

M1D1: Complete in silico cloning and induce TDP43 protein expression

1. Laboratory Orientation quiz
2. Prelab discussion
3. Build protein expression vector – *in silico*
4. Confirm protein expression vector – in lab

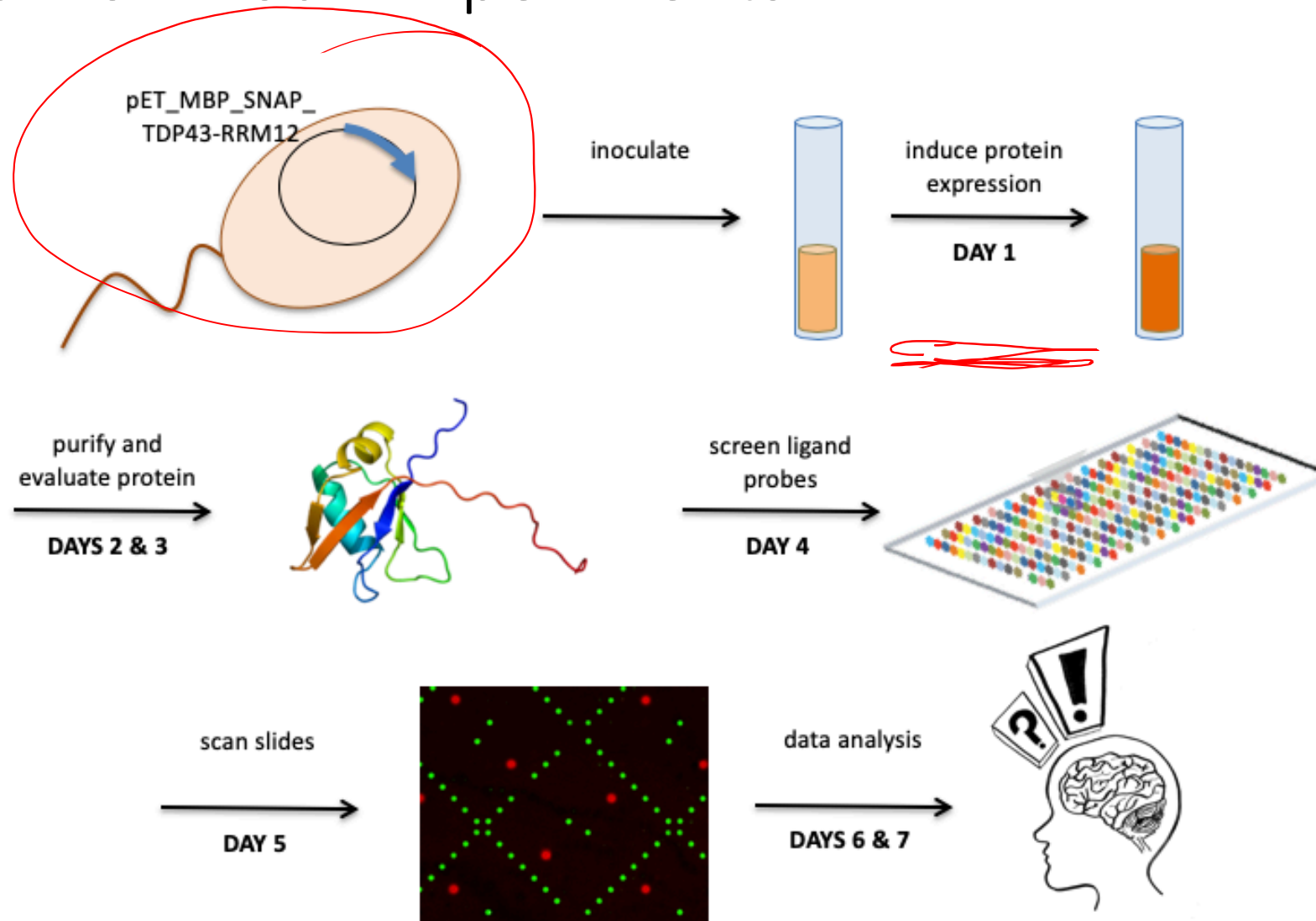


# Important Dates for Mod 1!

- **Data summary** (15%)
  - completed in teams and submitted via Stellar
  - draft due 3/8, final revision due 3/22
  - format in bullet points
- **Mini-presentation** (5%)
  - completed individually and submitted via Gmail
  - due 3/15
- **Laboratory quizzes**
  - scheduled for M1D4 and M1D7
- **Notebook** (part of 10% Homework and Notebook)
  - one entry will be graded by Joe 24 hr after M1D7
- **Blog** (part of 5% Participation)
  - due 3/16 via Blogspot

