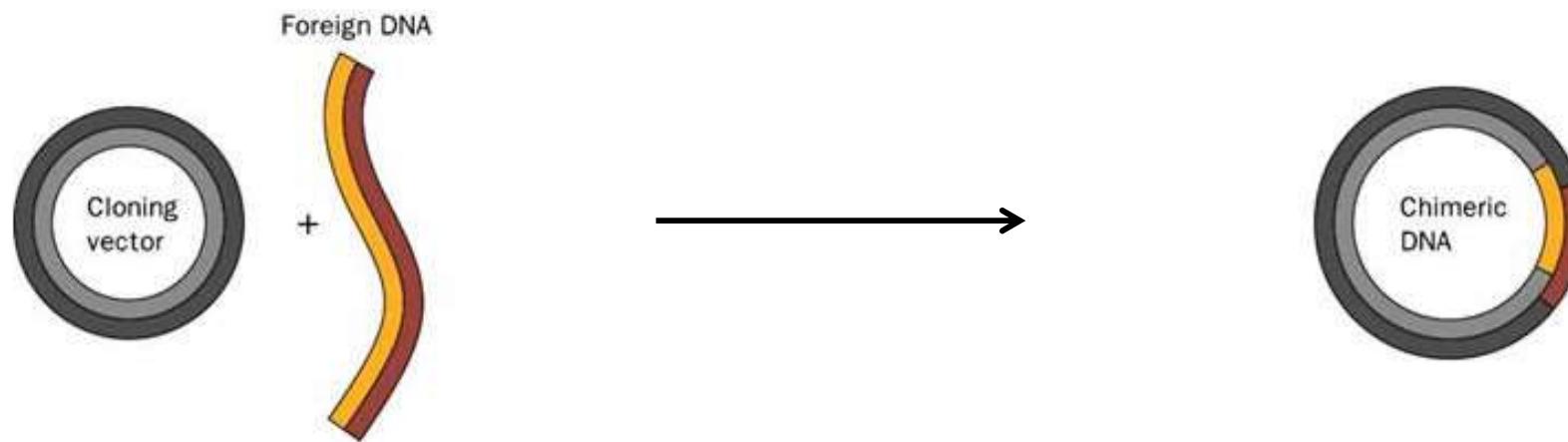


Molecular Cloning for Biological Expression Design

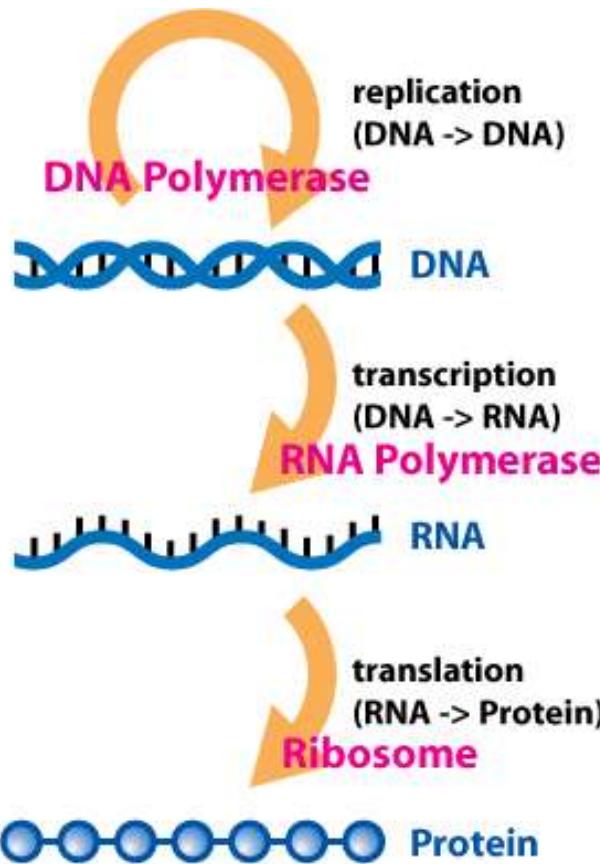
UE2.1 Biological Parts and Devices



Manish Kushwaha

4 October, 2024

Central Dogma: Relevance for Expression Design



- Gene/s of interest (Coding sequence)
- Antibiotic Selection Marker

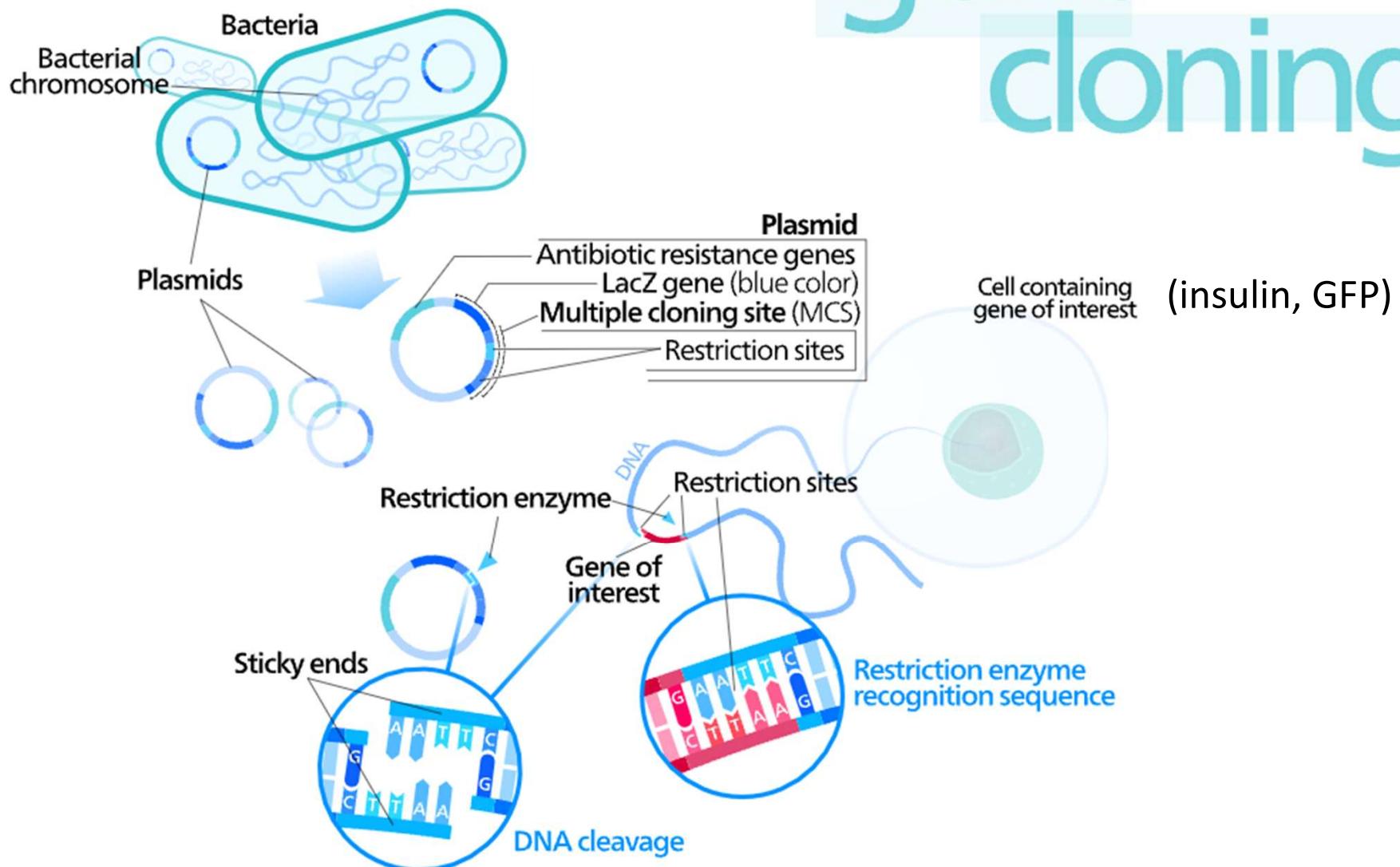
- Replication Origin
 - Copy Number
 - Relaxed/ Stringent control
- Promoter
 - Constitutive
 - Inducible
- Terminator
 - Intrinsic
 - Rho-dependent
- Ribosome Binding Site (RBS)
- Kozak Sequence
- IRES

Image source:

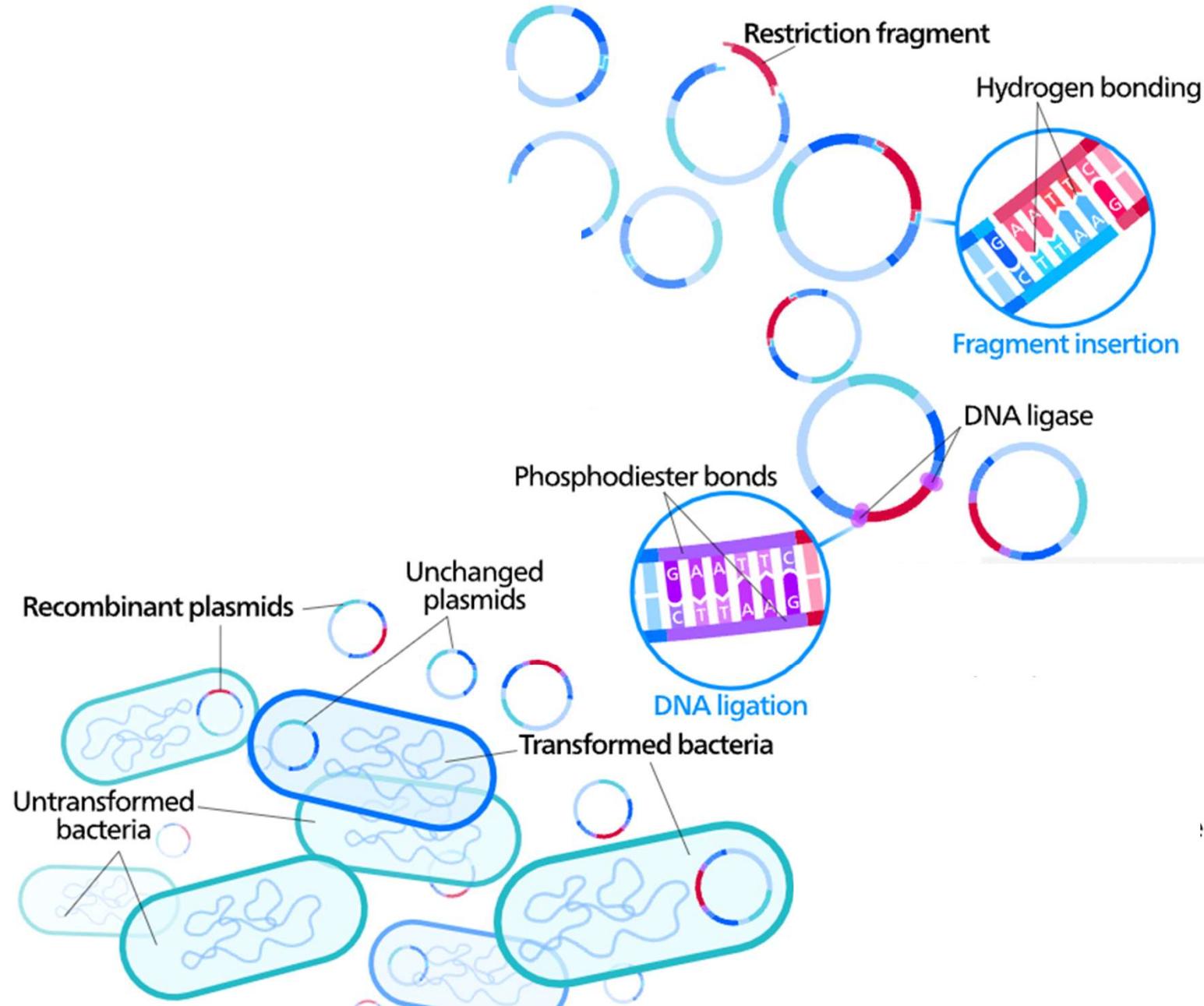
https://en.wikipedia.org/wiki/Central_dogma_of_molecular_biology

