

M1D1:

In silico cloning and confirmation digest of protein expression vector

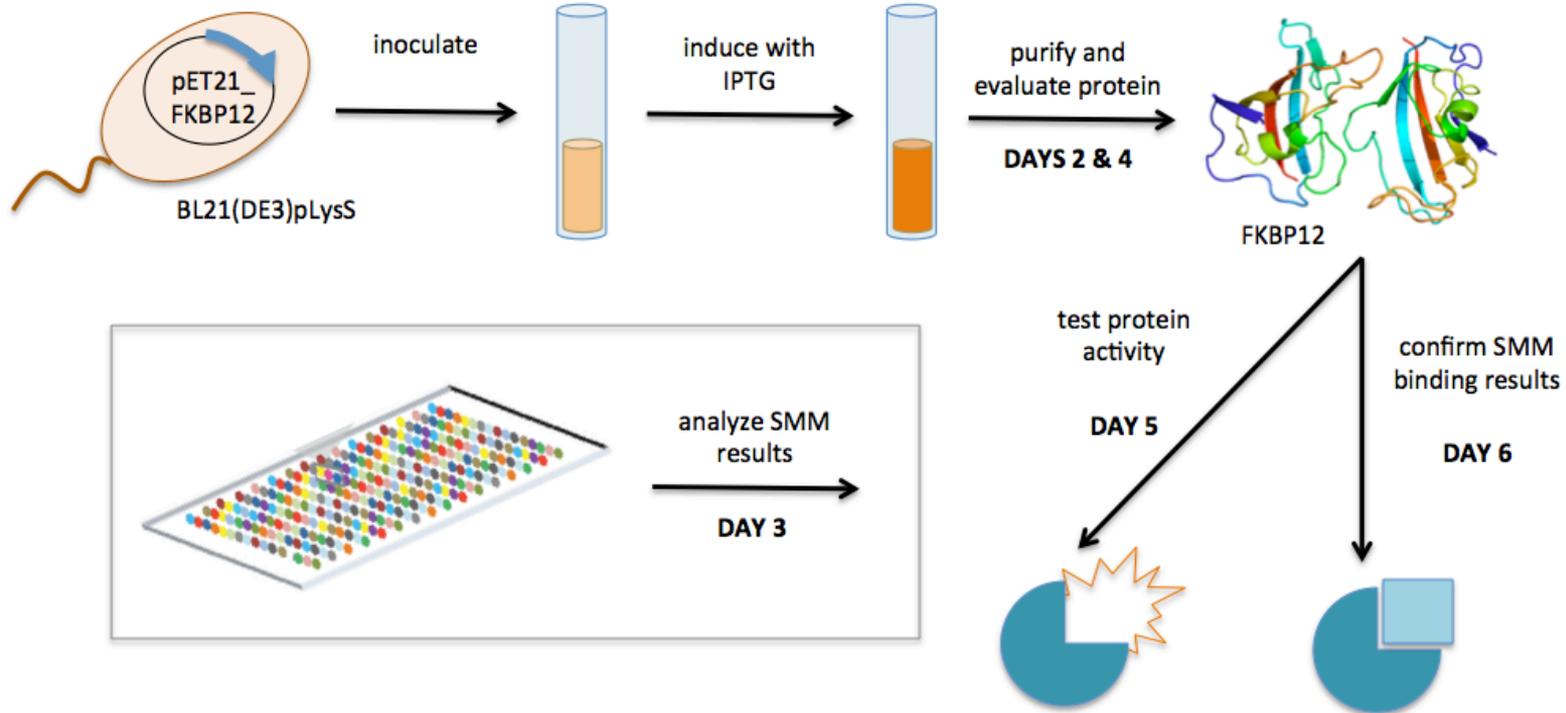
1. Laboratory Orientation quiz
2. Prelab discussion
3. Build protein expression vector - virtually
4. Confirm protein expression vector - actually

Mark your calendars!