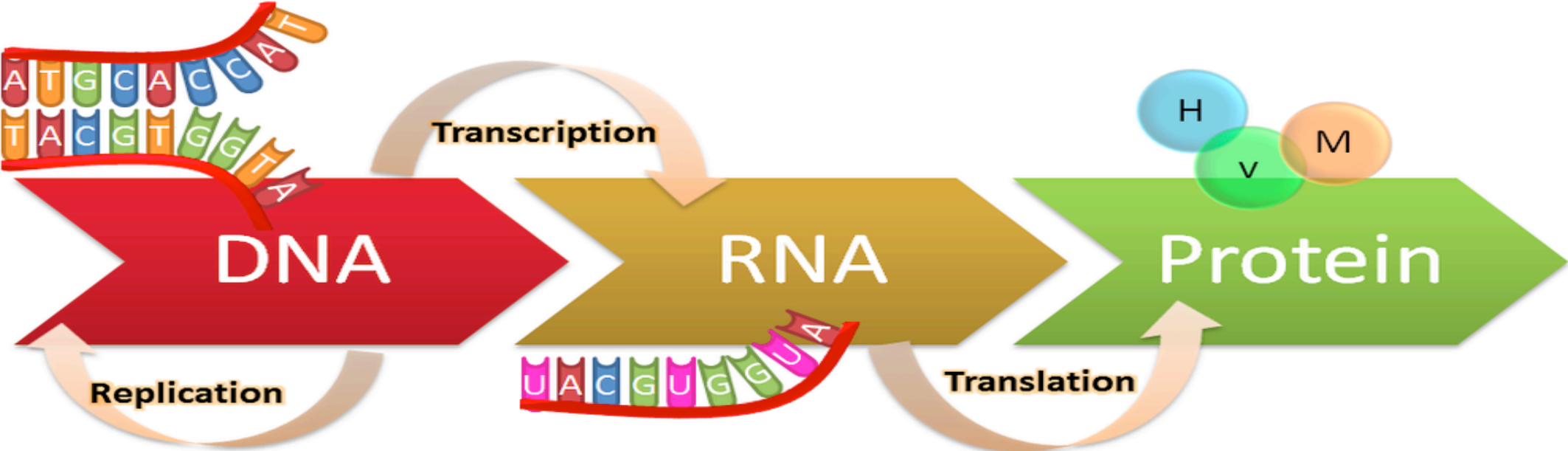


# Overview of Mod1 Experiments



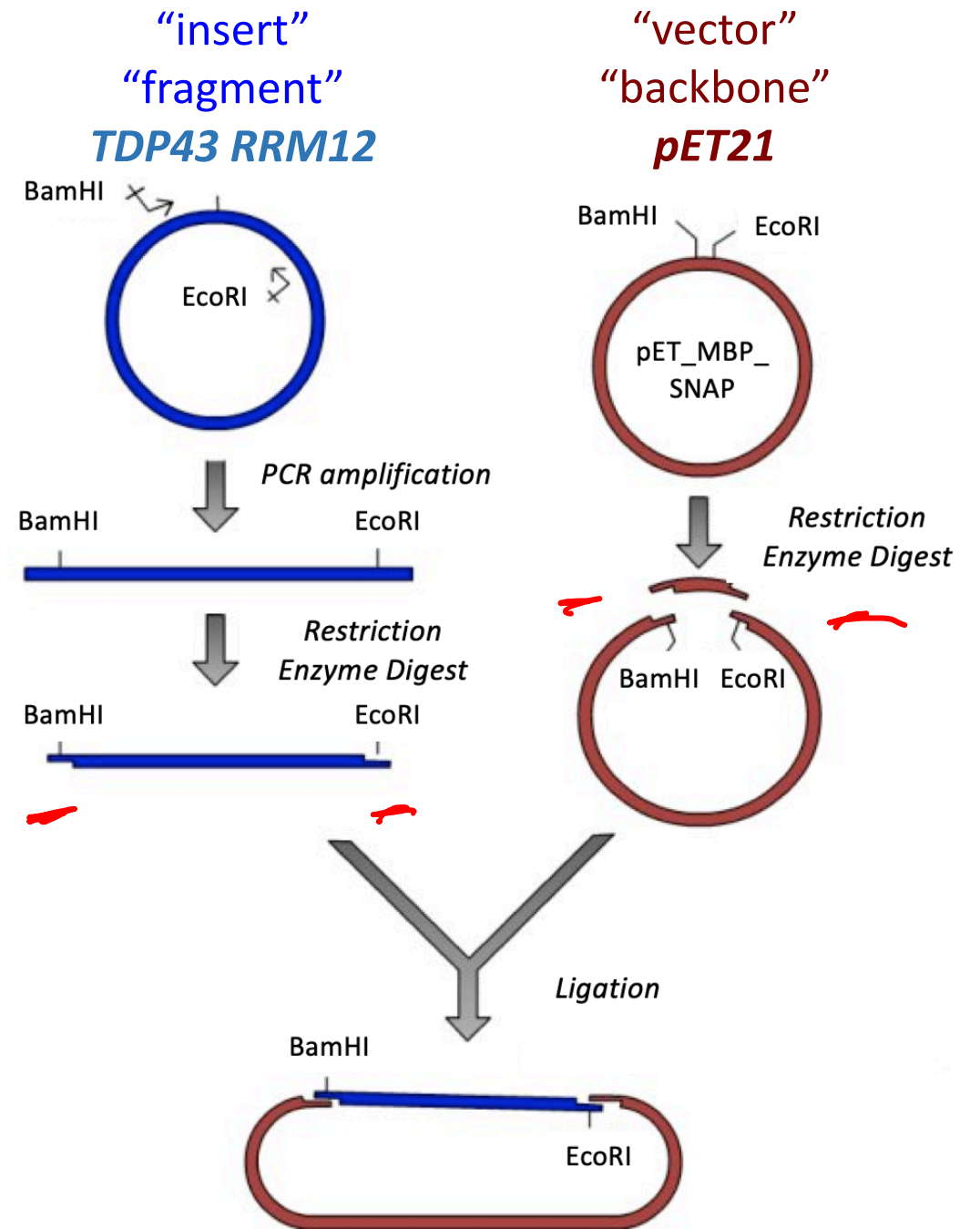
How are proteins made?