Molecular Cloning: Overview

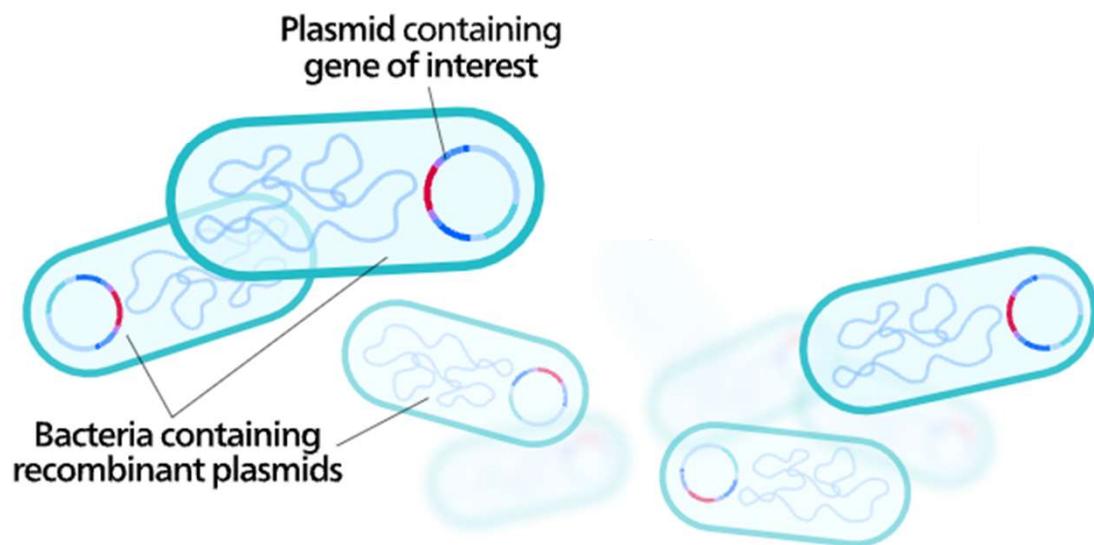
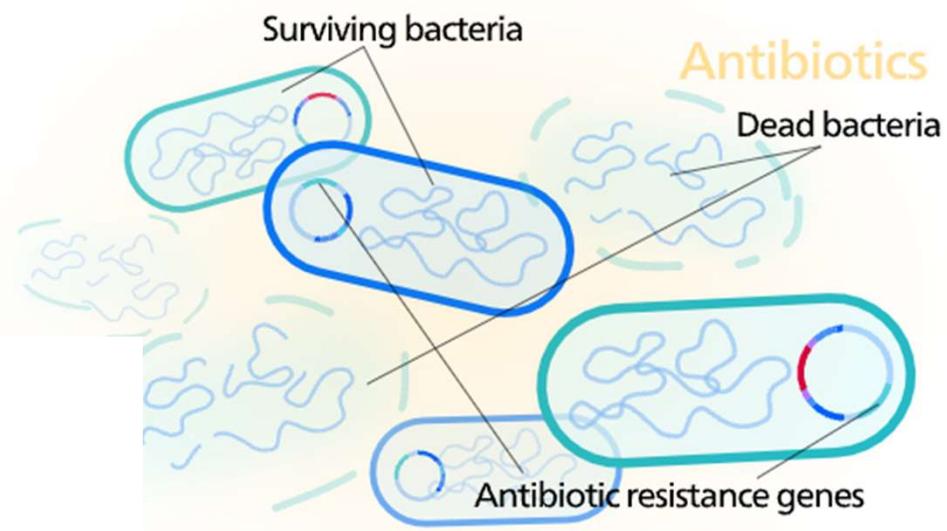
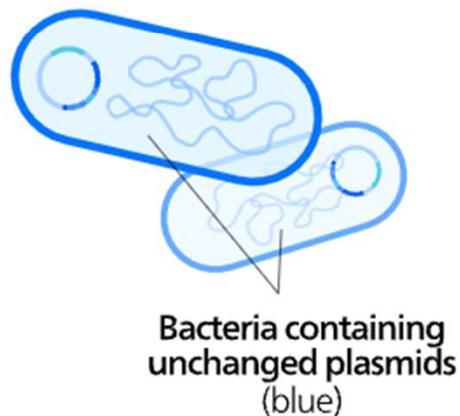
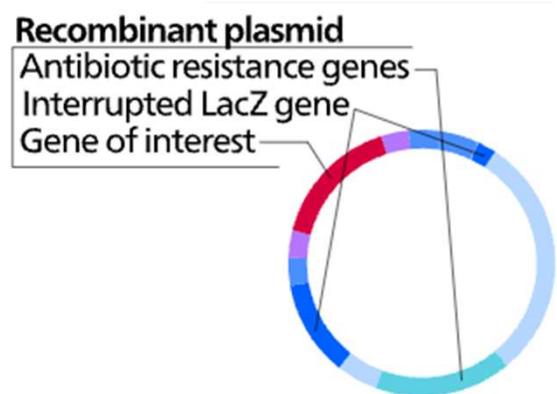
gene
cloning



Molecular Cloning: Overview



Molecular Cloning: Overview



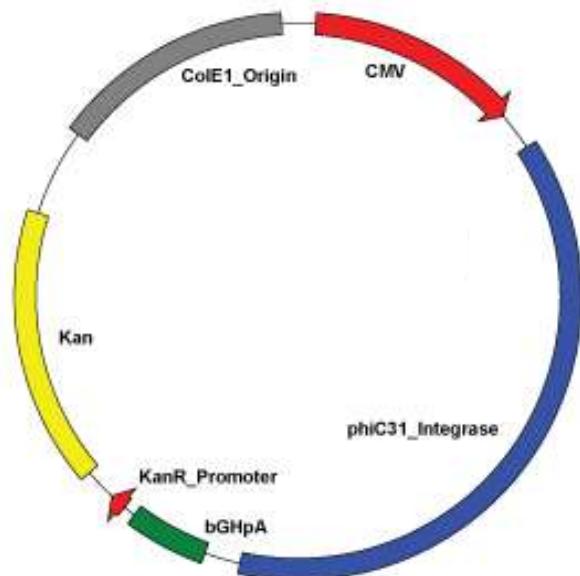
Molecular Cloning: the Plasmid Vector

Plasmid Vectors

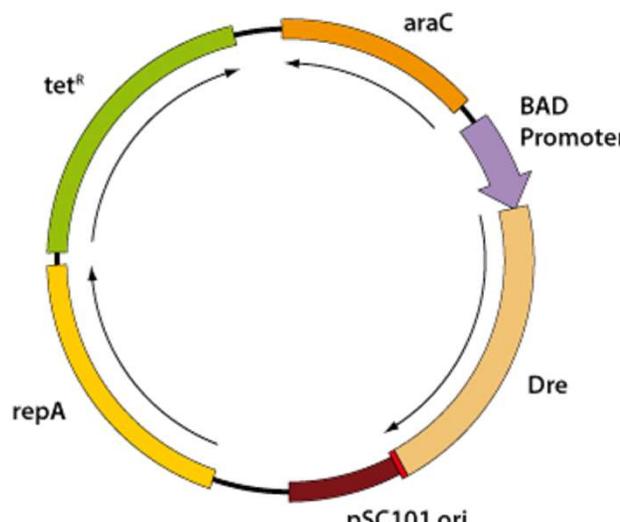
Plasmids must have two required signals:

1. An **origin of replication** to use the host's DNA replication machinery for self-maintenance.
2. An **antibiotic selection marker** to provide a selective advantage to the cells that contain the plasmid.

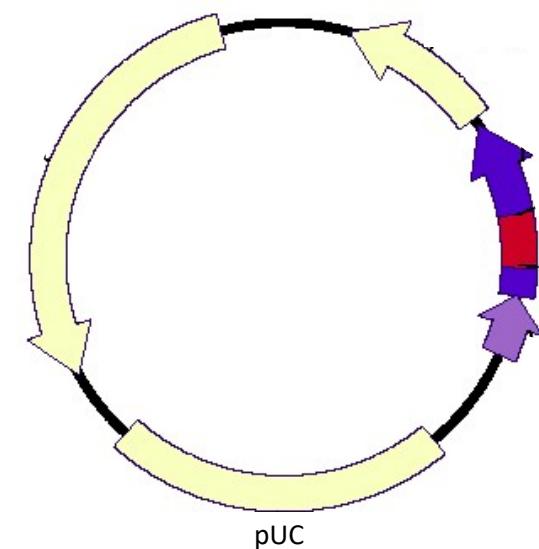
1. ColE1 origin, 40-60 copies
2. Kanamycin resistance



1. pSC101 origin, ~5 copies
2. Tetracycline resistance



1. pUC origin, ~200 copies
2. Ampicillin resistance

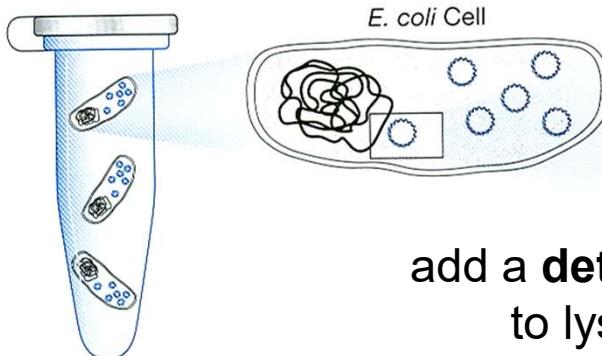


Molecular Cloning: DNA purification

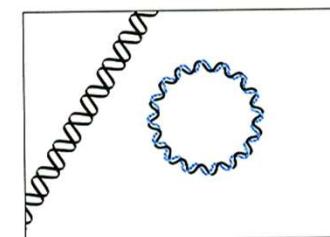
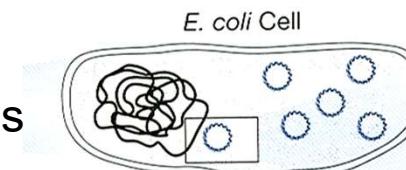
*Once your microbial cells have a plasmid, **they amplify it.***

DNA Extraction

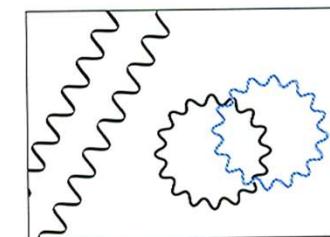
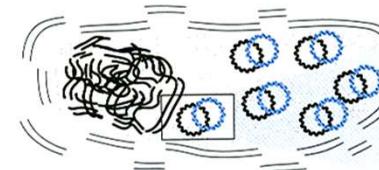
- DNA is very hydrophilic, and can be separated & purified using silica columns.
- Standard protocols are available for purifying small DNA molecules (e.g. plasmids) and large DNA molecules (whole chromosomes).



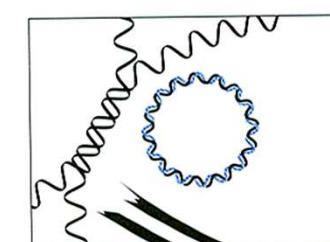
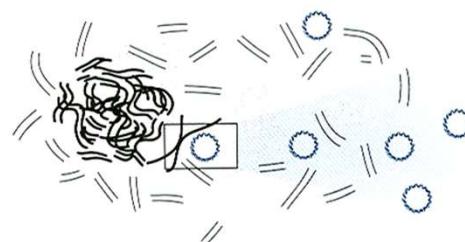
centrifuge
to pellet your cells



add a **detergent + strong base**
to lyse open your cells
and denature the DNA



add a **weak acid** to neutralize
The plasmid DNA re-anneals quickly,
but not the chromosomal DNA
(too big for quick reannealing!)