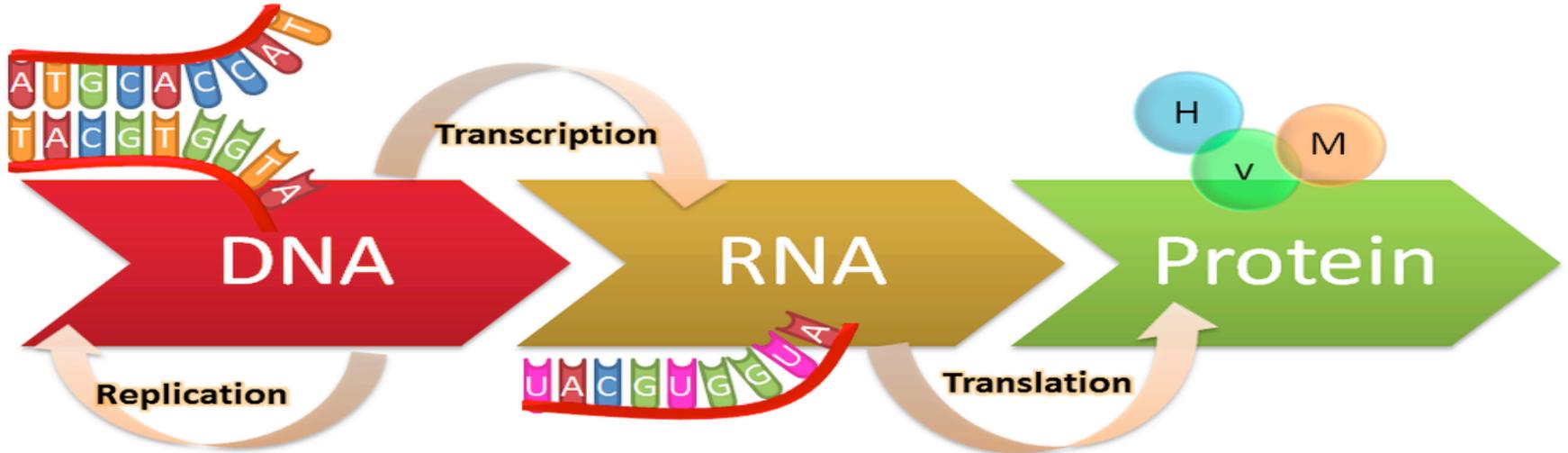
- **Data summary** (15%)
 - completed in teams and submitted via Stellar
 - draft due 3/11, final revision due 3/25
 - format in bullet points
- **Mini-presentation** (5%)
 - completed individually and submitted via Gmail
 - due 3/16
- **Laboratory quizzes**
 - scheduled for M1D4 and M1D7
- **Notebook** (part of 10% Homework and Notebook)
 - one entry will be graded by ~~Casper~~ 24 hr after M1D7
- **Blog** (part of 5% Participation) *Michaela*
 - due 3/17 via Blogspot



Overview of Mod 1 experiments



How are proteins made?



What if we want a specific protein?