### The Central Dogma

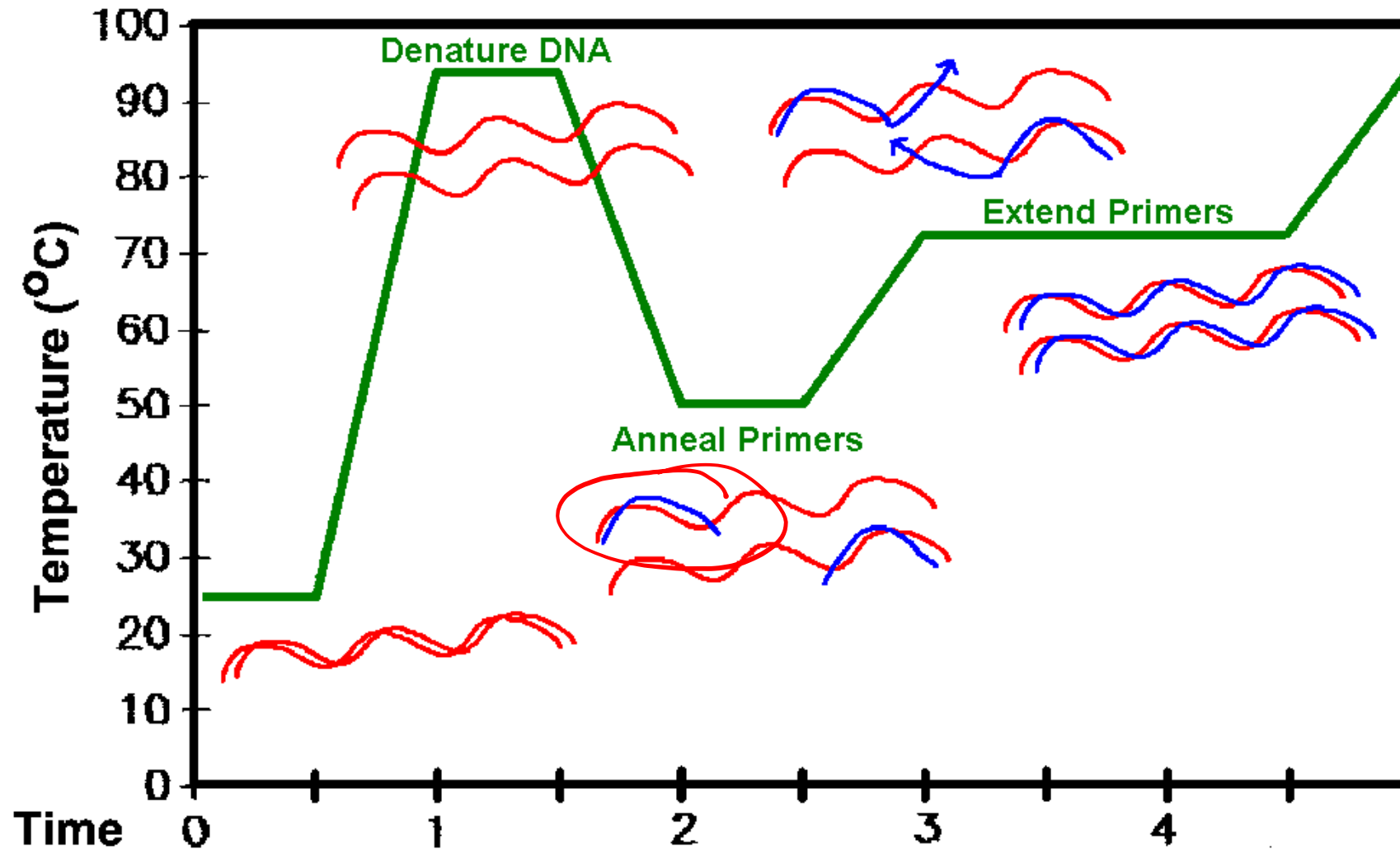


# What if we want a specific protein?

- Amplification
- Digestion
- Ligation

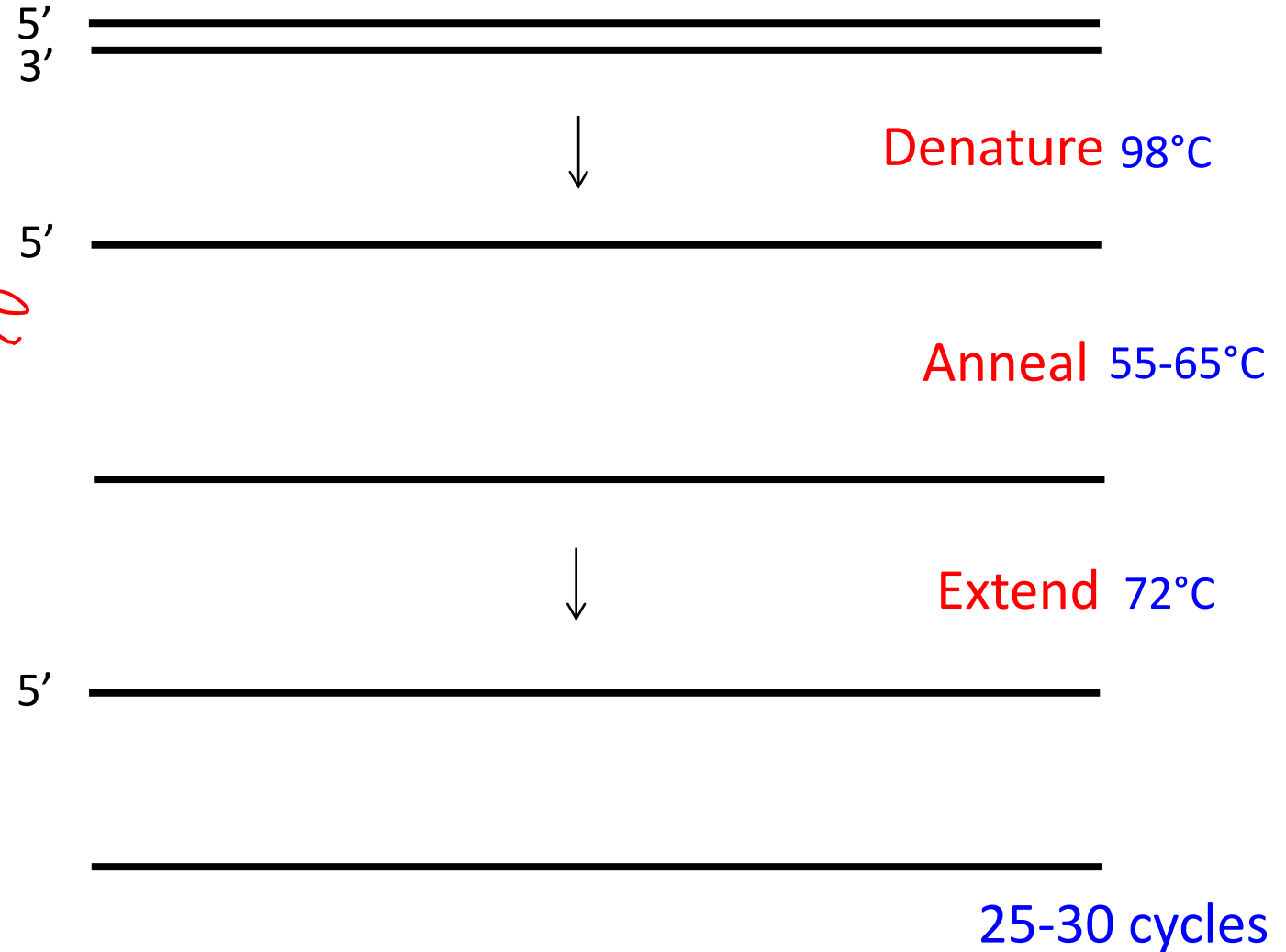


# Amplification: PCR cycling



# 1) Amplification– PCR reagents and conditions

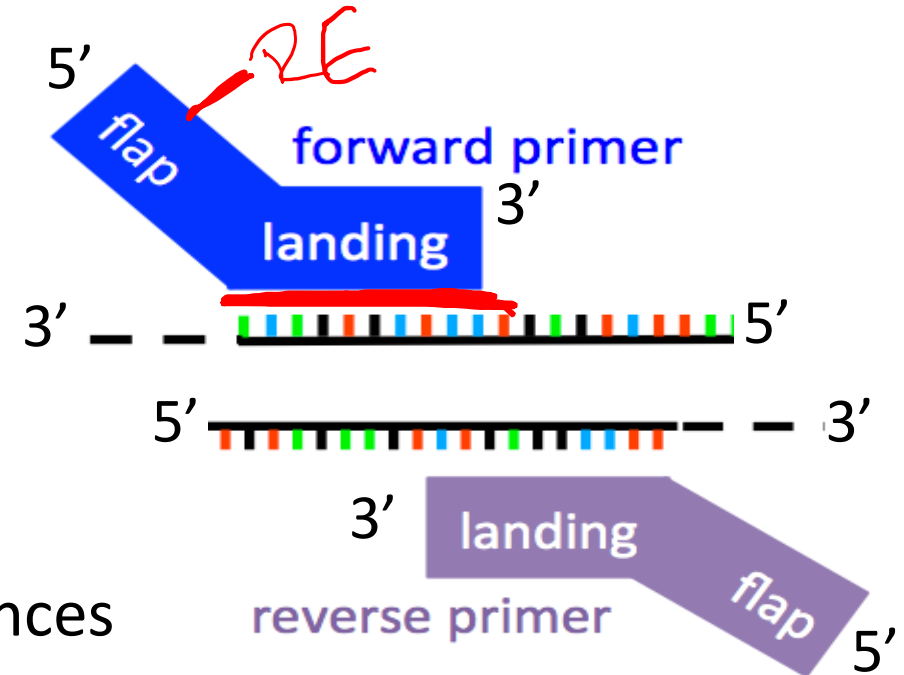
Reagents
Primers
DNA Template
<del>DNB</del> dNTPS
DNA polymerase
Buffer ( $Mg^{2+}$ )