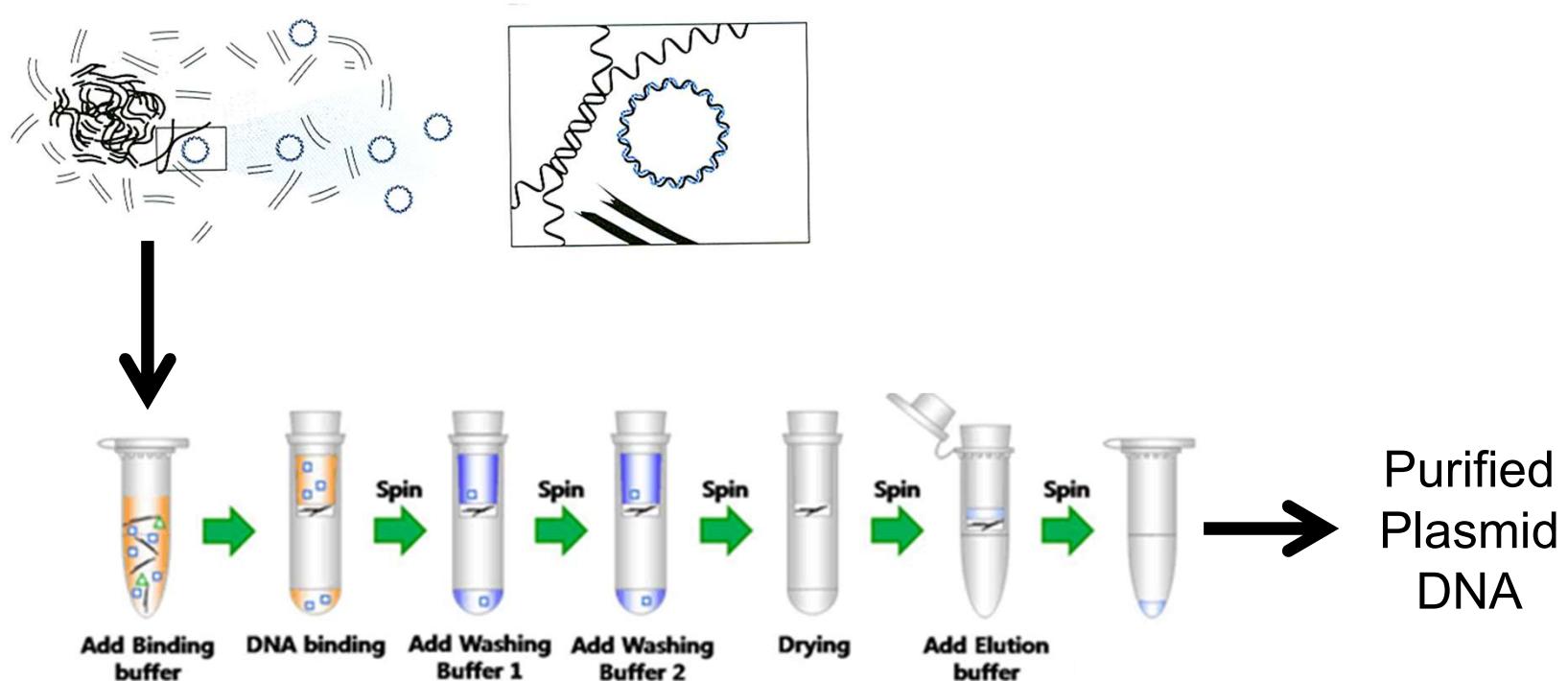


Molecular Cloning: DNA purification

From your amplified microbial cells, you can purify the plasmid.

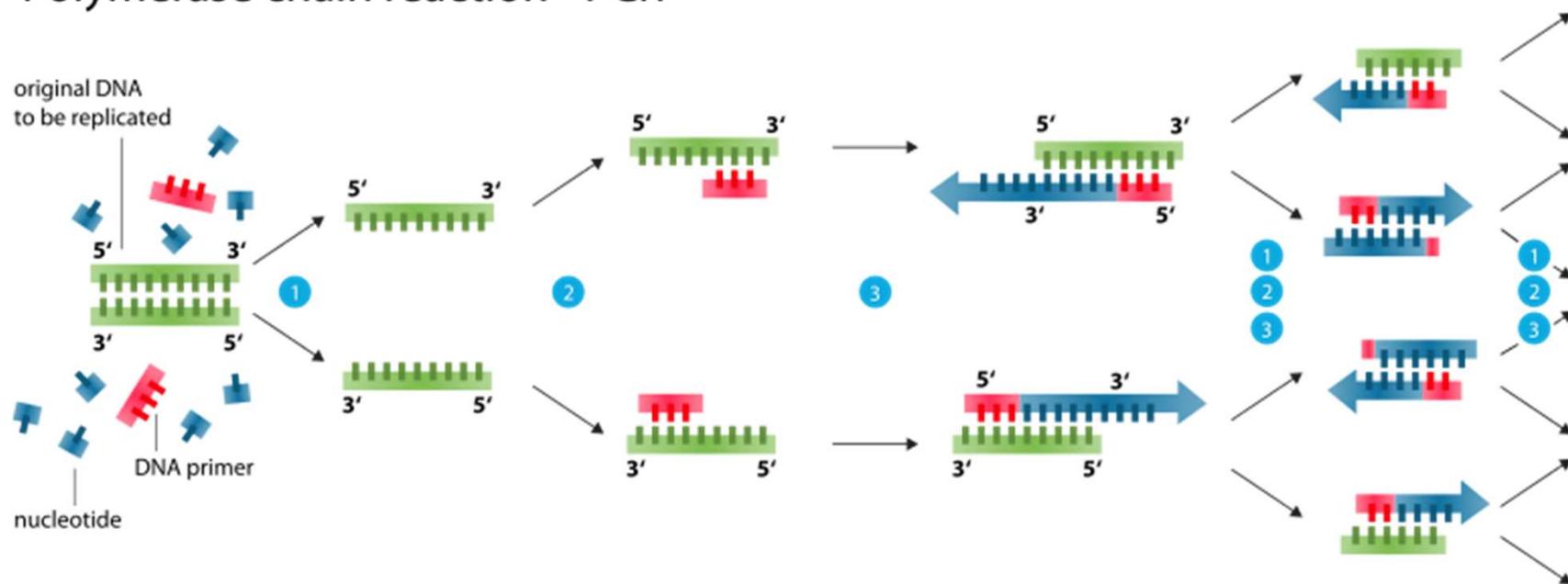
DNA Extraction

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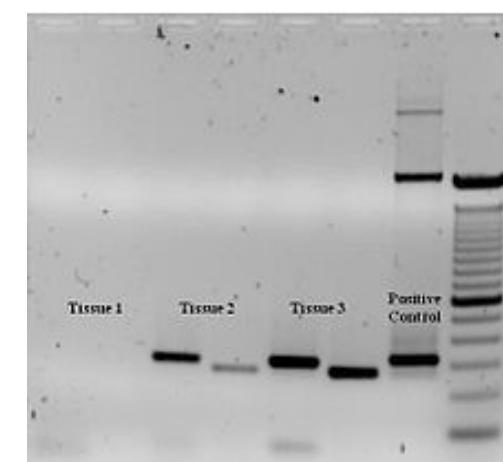


How else can we amplify DNA?

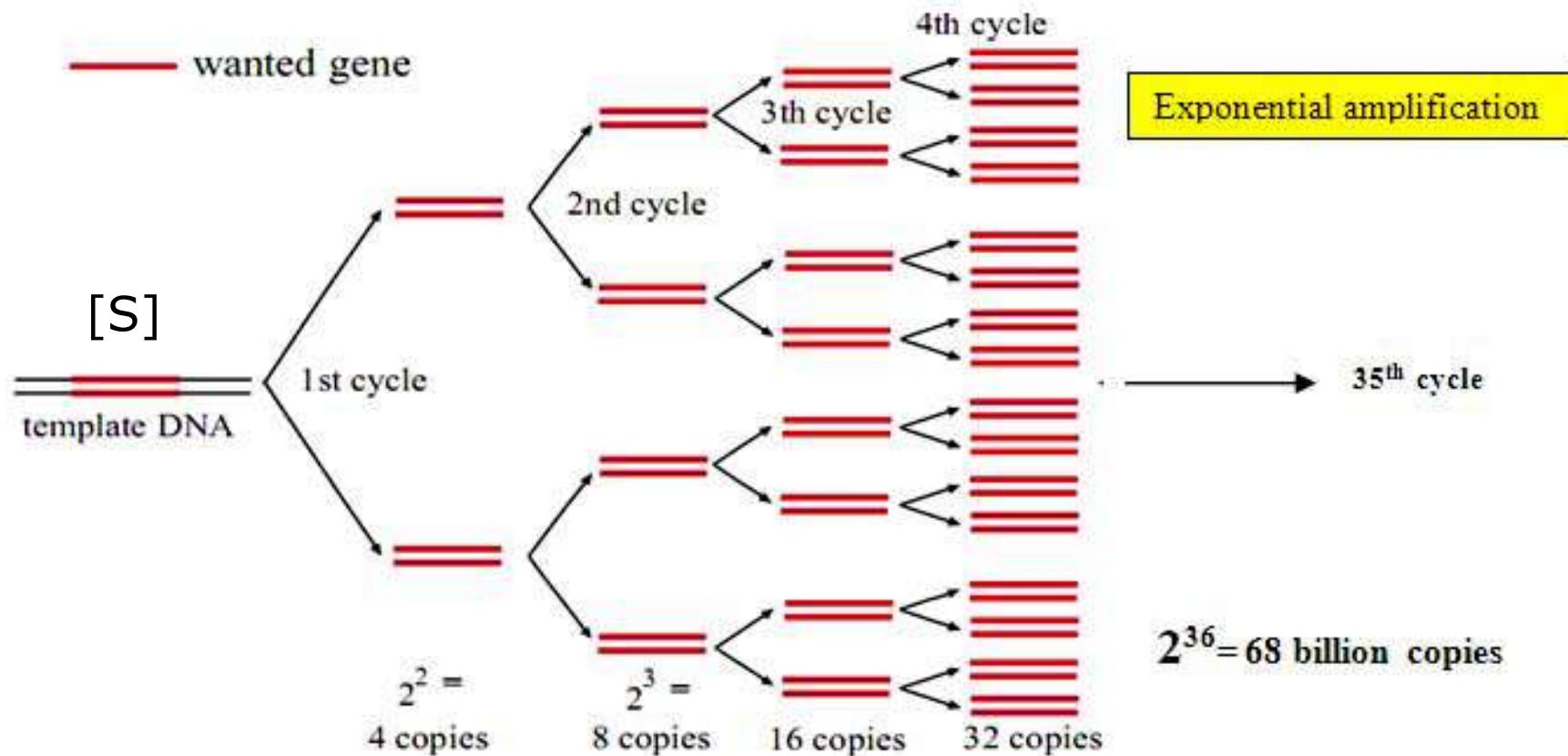
Polymerase chain reaction - PCR



- 1 Denaturation at 94-96°C
- 2 Annealing at ~68°C
- 3 Elongation at ca. 72 °C



Amplifying DNA using PCR



Exponential Amplification

Number of copies of ssDNA obtained after 'n' cycles = $[S] * 2^n$

Primer design

- Ideal primer length: ~20 nt
- Ideal primer Tm: 60 C
- 3' GC clamp: 3 out of the last 5 nt should be G/C

Basic Melting Temperature (Tm) Calculations

Two standard approximation calculations are used.

- For sequences less than 14 nucleotides the formula is:

$$Tm = (wA + xT) * 2 + (yG + zC) * 4$$

where w,x,y,z are the number of the bases A,T,G,C in the sequence, respectively.