- Amplification

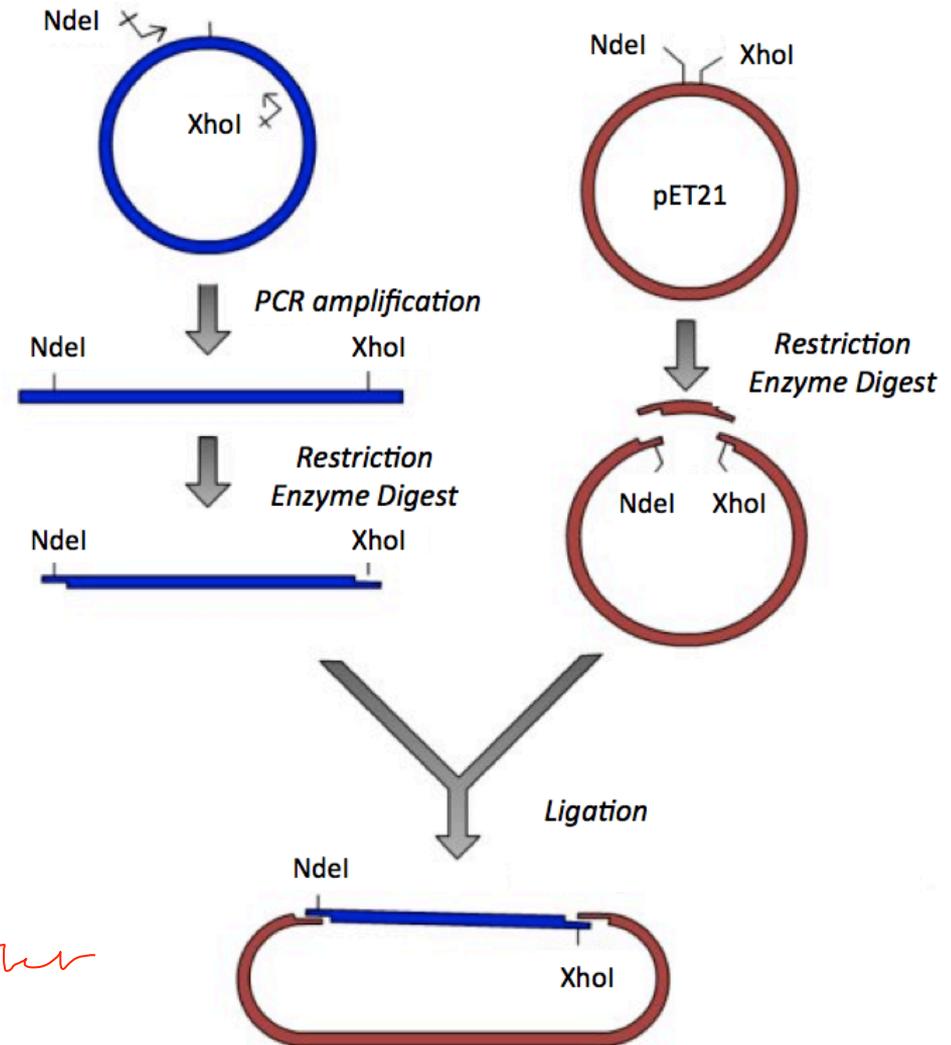
gene of interest

- Digestion

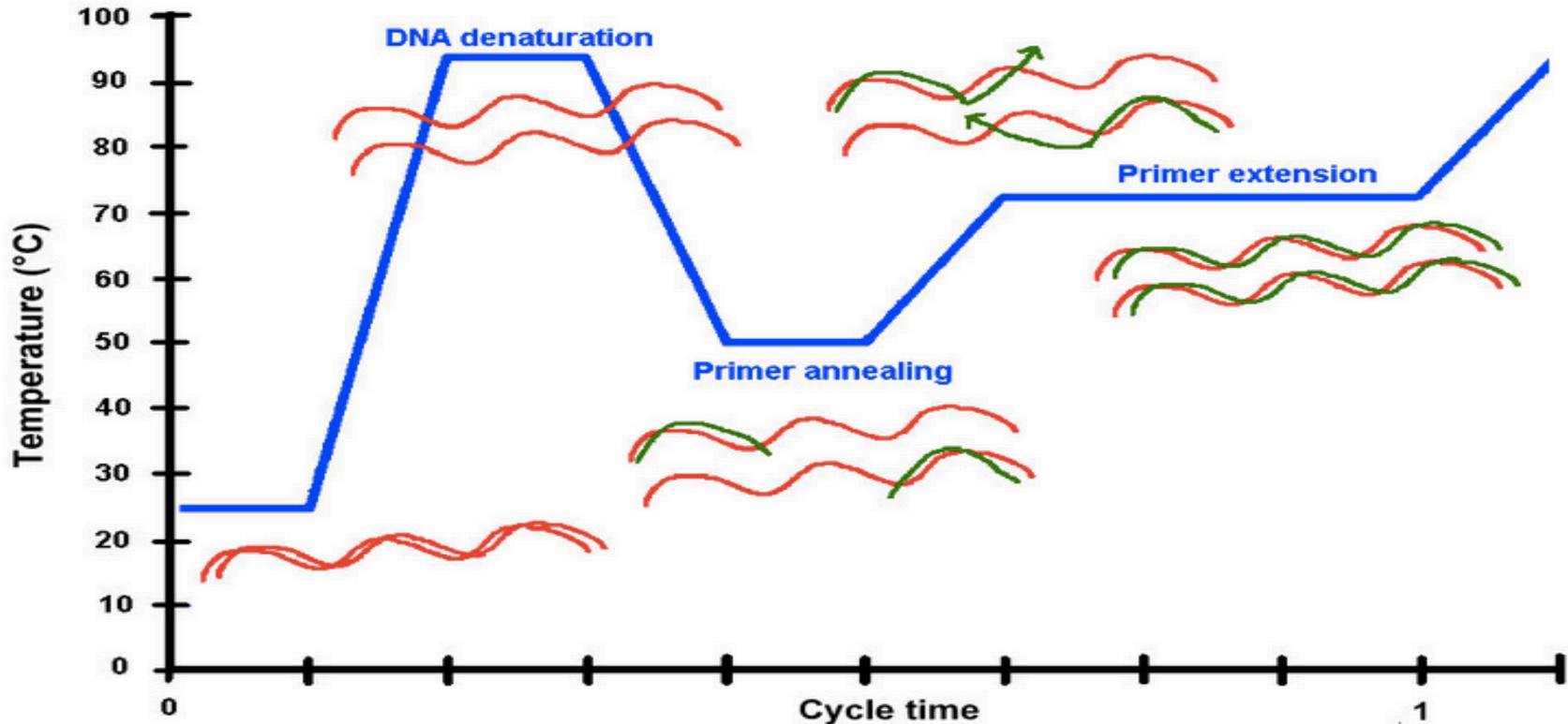
*generate sticky ends
open the vector*

- Ligation

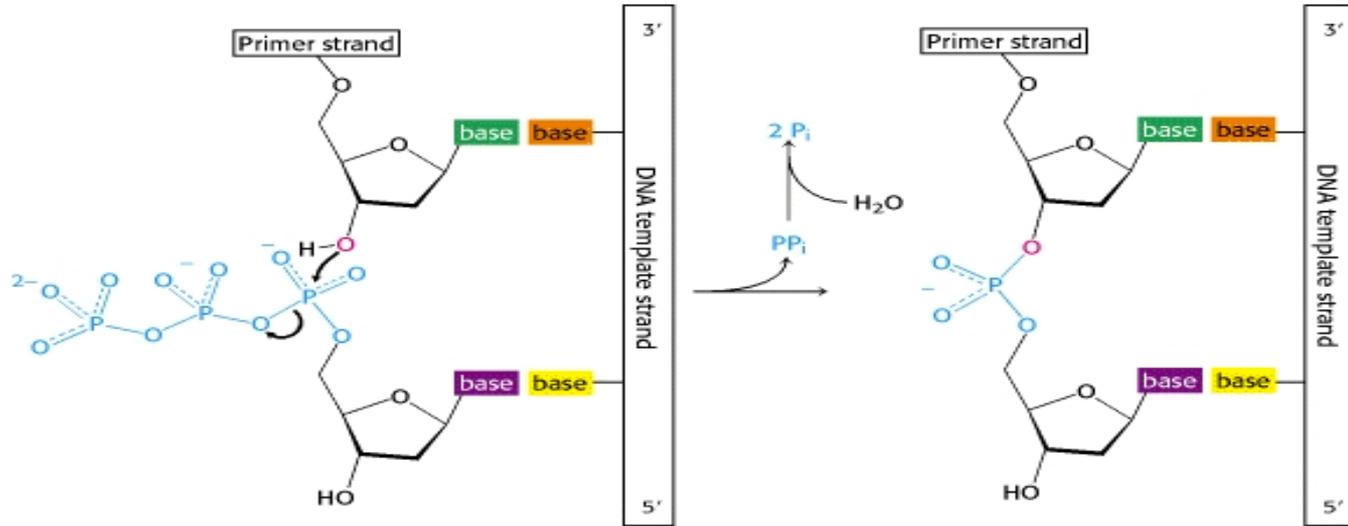
glues everything together



Amplification: PCR cycling