# 1) Amplification—Guidelines for primer design

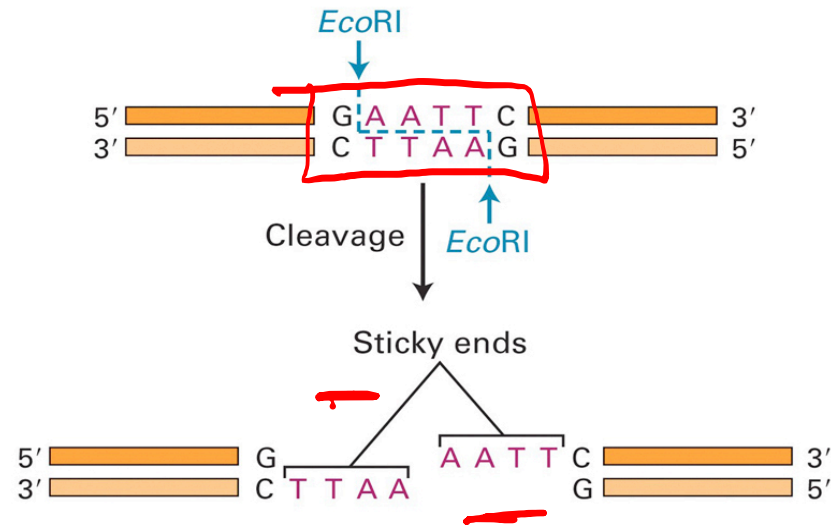
- **Landing sequence:** match to TDP43 gene, RRM12 region
- **Flap sequence:** endonuclease recognition sequence, junk DNA

- Length (landing sequence): 17-28 bp
- GC content: 40-60 %
- Melting temp of primer : < 65 °C
- Avoid secondary structure and repeat sequences  
(e.g. hairpins, primer dimers, ATATAT)

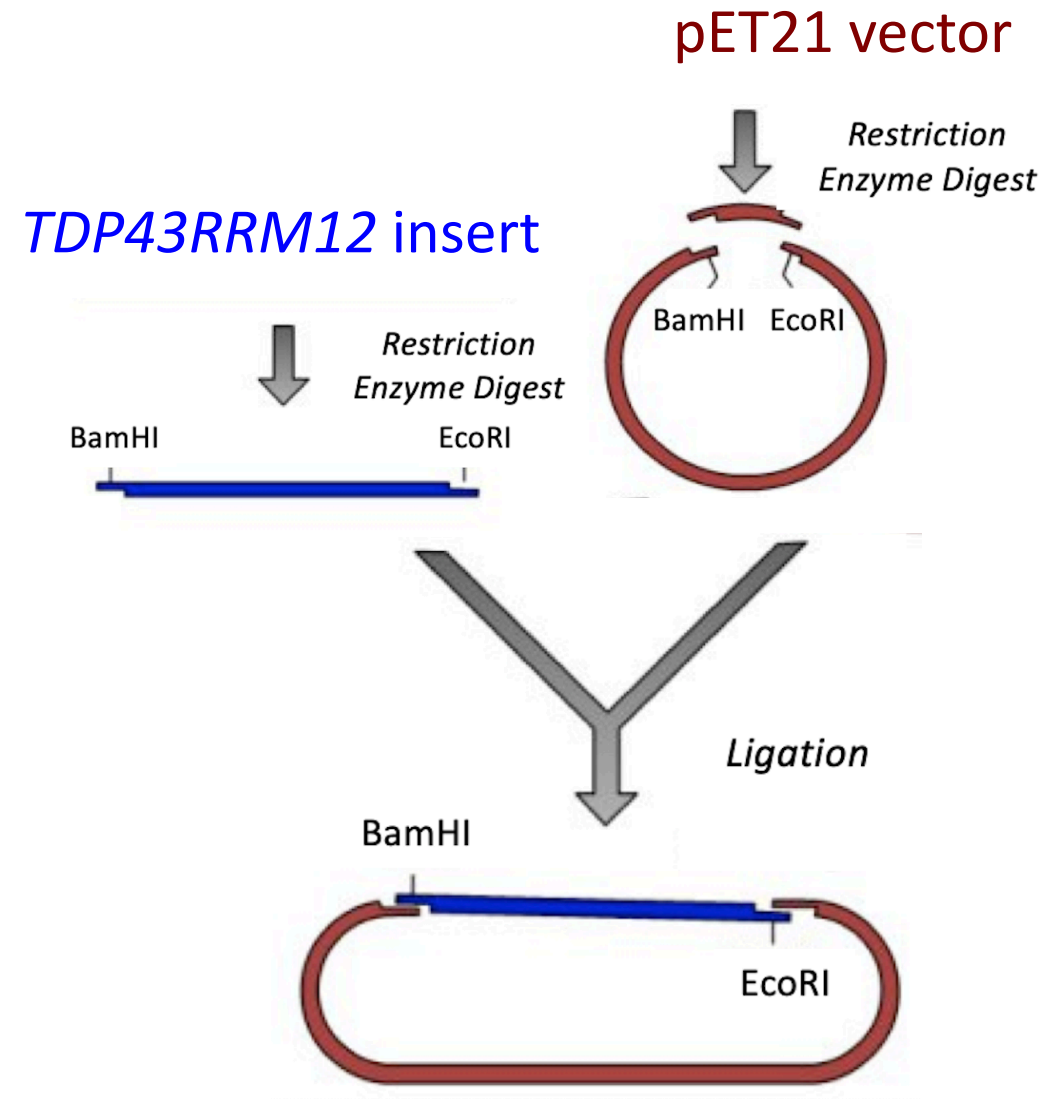
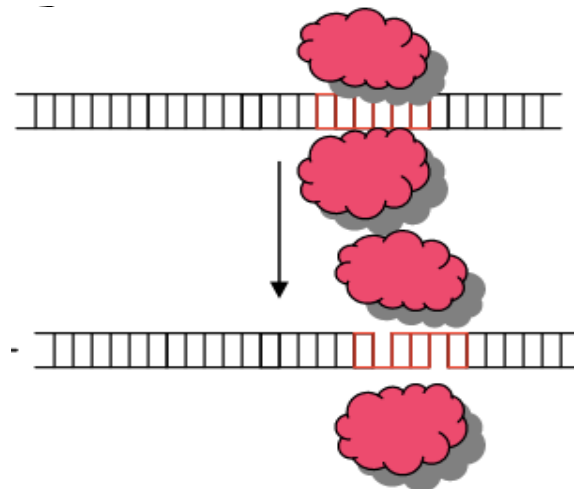