- For sequences longer than 13 nucleotides, the equation used is

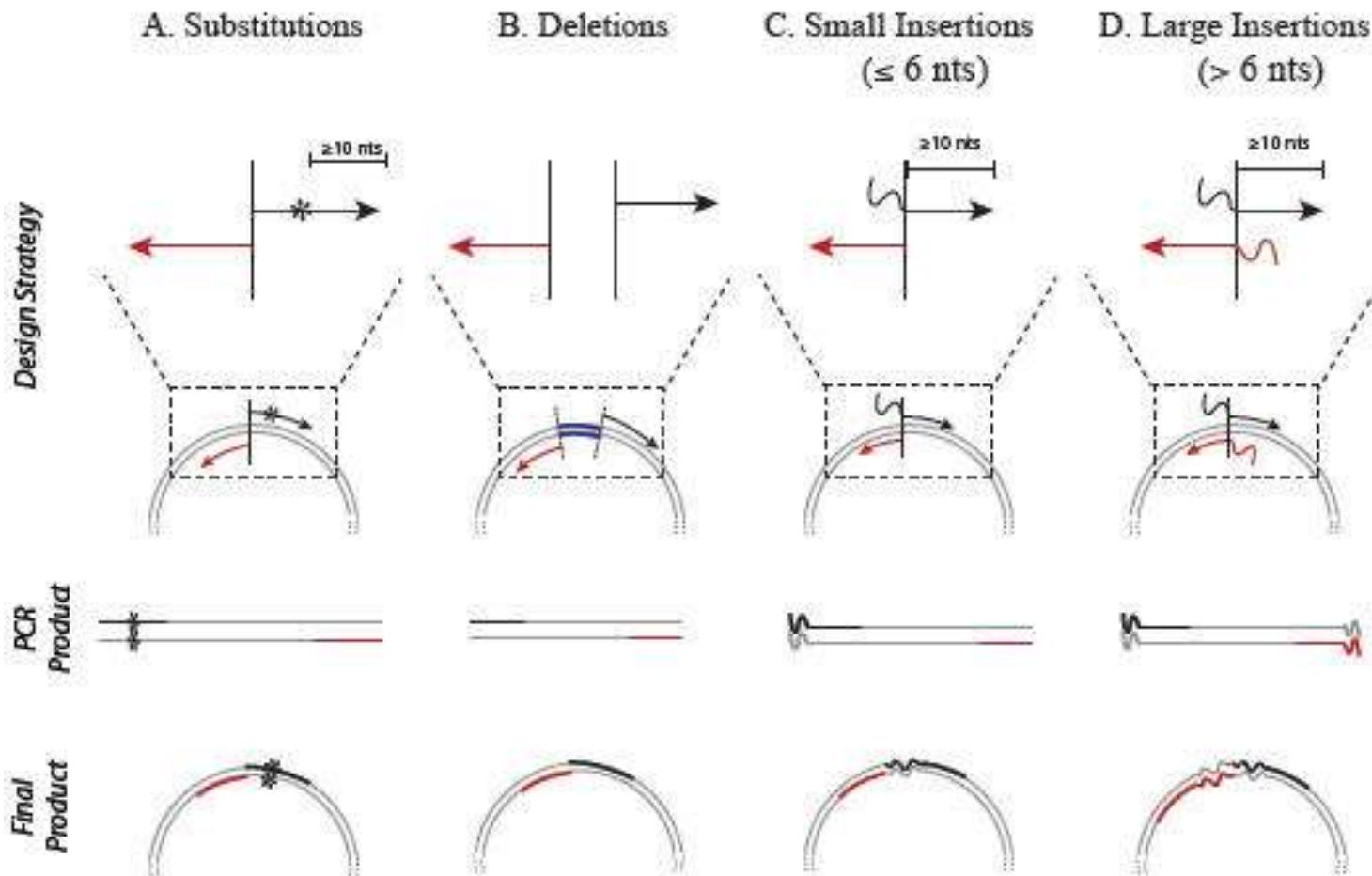
$$Tm = 64.9 + 41 * (yG + zC - 16.4) / (wA + xT + yG + zC)$$

Primer3

<https://bioinfo.ut.ee/primer3-0.4.0/>

<http://insilico.ehu.es/tm.php?formula=basic>

PCR to modify DNA (ends)



Molecular Cloning Toolkit

Once you have DNA in a tube, you can cut, paste, & modify it.

Enzymes to Chemically Modify DNA

Restriction endonuclease:

- Binds to a defined DNA sequence, and cuts the DNA.
- Creates “sticky” or “blunt” ends to be used for ligation.

DNA Ligase:

- Binds to two DNAs and creates a covalent bond

Two types of ligation reactions: sticky end & blunt end

- DNA ends must have 3'-OH and 5'-PO₄

T4 Polynucleotide kinase (PNK): Adds a phosphate to the 5' ends of DNA fragments

DNA Phosphatases:

- Removes the 5'-PO₄ from DNA fragment ends

Antartic Phosphatase (5' only), Shrimp Alkaline Phosphatase (5' & 3')

Exonucleases:

Mung Bean Nuclease:

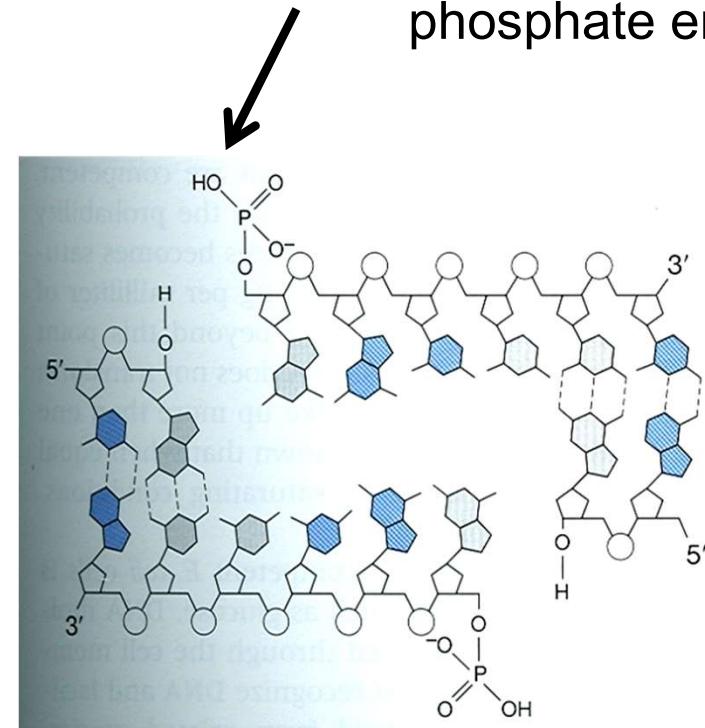
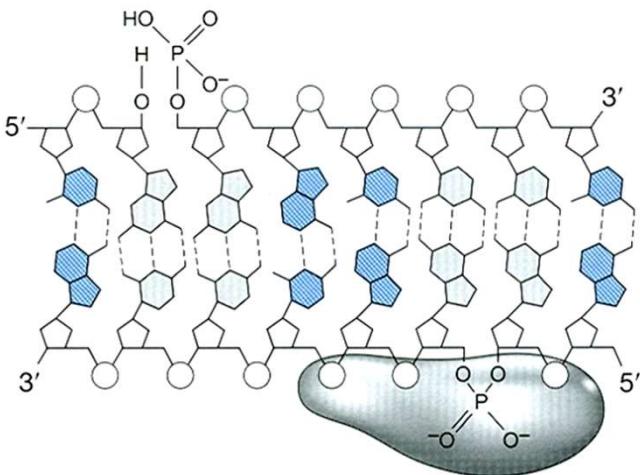
- Chews back both 5' and 3' sticky ends.

T7 Exonuclease:

- Chews back 5' sticky ends

Restriction Digestion

- Restriction Endonucleases cut DNA on both strands. Restriction digested DNA has phosphate ends
- Creates two DNA fragments from one.
(Or one DNA fragment from a circular DNA.)



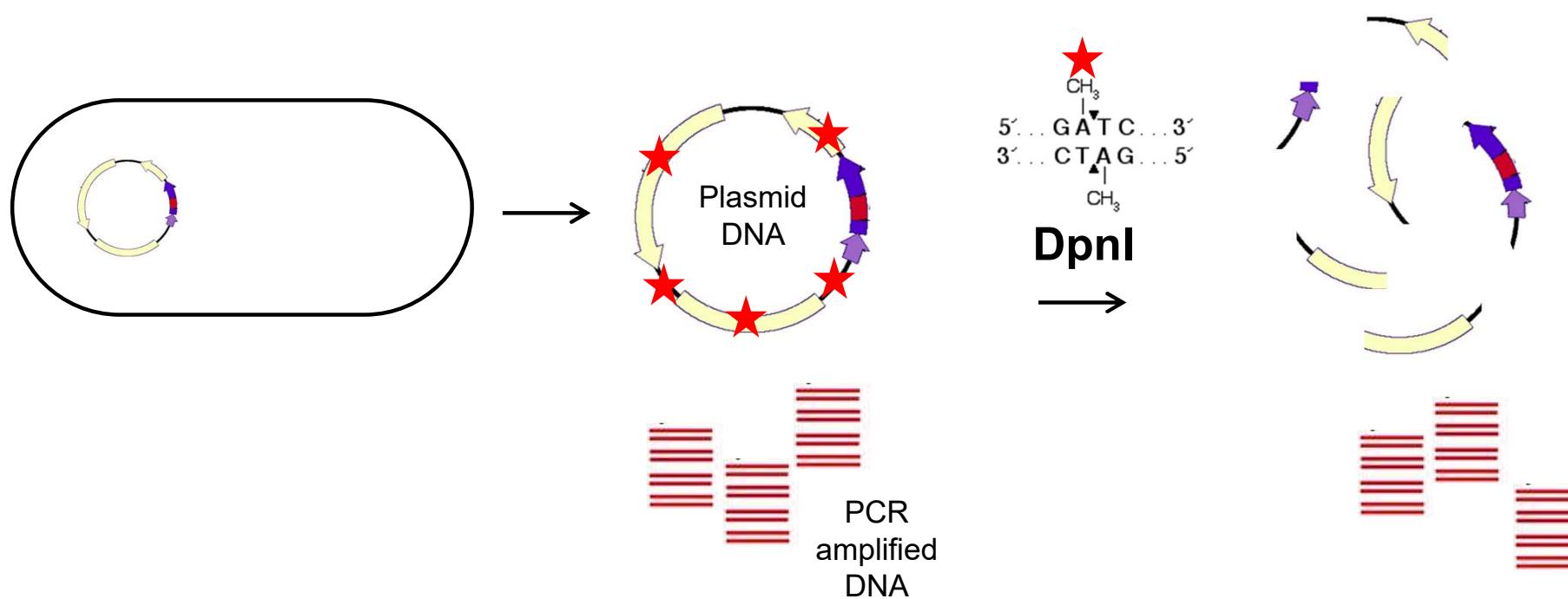
- The recognition sequence for a restriction enzyme is 4 to 8 base pairs long (**typically a palindrome**)
EcoRI: G^AAATTC
Ascl: GG^CCGCGCC
- Many restriction enzymes need some **flanking/ landing space** (they may not bind to their DNA sequence if it is too close to the end)

Restriction Digestion

Dam methylase (*dam* gene): GATC (methylates N6 in A)

Mec methylase (*dcm* gene): CCAGG and CCTGG (methylates C5 position in the 2nd C)

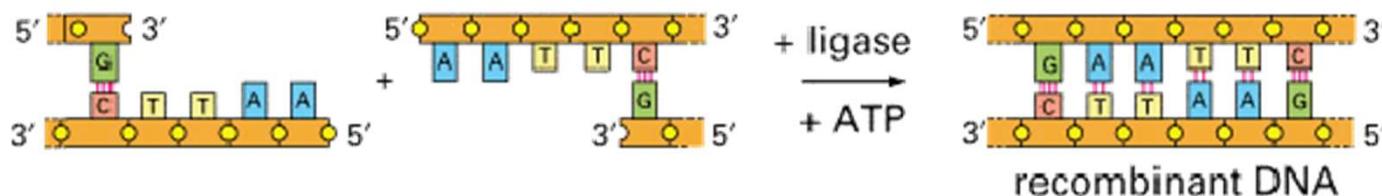
- Methylation of restriction sites often makes them resistant to restriction digestion.
- However, some methylated sites become sensitive to specific restriction enzymes.
- **This can be used to remove template DNA (methylated) after PCR.**