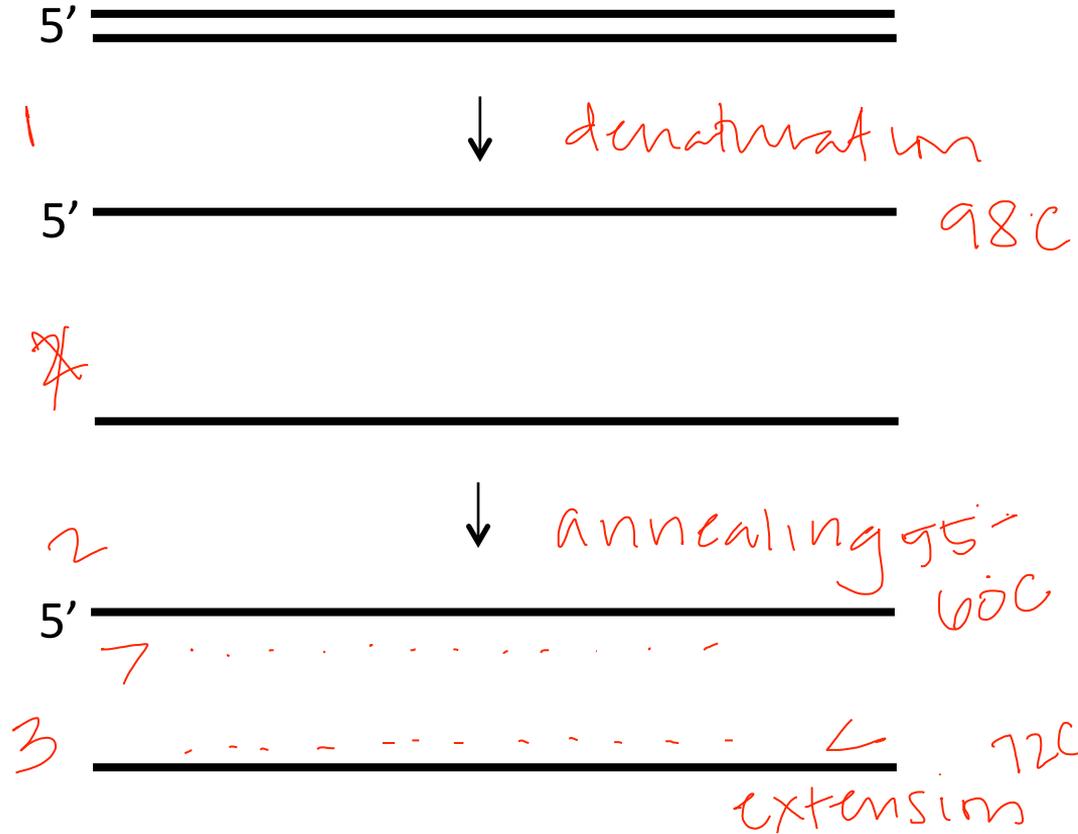
Amplification: DNA polymerase



- Catalyzes formation of polynucleotide chains
- Requires a primer base-paired to template

PCR reagents and conditions

| Reagents |
|------------|
| dNTPs |
| polymerase |
| primers |
| template |
| buffer |