## 2) Digestion—Create compatible ends on insert fragment and backbone



- many restriction enzymes function as homodimers
- binds palindromic sequences
- cleaves backbone



## 2) Digestion– Reagents and conditions

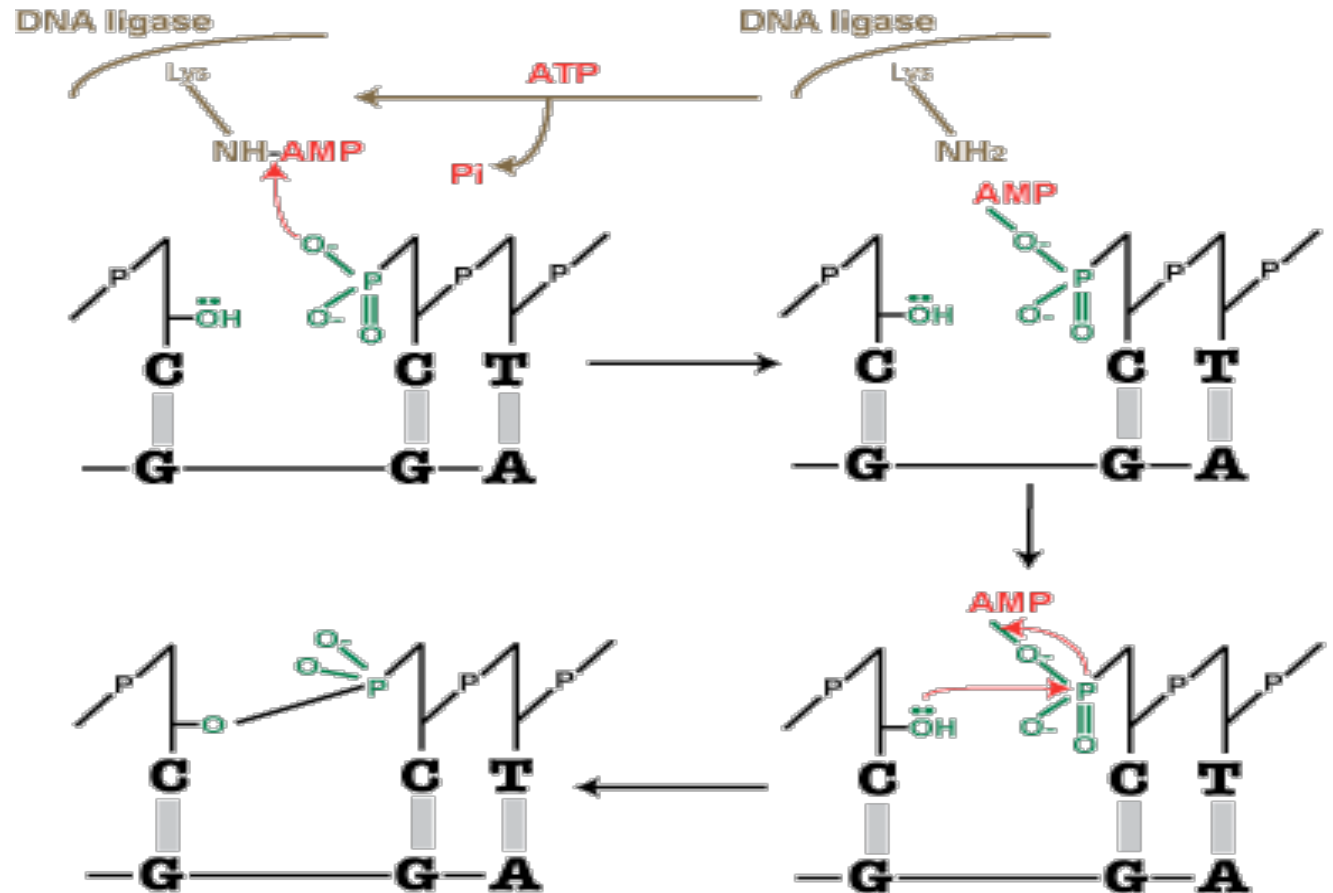
Reagents
RES
Buffer (ATP)
DNA

- Temperature

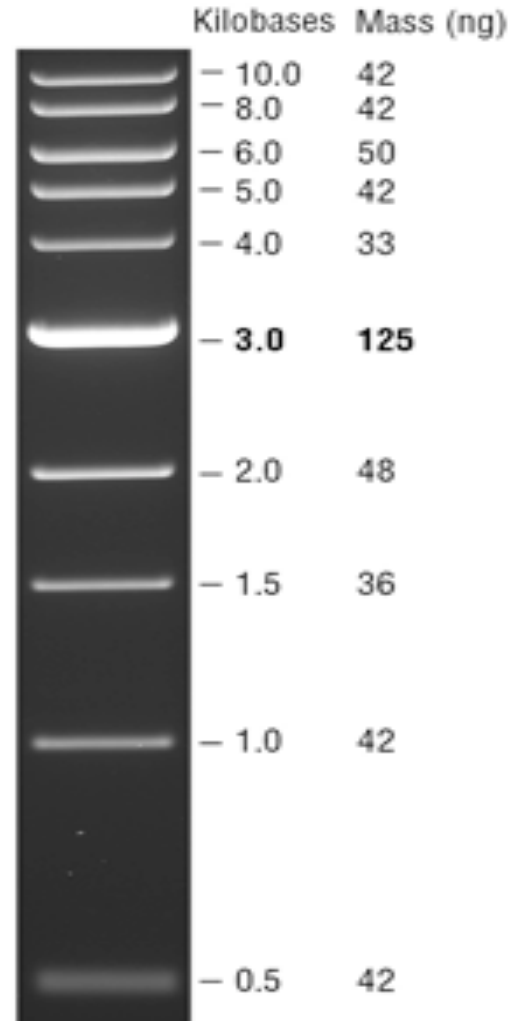
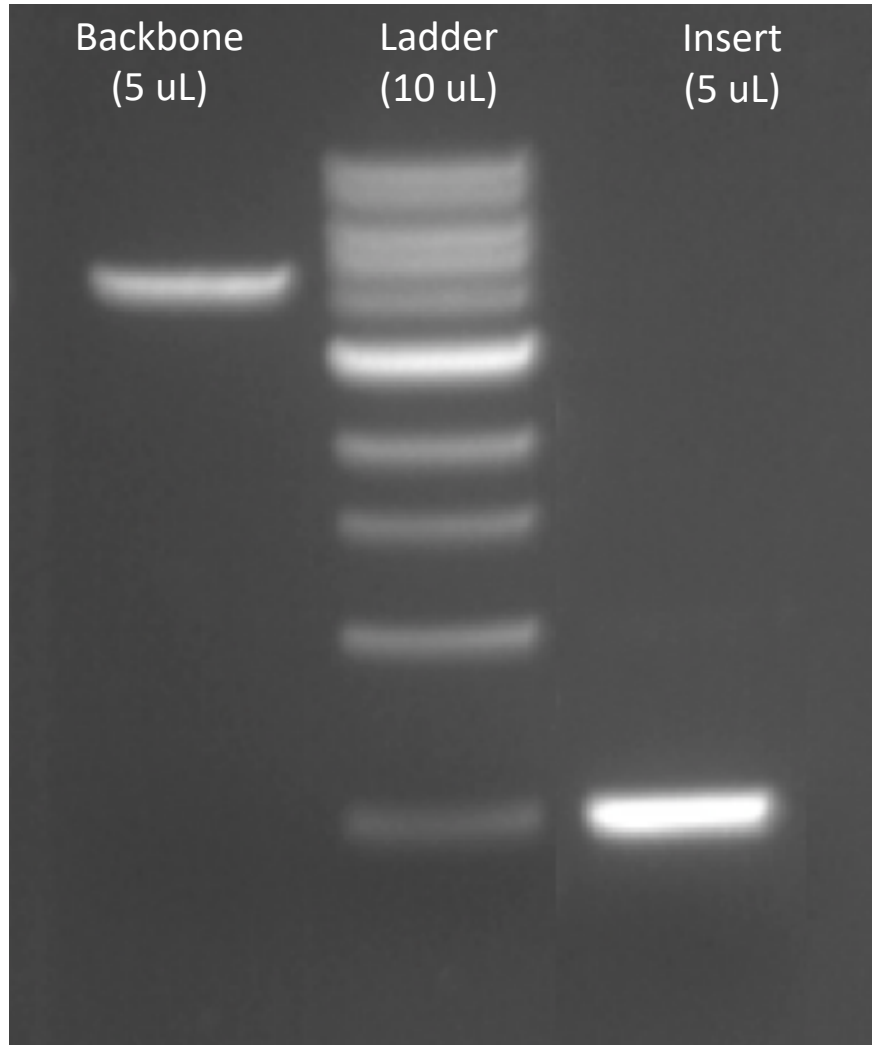
- Time

### 3) Ligation: T4 DNA ligase

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