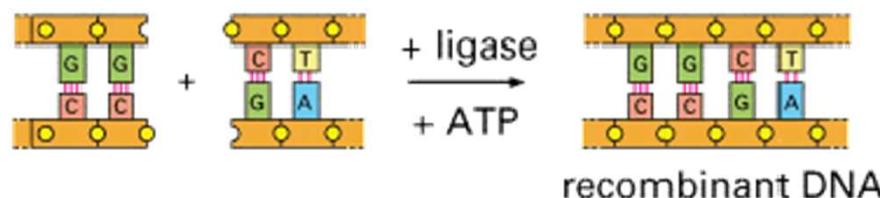
DNA Ligase connects sticky ends and blunt ends

3'-OH and 5'-PO₄

(A) JOINING TWO COMPLEMENTARY STAGGERED ENDS

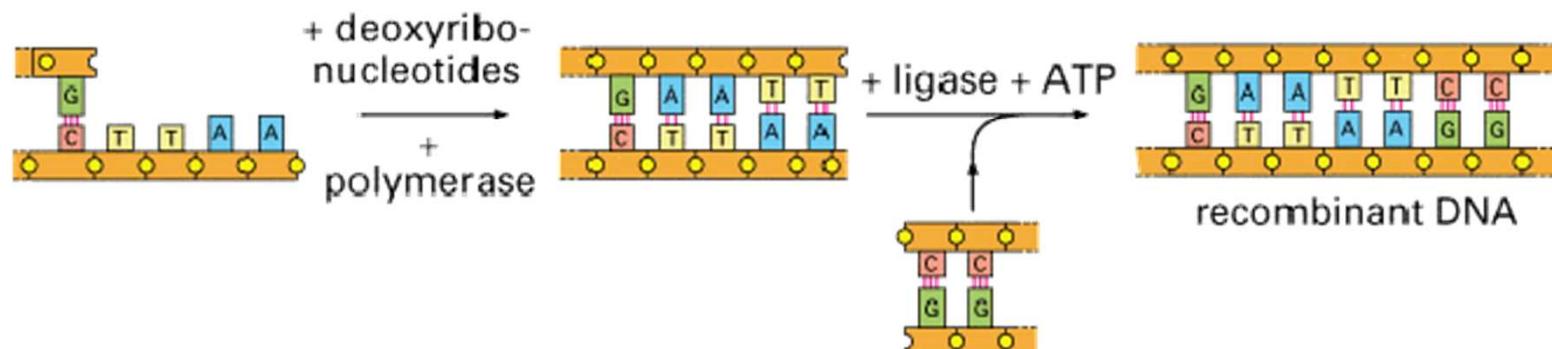


(B) JOINING TWO BLUNT ENDS

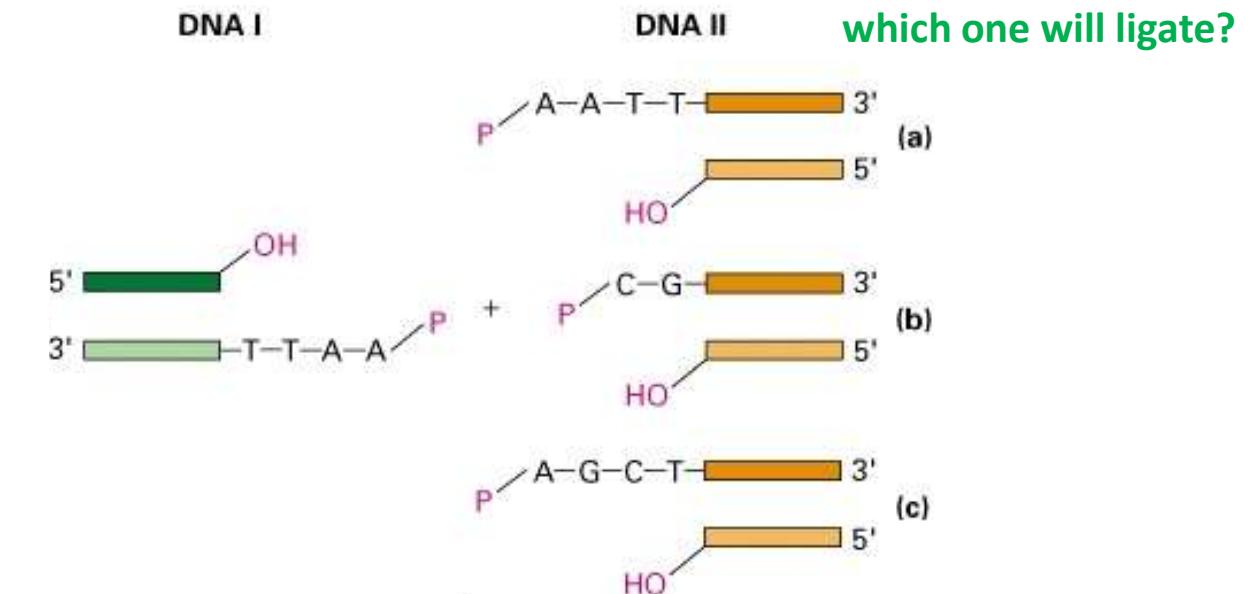
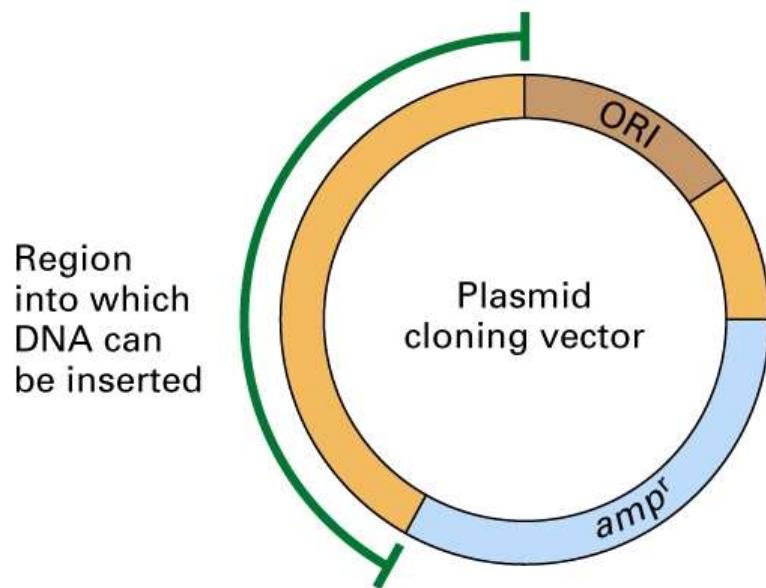


Requires much more ligase
and/or longer incubation time
(2 hours at room temperature)

(C) JOINING A BLUNT END WITH A STAGGERED END

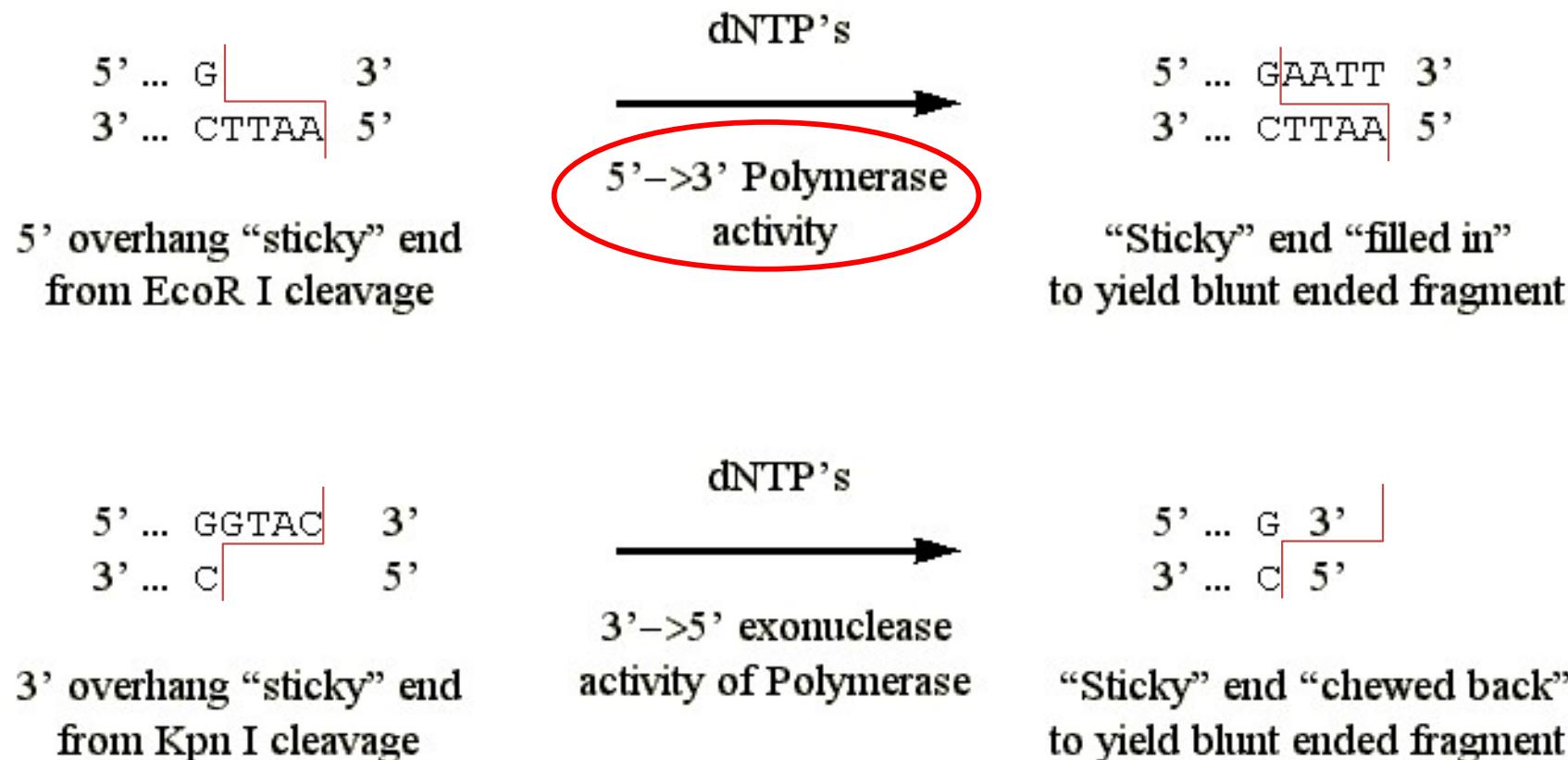


Restriction fragments with complementary “sticky ends” are ligated easily



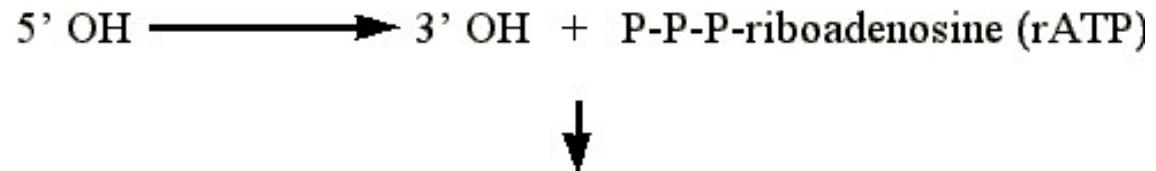
Other DNA modifying enzymes (Blunting)

- T4 DNA polymerase
 - Polymerase activity (fill, 5' → 3')
 - Nuclease activity (chew, 3' exonuclease)