| |
| |



A closer look at primer design

- Length: 17-28 bp

Specificity of binding (to template)

- GC content: 40-60 %

DNA binding efficiency

- T_m : < 65 °C

DNA binding efficiency

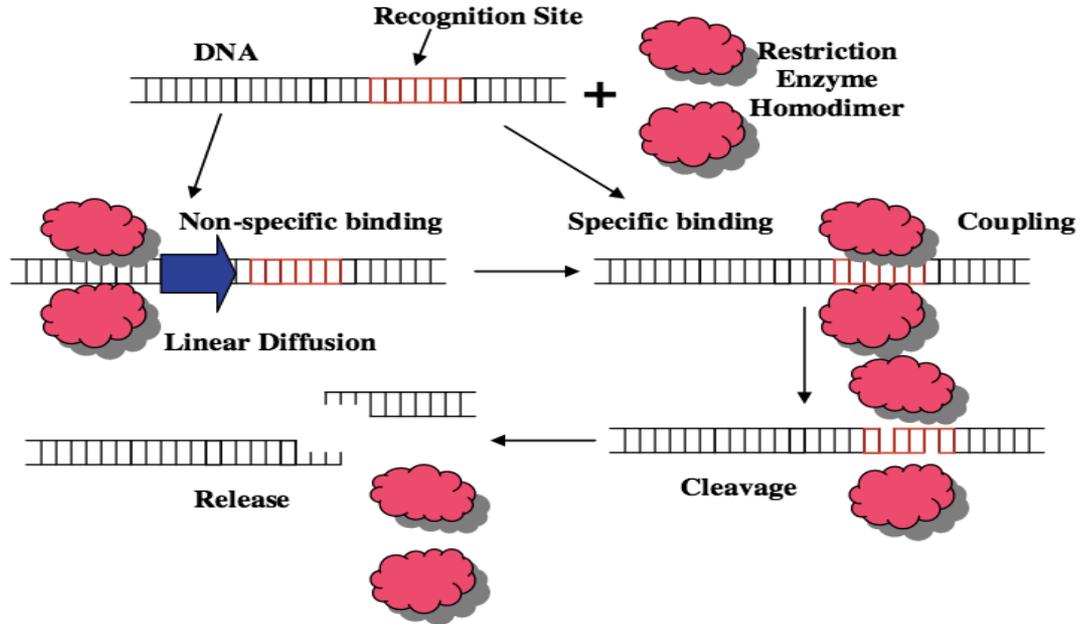
- Avoid secondary structure and repeat sequences