# 3) 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 = 50 ng/uL
  - Want 50 – 100 ng
2. Calculate moles of backbone
  - Vector = 6837 bp, MW bp = 660 g/mol
3. Calculate moles of insert
  - Insert = 527 bp, **3:1 ratio** of insert:backbone
4. Calculate volume of insert
  - Use insert concentration = 20 ng/uL

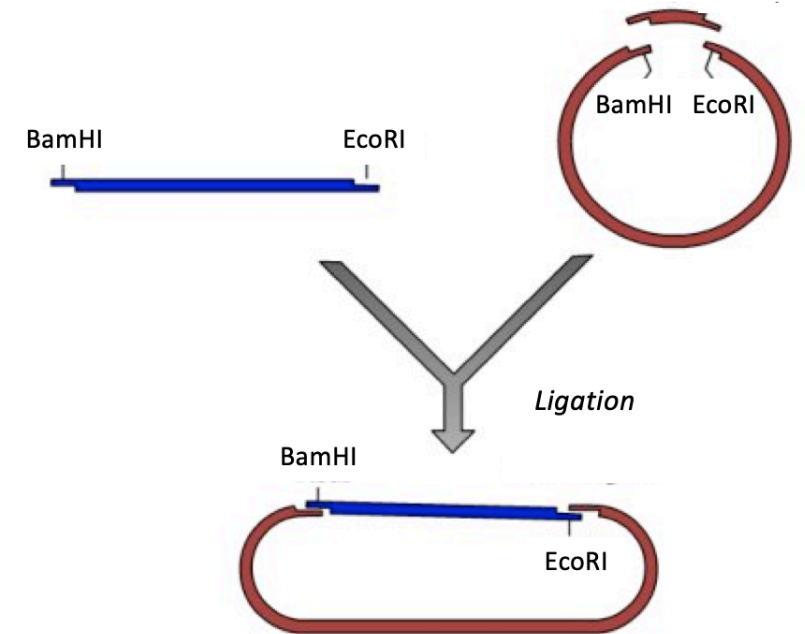
# How do we confirm successful ligations/ DNA plasmid production?