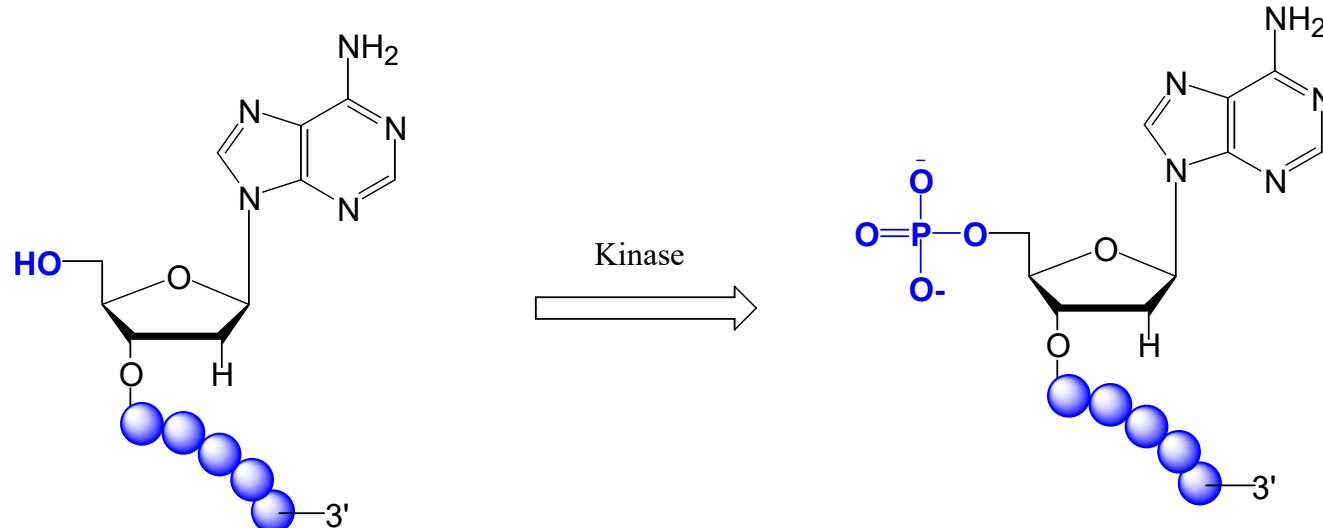


Polynucleotide Kinase (PNK)

Adds 5'phosphate



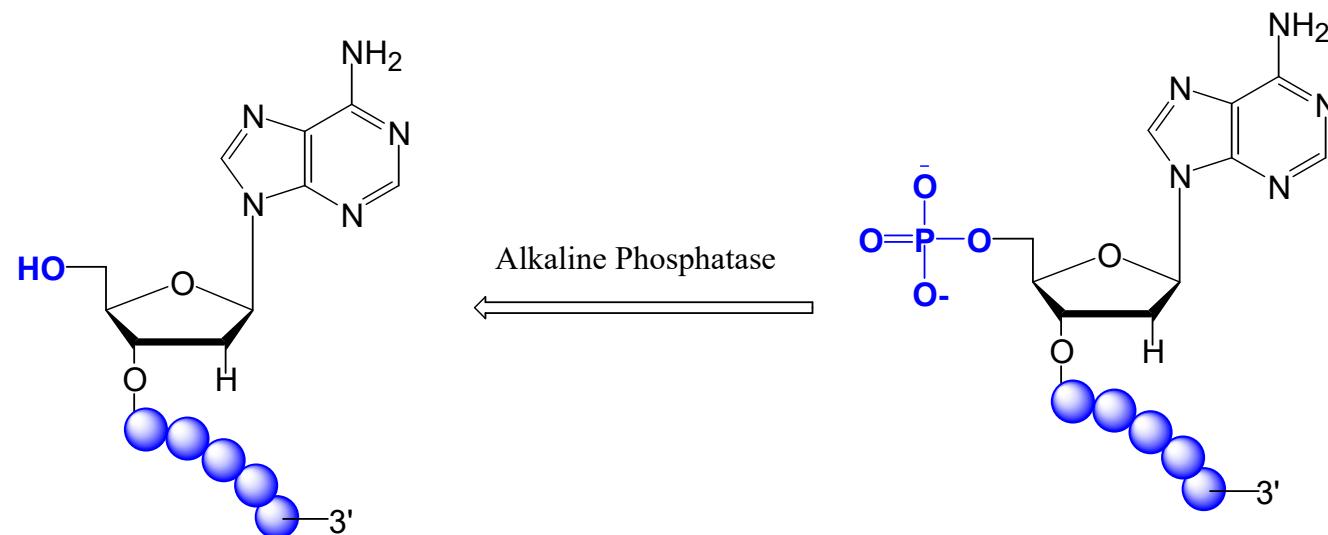
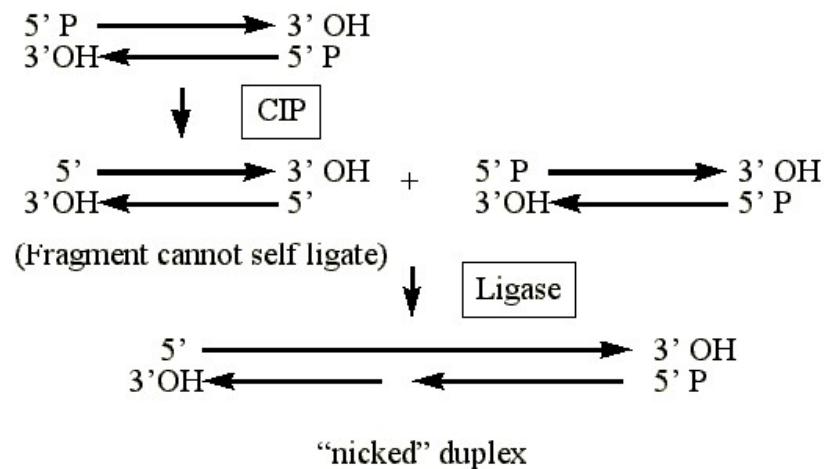
γ -Phosphate group is transferred from rATP



Synthetic oligonucleotides are unphosphorylated at the 5' end.
A very useful enzyme to radiolabel DNA fragments.

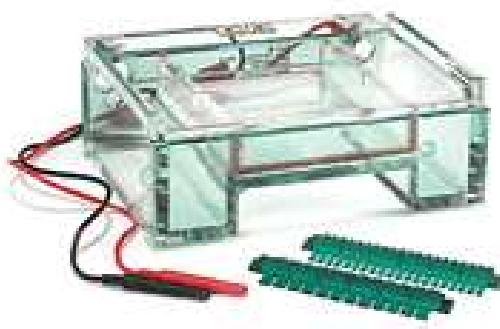
Phosphatase

Removes 5' phosphate



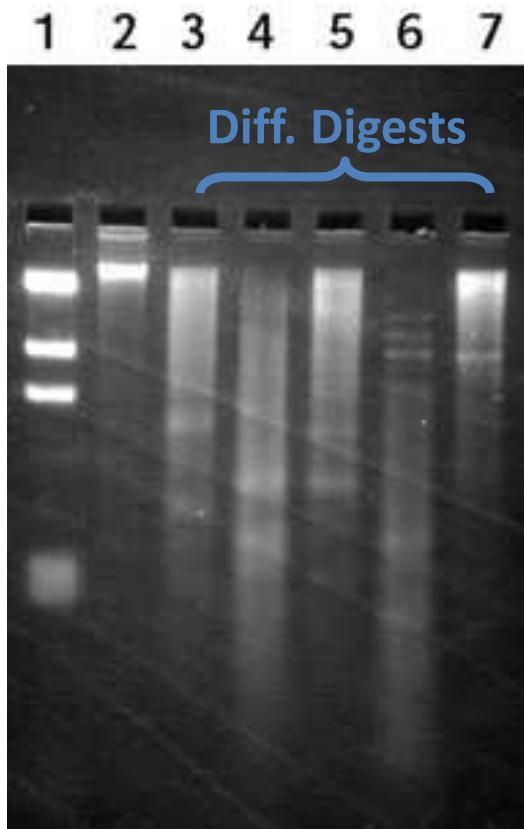
A useful enzyme to reduce the background of cloning.

Visualization and Separation of DNA

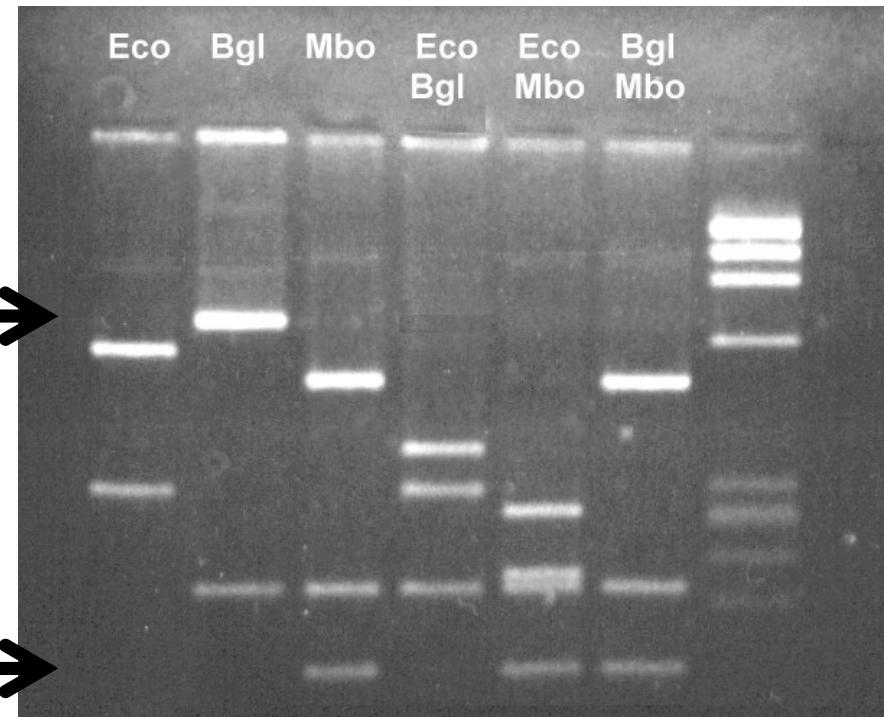


Gel Electrophoresis in Action.

<http://www.youtube.com/watch?v=QEG8dz7cbnY>

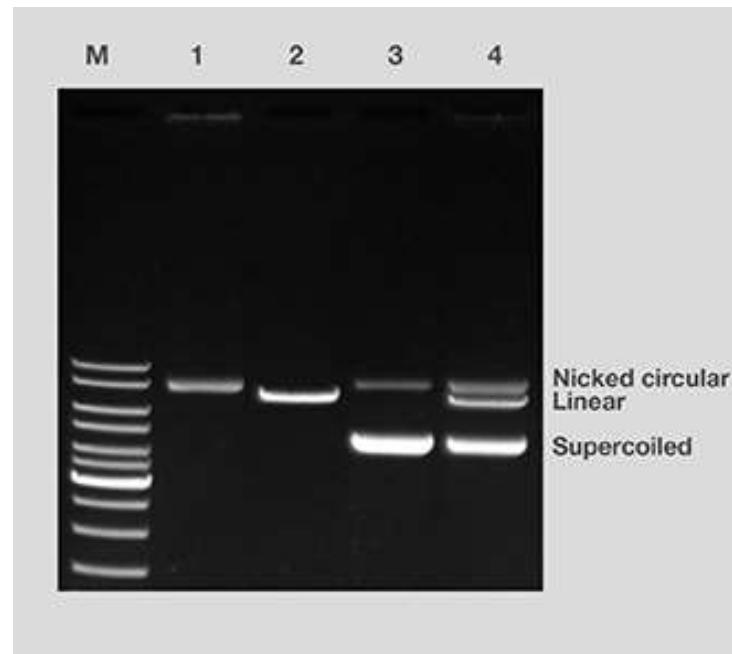
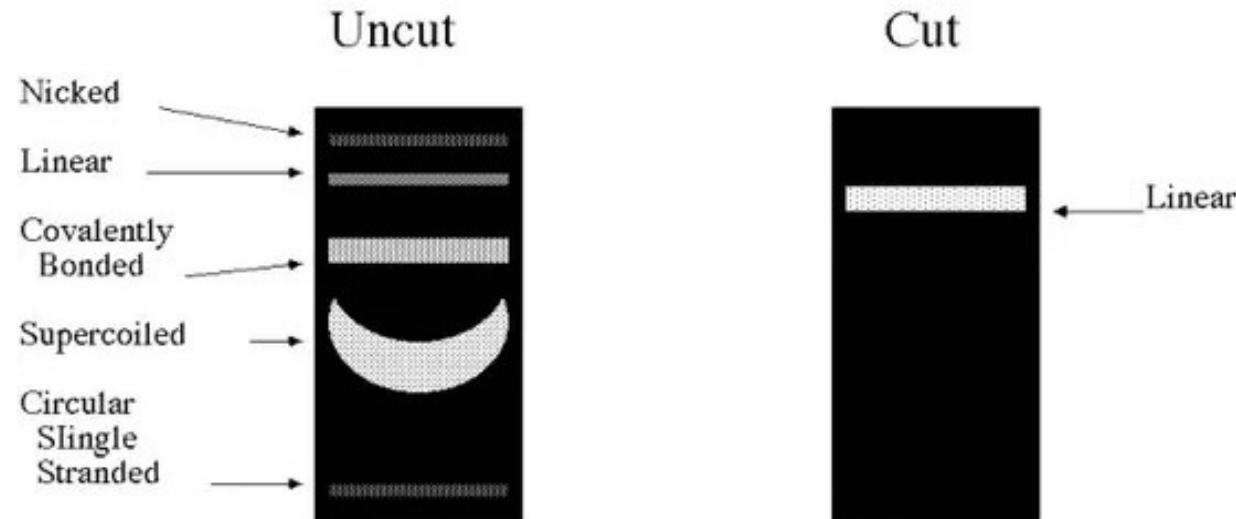