R

ATATATAT

Digestion: restriction enzymes

- Function as homodimers
 - Each dimer cleaves backbone at site of palindromic recognition sequence



Digest reagents and conditions

| Reagents |
|--------------|
| enzyme |
| target (DNA) |
| buffer |
| |
| |
| |
| |
| |

- Temperature

37°C or 25°C

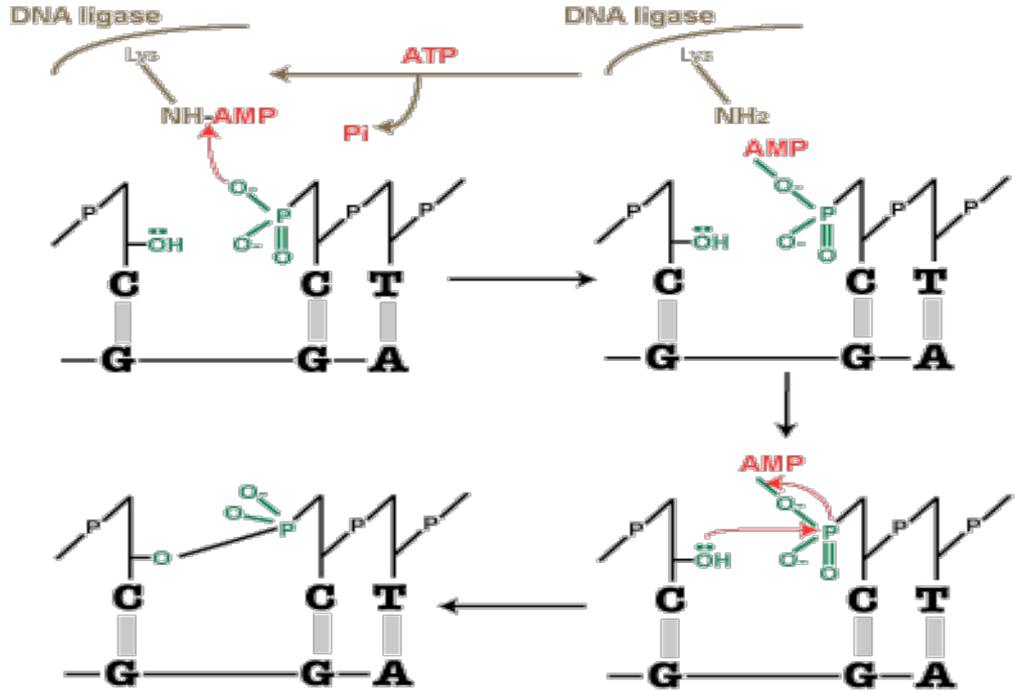
- Time

1 hr - ~~24h~~

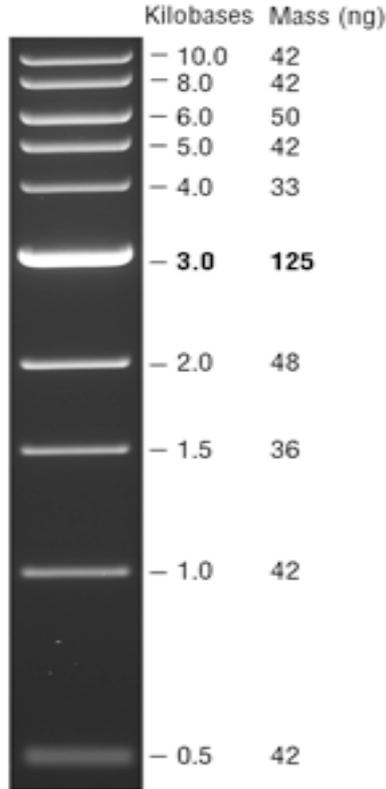
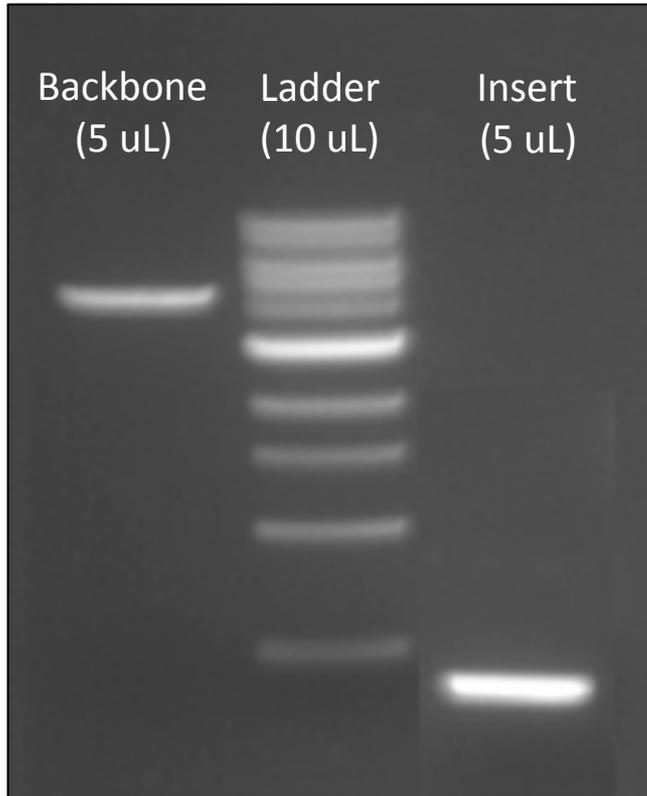
overnight.