Method 1:

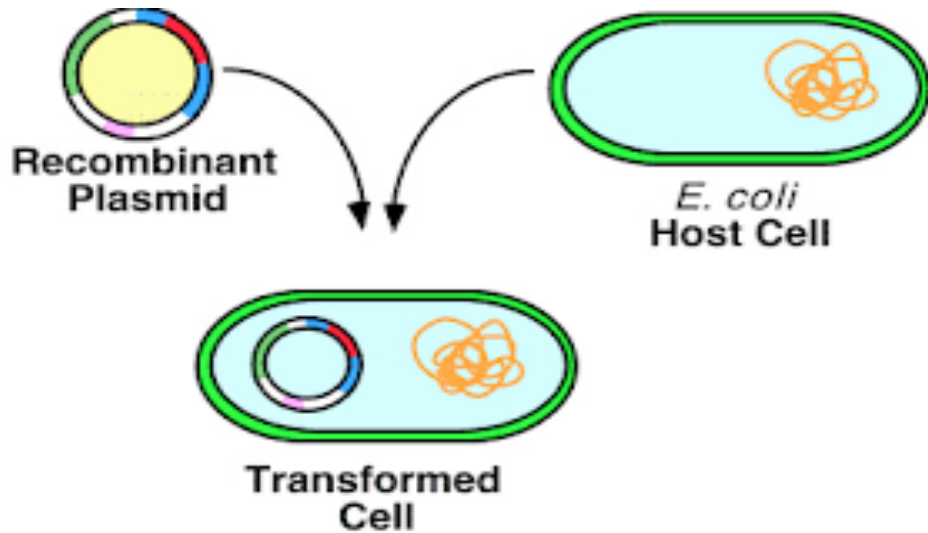
*Sequencing*

Method 2: Diagnostic Digest

- Amplify plasmid
  - Transform into bacteria
- Purification
  - Separate plasmid from chromosomal DNA
- Digestion
  - Confirm the plasmid contains expected fragments



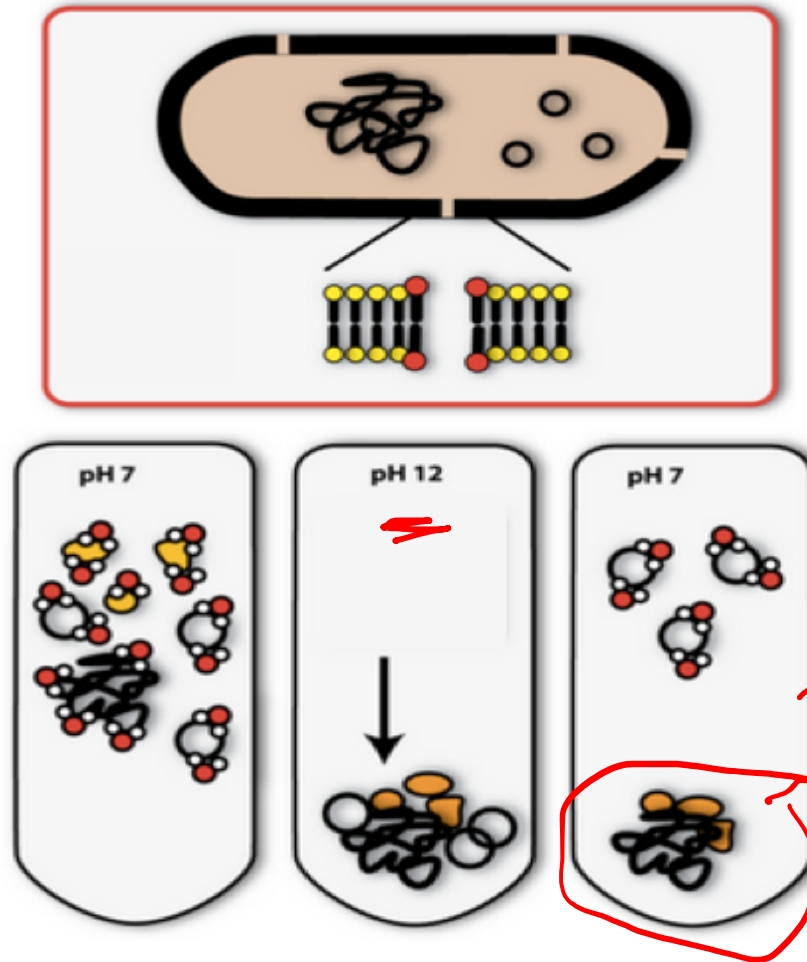
# Diagnostic Digest: Transformation to amplify DNA plasmid



1. Incubation of bacteria and DNA plasmid
2. Heat shock (or electroporation)  
-- DNA taken in by competent cells
3. Recovery at 37C
4. Selection for bacteria that have taken up the plasmid