Longer DNA fragments
Shorter DNA fragments

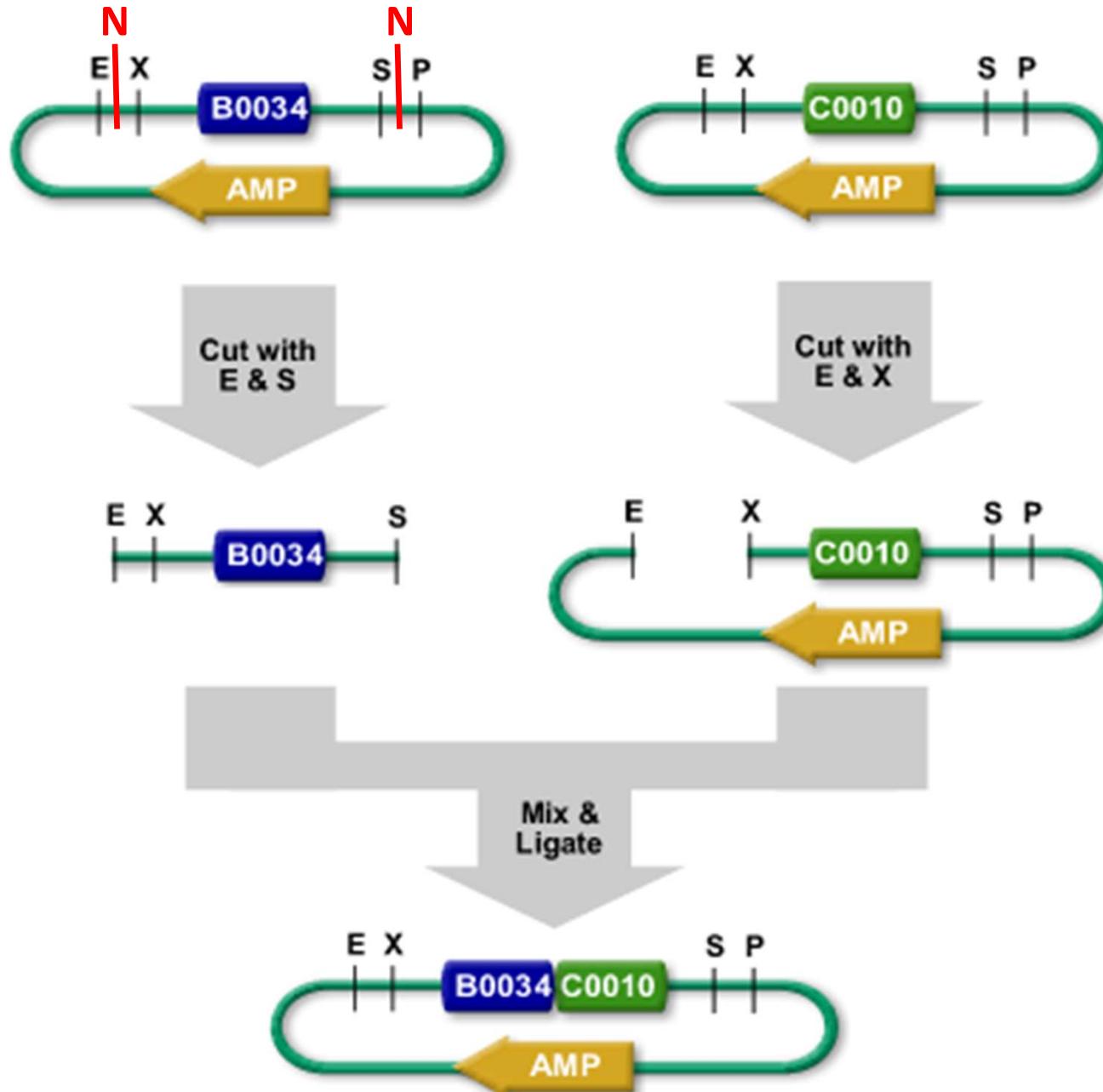


Visualization and Separation of DNA

Plasmid DNA



BioBrick Cloning: step-wise addition of parts



E = EcoRI

X = XbaI

S = SphI

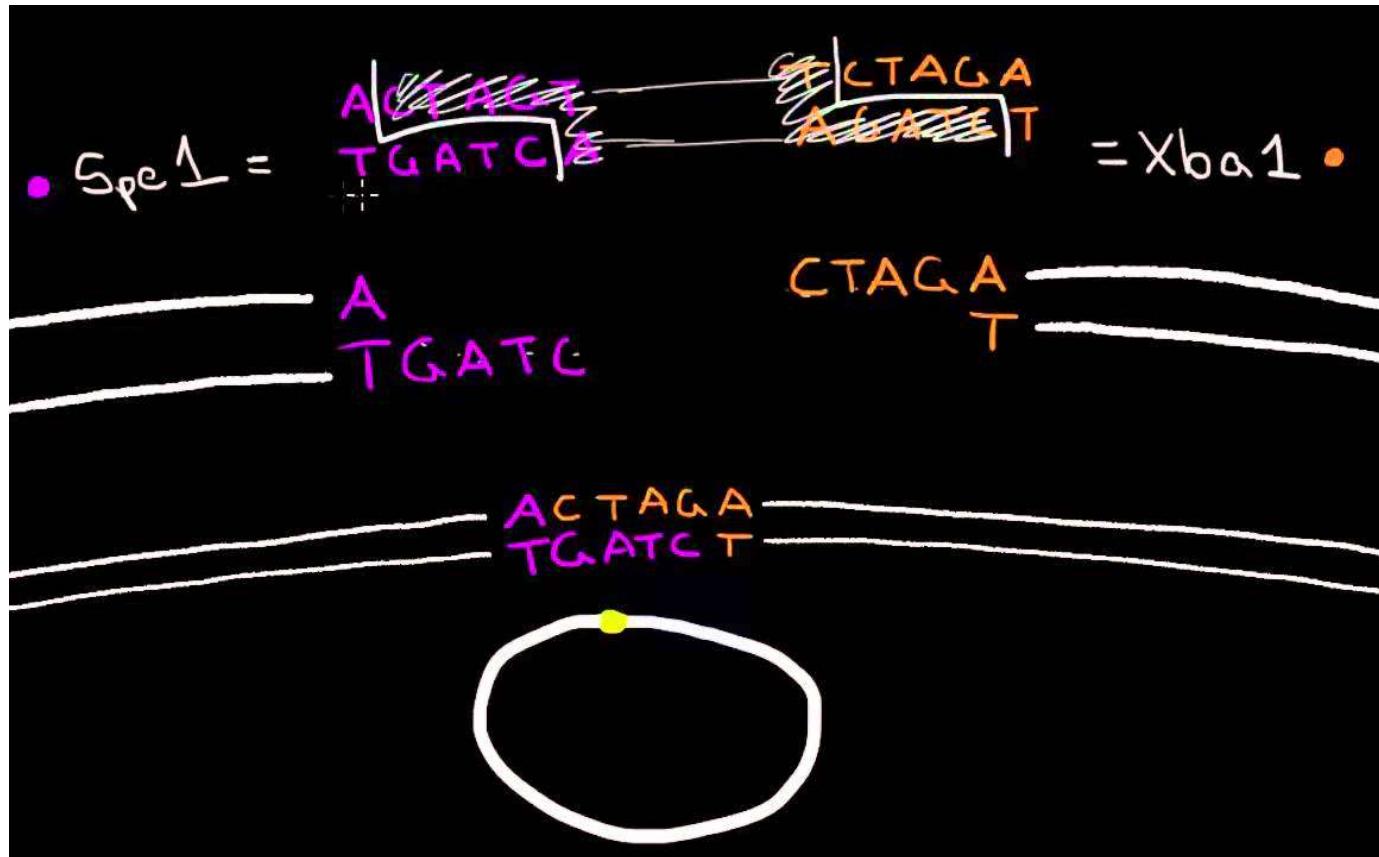
P = PstI

N = NotI

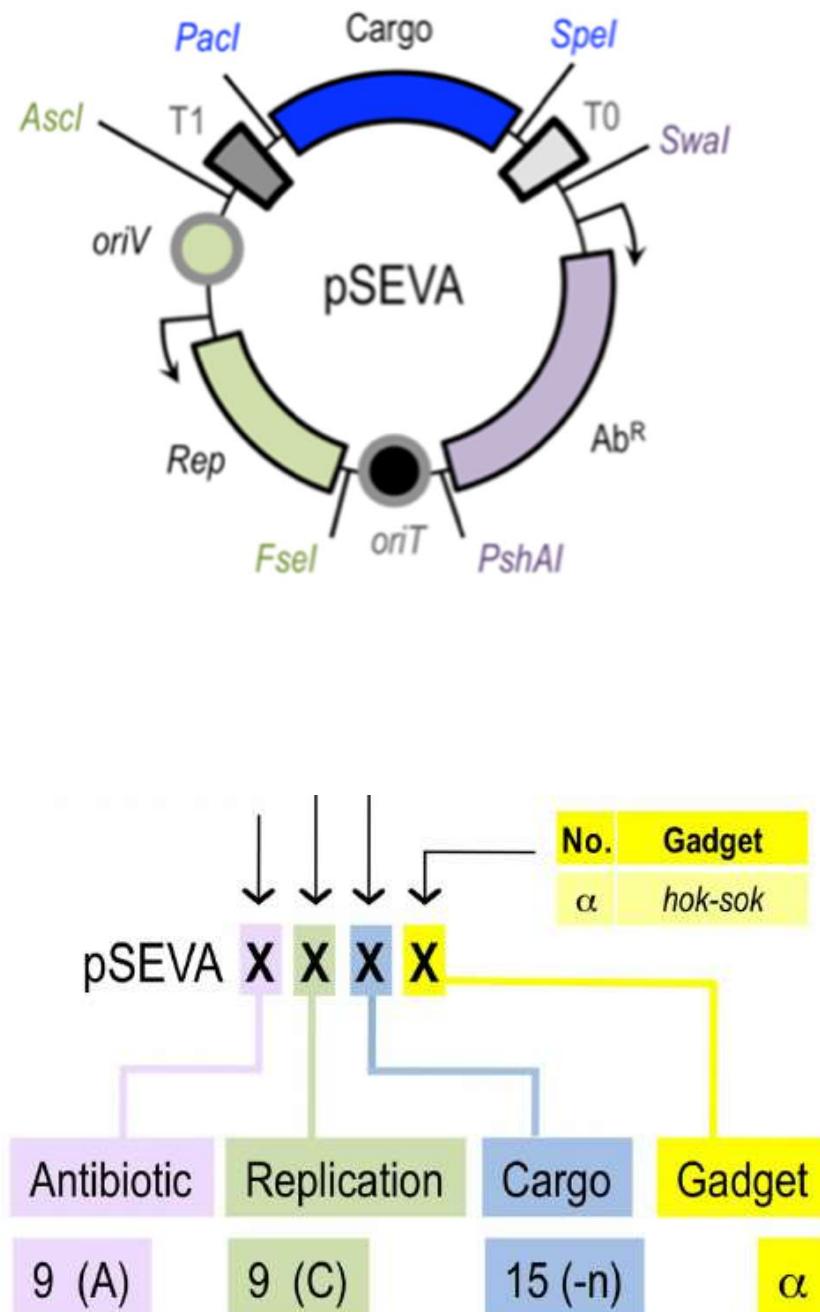
BioBrick vector standards

BioBrick Cloning

Spel and XbaI have compatible ends



The Standard European Vector Architecture (SEVA 2.0)