Ligation: T4 DNA ligase

- Forms covalent phosphodiester bond between 3' OH acceptor and 5' phosphate donor
- Requires ATP



Ligation conditions



- Ideally, want 4:1 **molar** ratio of insert:backbone
- Calculate molar amounts from concentrations and sizes of DNA molecules

Ligation calculations

1. Determine volume of backbone
 - Use backbone concentration = 40 ng/uL
 - Want 50 – 100 ng
2. Calculate moles of backbone
 - Vector = 5367 bp, MW bp = 660 g/mol
3. Calculate moles of insert
 - Insert = 351 bp, 4:1 ratio of insert:backbone
4. Calculate volume of insert
 - Use insert concentration = 20 ng/uL

How do we confirm the product?

- Transformation

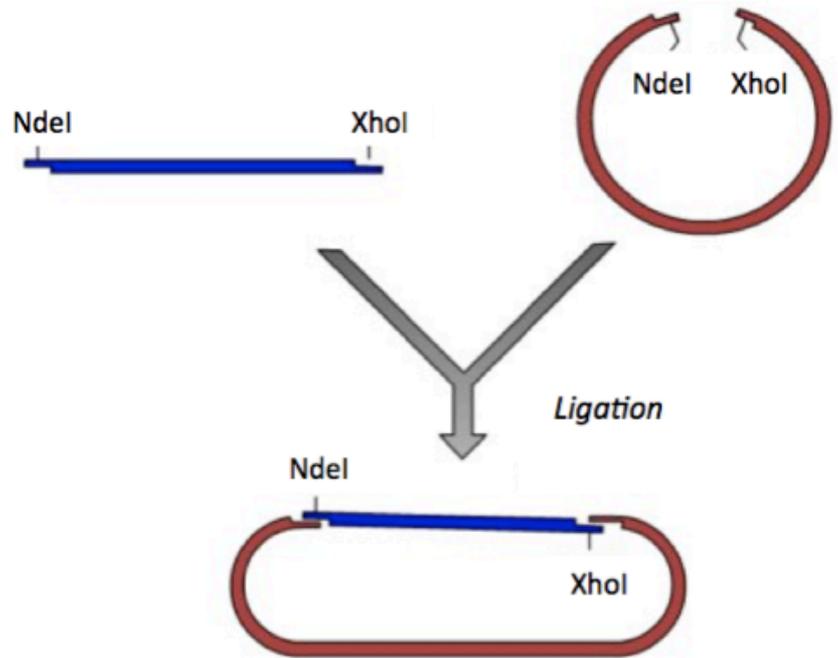
amplify cloning product

- Purification

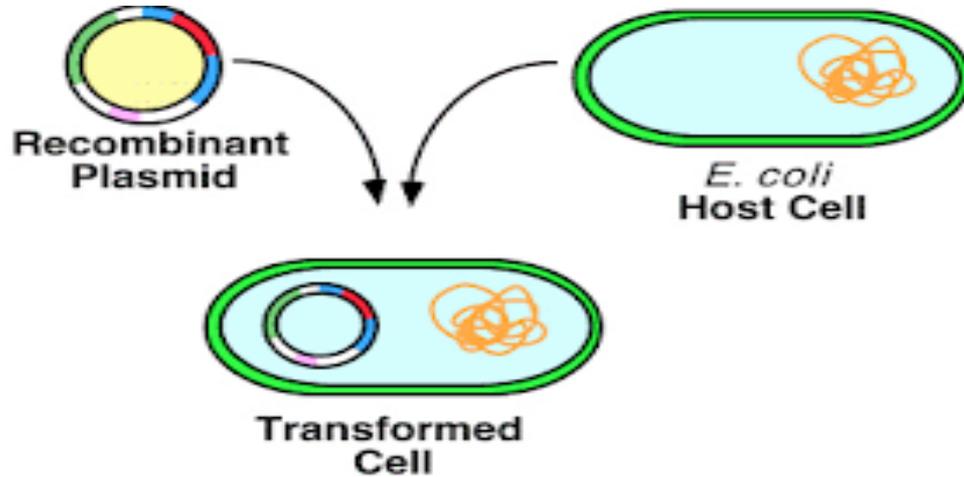
retrieve from bacteria

- ~~•~~ Digestion

check

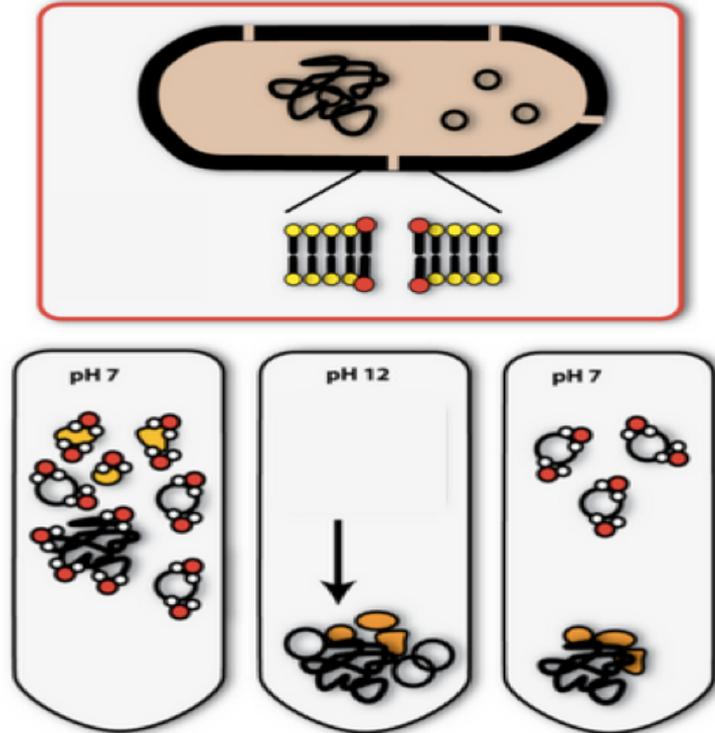


Transformation



1. Incubation
2. Heat shock
 - DNA taken in by competent cells
3. Recovery
4. Selection

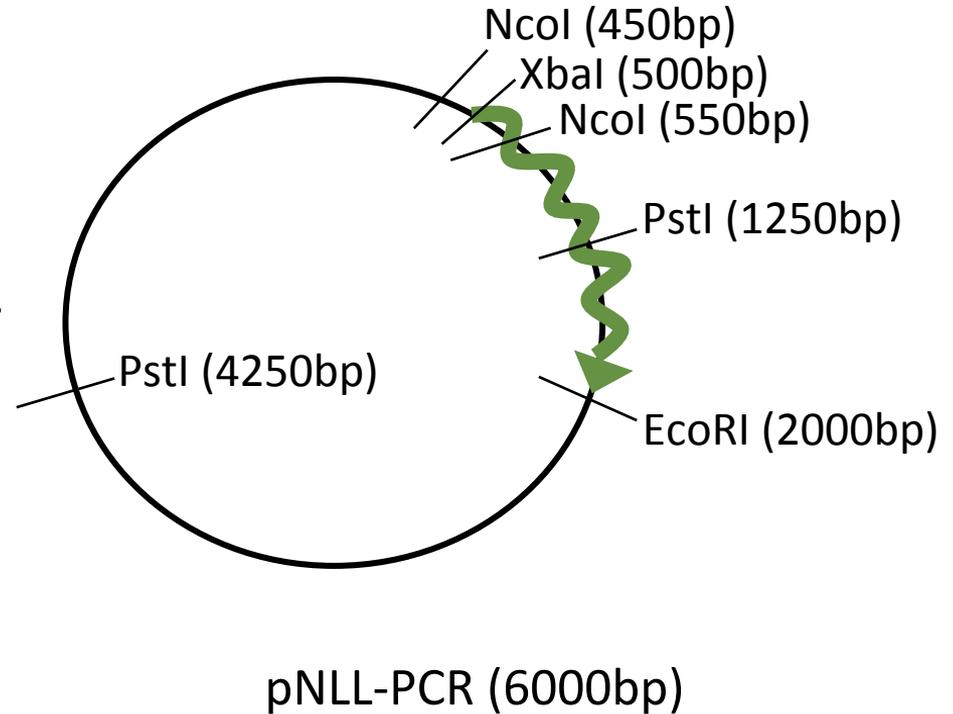
Purification



1. Resuspend cells
2. Lysis
3. Neutralization
 - Separates chromosomal DNA from plasmid DNA
4. Wash
5. Resuspend or elute DNA