# Diagnostic digest: DNA Purification

**AKA: the mini-prep**



1. Resuspend cells

2. Lysis

3. Neutralization

- Separates chromosomal DNA from plasmid DNA

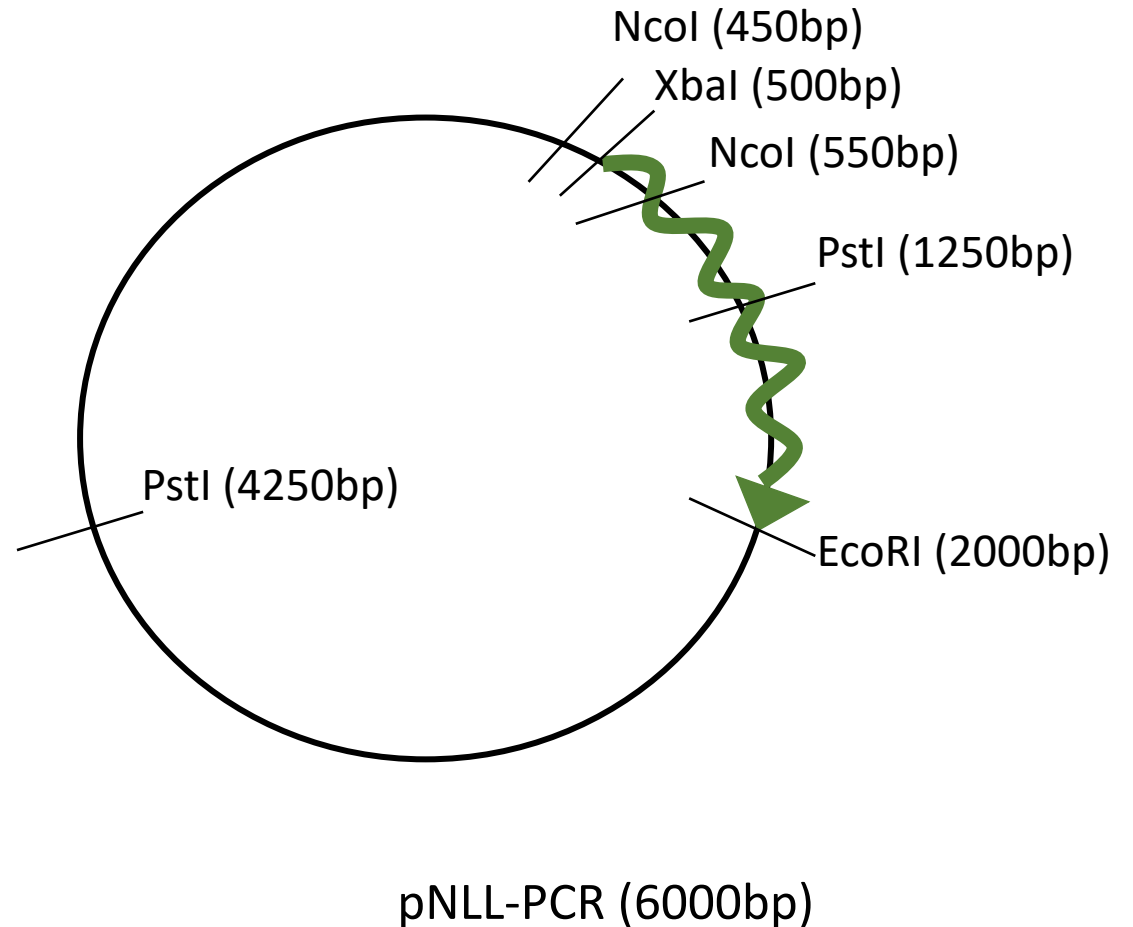
4. Wash

5. Resuspend or elute DNA



# Diagnostic Digest: 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?

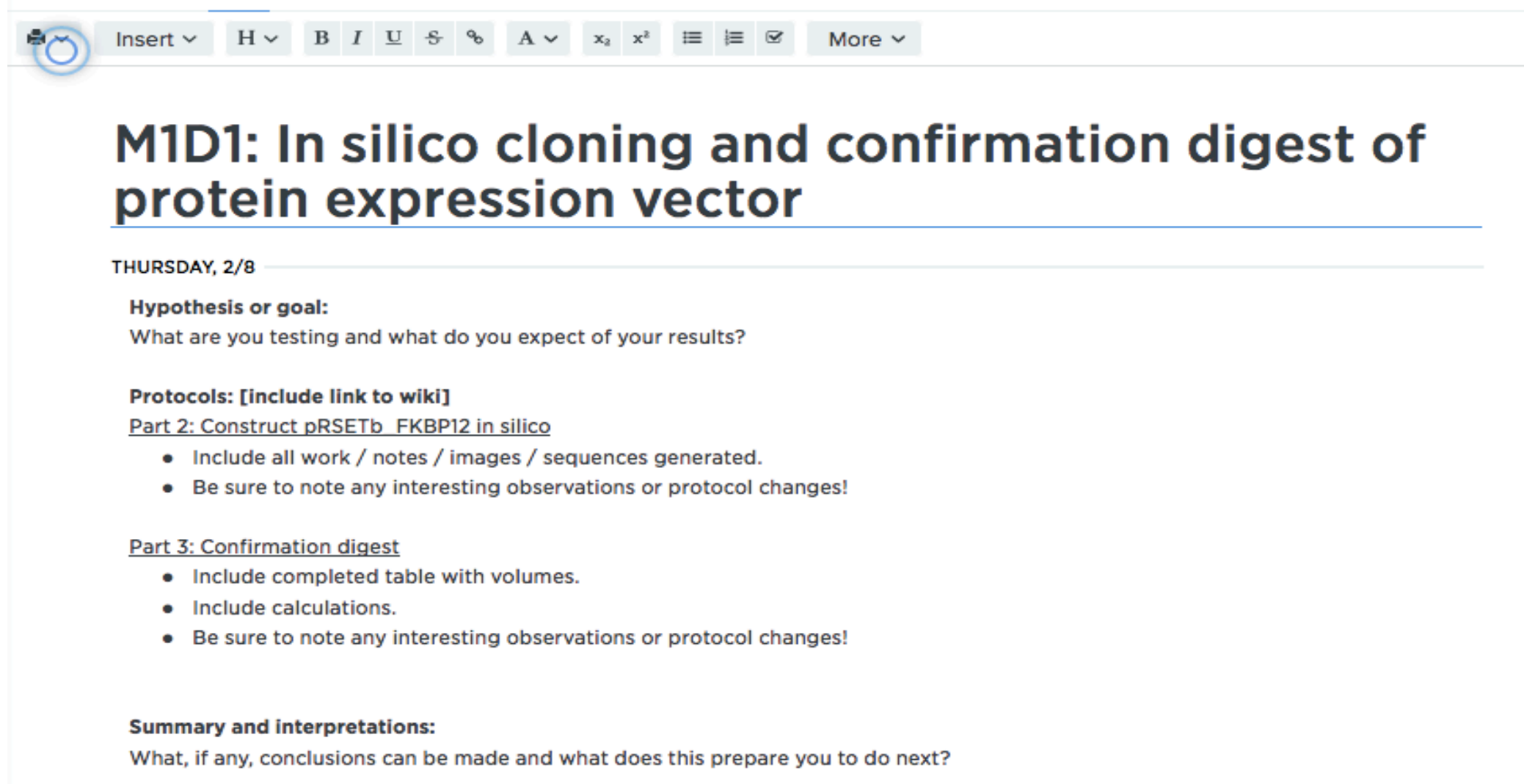
## Laboratory notebook entry component:

## 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 screenshot shows a notebook interface with a toolbar at the top containing icons for insert, heading, bold, italic, underline, strikethrough, link, text color, background color, list, and more options. The main content area is titled "M1D1: In silico cloning and confirmation digest of protein expression vector" and is dated "THURSDAY, 2/8". The notebook content is organized into several sections:

**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(S20)\_YourName”
  - Make each module a new folder
  - Make each day a new entry within module folder

- Share the project with:

**Becky (rcmeyer@mit.edu) and Joe (jkreitz@mit.edu)**

- Right-click and choose ‘settings’
- Add collaborators by email

## For today...

- Virtual cloning exercise to build pET\_MBP\_SNAP\_TDP43-RRM12 expression plasmid
- Confirmation digest of pET\_MBP\_SNAP\_TDP43-RRM12

## For M1D2...

- Prepare a template for Benchling entries
- Complete in class exercises (ligation calculation, etc)