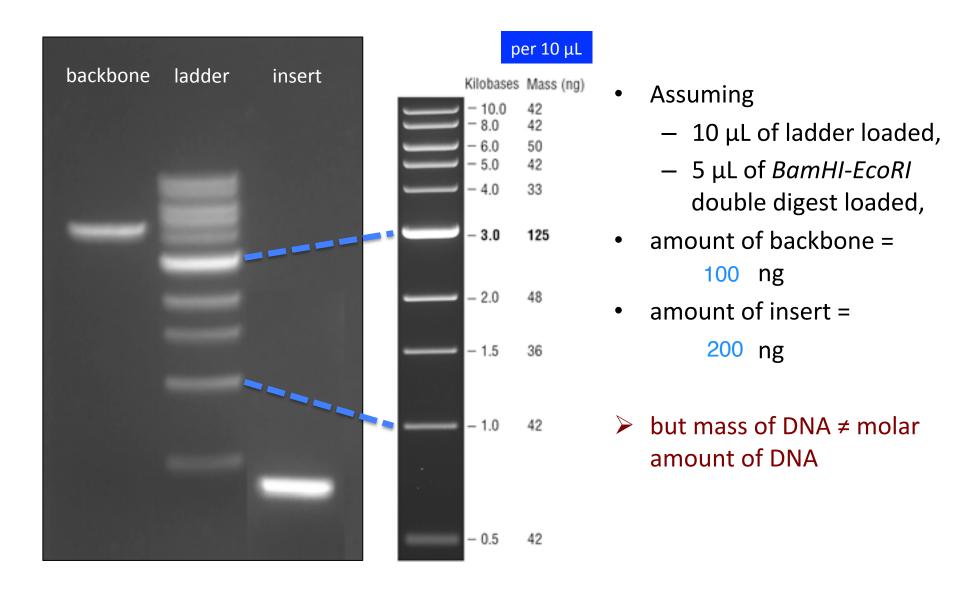


backbone ladder insert (vector) (fragment)

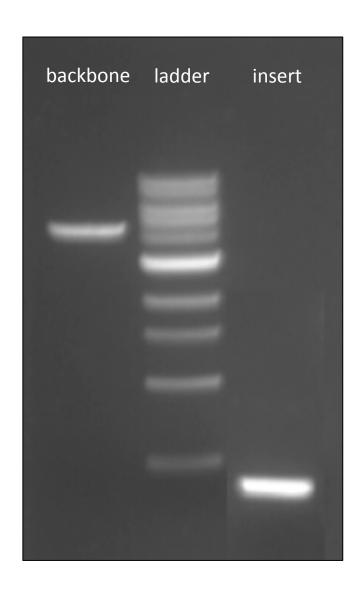
pRSETb-FKBP12 cloning strategy

recovery gel

For ligation, mix 1:4 *molar* backbone : insert



Calculate the 1:4 molar amounts for ligation



1. From recovery gel, estimate

- backbone: 100 ng / 5 μL = 20 ng/μL - insert: 200 ng / 5 μL = 40 ng/μL

2. Determine volume of backbone needed

– 50-100 ng, choose 60 ng, *i.e.* 3 μL

3. Calculate moles of backbone

- 2776 bp * (660 g / (mol*bp)) = 1.83 x 10⁶ g/mol
- so 60 ng / (1.83 x 10⁶ g/mol) = 3.27 x 10⁻¹⁴ mol

4. Determine moles of insert needed (4X bkbn)

- $-4 \times 3.27 \times 10^{-14} \sim 1.31 \times 10^{-13} \text{ mol}$
- with 408 bp * (660 g / (mol*bp)) = 2.69 x 10⁵ g/mol
- so use 1.31 x 10^{-13} mol * 2.69 x 10^5 g/mol ~ 35.3 ng

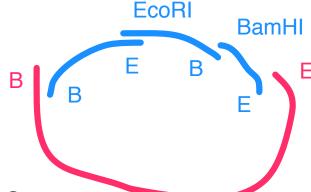
5. Calculate volume of insert needed

- 35.3 ng / (40 ng/ μ L) ~ 1 μ L

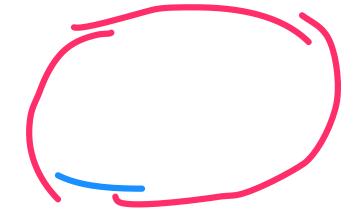
Optimal backbone-to-insert ratio

- ideally, want 1:4 backbone : insert
 - molar ratio, not mass or volume

What if too much insert?



• What if too much backbone?



How do we confirm our product?

1. Transformation

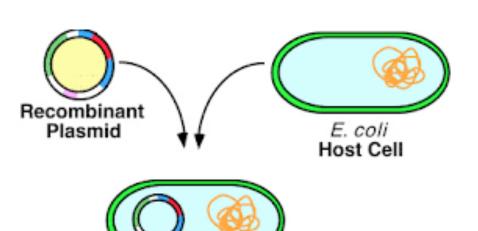
- of "competent cells"
- incubation
- heat shock
- recovery
- selection by antibiotics
 resistance pRSETb contains an ampicillin resistance cassette

2. Purification (mini-prep)

separate plasmid from host (chromosomal) DNA

3. Digestion

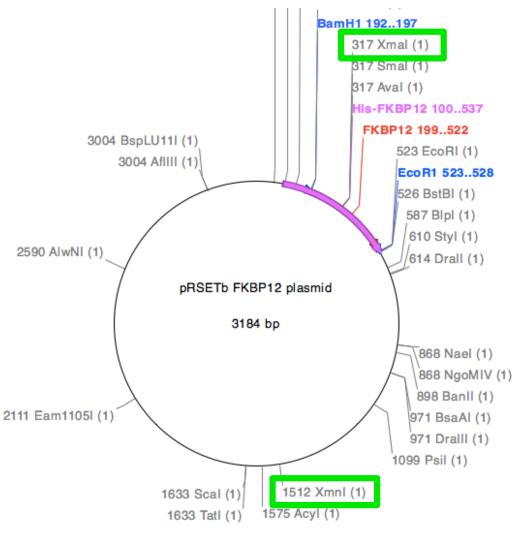
- again
- by different restriction enzymes

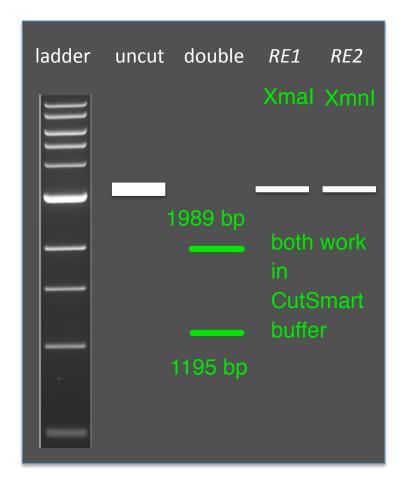


Confirmation digest

Goal: 1 cut only in backbone + 1 cut only in insert

- Are fragments easily distinguished on an agarose gel? > 500 bp
- Do you have access to the enzymes?
- Are the two enzymes compatible? work well in same buffer





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Make sure to keep notes in Benchling