Digestion, again

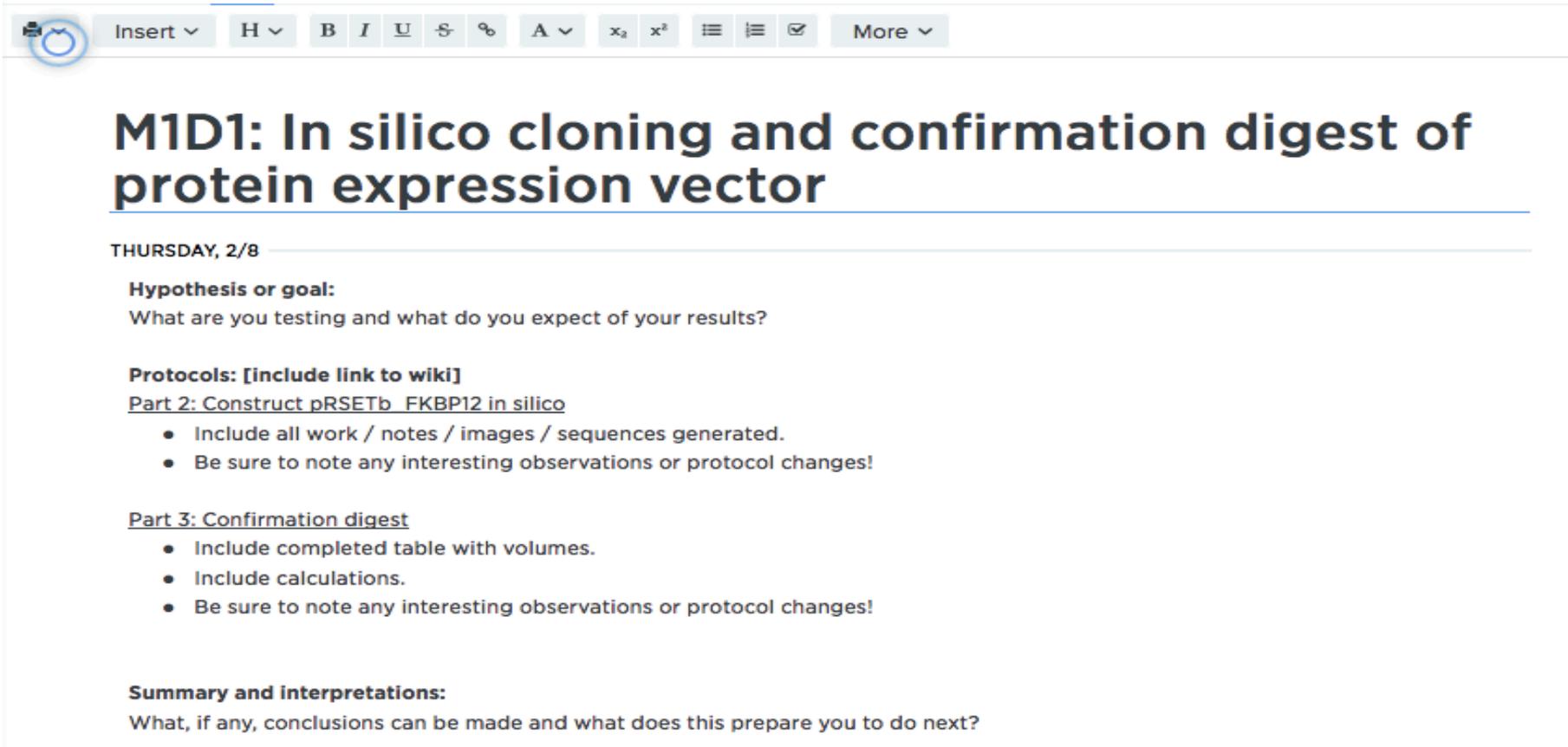
- Confirmation digests
- Ideally, will cut once in insert and once in vector
 - XbaI and EcoRI?
 - PstI?
 - NcoI?



What should go in your notebook?

| Laboratory notebook entry component: | Points: | | |
|--|----------|---------|------------|
| | Complete | Partial | Incomplete |
| Date of experiment (include Module#/Day#) and Title for experiment | 1 | 0.5 | 0 |
| Hypothesis or goal / purpose | 1 | 0.5 | 0 |
| Protocols (link to appropriate wiki sections) | 1 | 0.5 | 0 |
| Notes on protocol changes / clarifications | 1 | 0.5 | 0 |
| Observations | 2 | 1 | 0 |
| *Visual details | | | |
| *Qualitative information | | | |
| *Raw data | | | |
| Data analysis | 3 | 1.5 | 0 |
| *Calculations | | | |
| *Graphs and Tables | | | |
| Summary and interpretation of data | 3 | 1.5 | 0 |
| *What did you learn? | | | |
| *How does this information fit into the larger scope of the project? | | | |
| Information is clear | 2 | 1 | 0 |
| All days represented | 1 | 0.5 | 0 |
| OVERALL /15 | | | |

How should you format your notebook?



The image shows a digital notebook interface with a toolbar at the top containing options like Insert, H, B, I, U, S, A, x₂, x², and More. The main content area displays a notebook page with a title, a date, and several sections of text and bullet points.

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THURSDAY, 2/8

Hypothesis or goal:
What are you testing and what do you expect of your results?

Protocols: [include link to wiki]
Part 2: Construct pRSETb_FKBP12 in silico

- Include all work / notes / images / sequences generated.
- Be sure to note any interesting observations or protocol changes!

Part 3: Confirmation digest

- Include completed table with volumes.
- Include calculations.
- Be sure to note any interesting observations or protocol changes!

Summary and interpretations:
What, if any, conclusions can be made and what does this prepare you to do next?

How should you organize your notebook?

- Entitle your project “20.109(S19)_YourName”
 - Make each module a new folder
 - Make each day a new entry within module folder
- Share the project with Noreen and Michaela
 - Right-click and choose ‘settings’
 - Add collaborators by email

For today...

- Virtual cloning exercise to build pET21_FKBP12 expression plasmid
- Confirmation digest of pET21_FKBP12

For M1D2...

- Prepare a template for Benchling entries
- Complete in class exercises