| No. | Ori V |
|-----|---------------|
| 1 | R6K |
| 2 | RK2 |
| 3 | pBBR1 |
| 4 | pRO1600/ColE1 |
| 5 | RSF1010 |
| 6 | p15A |
| 7 | pSC101 |
| 8 | pUC |
| 9 | pBBR322/ROP |

| No. | Antb |
|-----|-------|
| 1 | Ap |
| 2 | Km |
| 3 | Cm |
| 4 | Sm/Sp |
| 5 | Tc |
| 6 | Gm |

| No. | Cargo |
|-----|--------------------------------------|
| 1 | MCS-default |
| 2 | <i>lacZ</i> α -pUC19 |
| 3 | <i>lacZ</i> α -pUC18 |
| 4 | <i>lac</i> β -P _{trc} |
| 5 | <i>lacZ</i> |
| 6 | <i>luxCDABE</i> |
| 7 | <i>GFP</i> |
| 8 | <i>xylS-Pm</i> |
| 9 | <i>alkS-Palk</i> |
| 10 | <i>araC-Pbad</i> |
| 11 | <i>chnR-PchnB</i> |
| 12 | <i>cprK1-PDB3</i> |
| 13 | PEM7 |

Golden Gate cloning enzyme

Bsa I

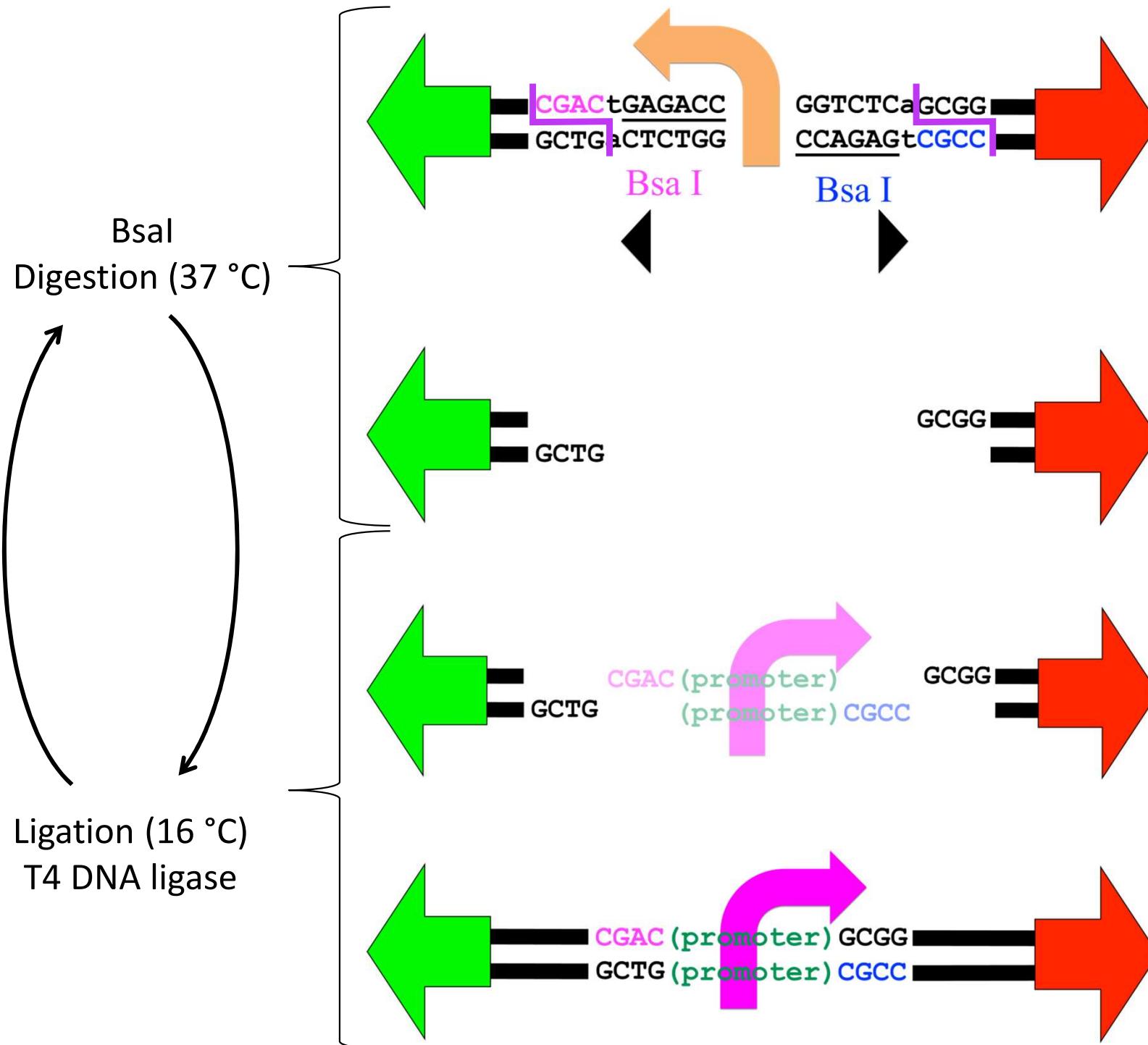
5'... GGTCTC (N)₁ ... 3'
3'... CCAGAG (N)₅ ... 5'



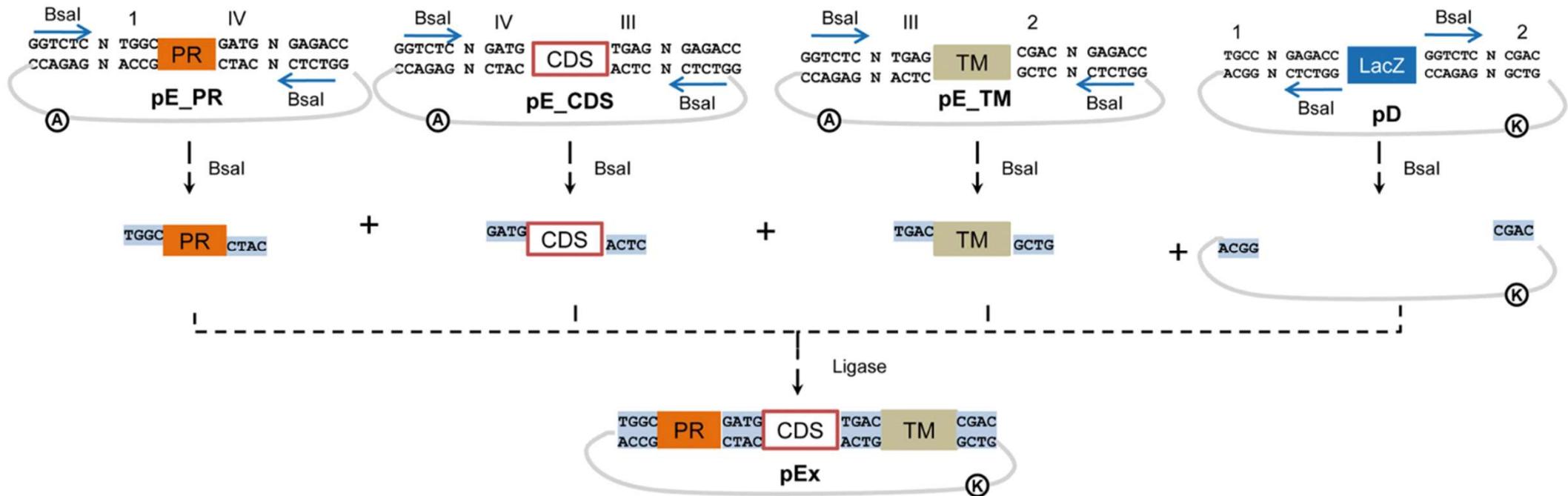
GGTCTCn-----
CCAGAGn1234

- Not Palindromic
- Type II S

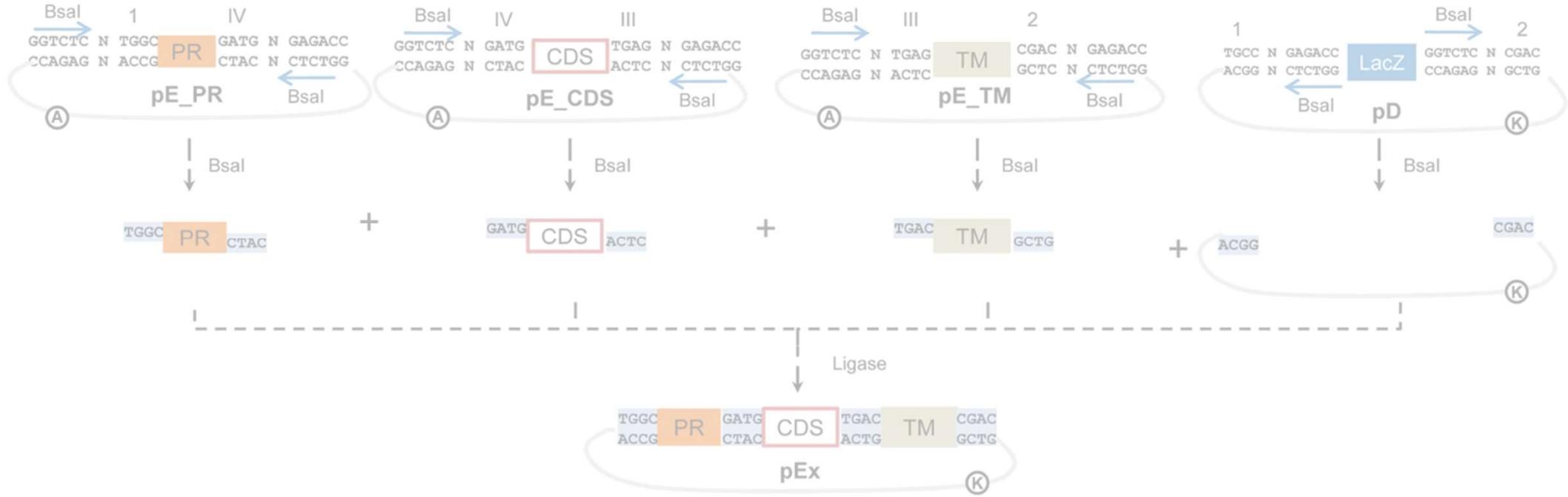
Golden Gate cloning



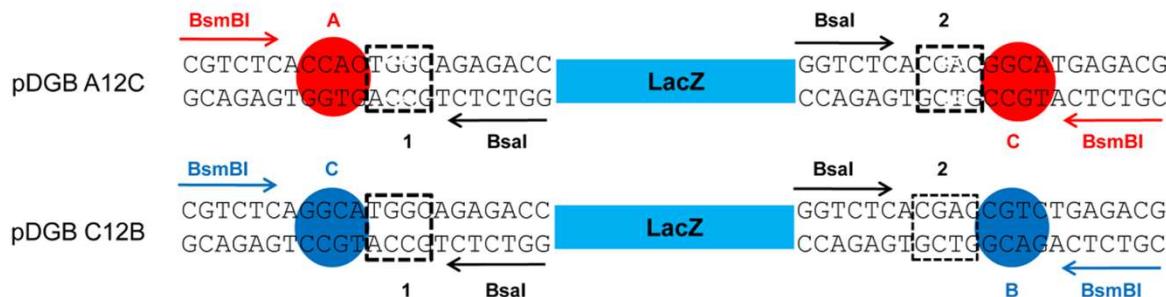
Golden Braid cloning



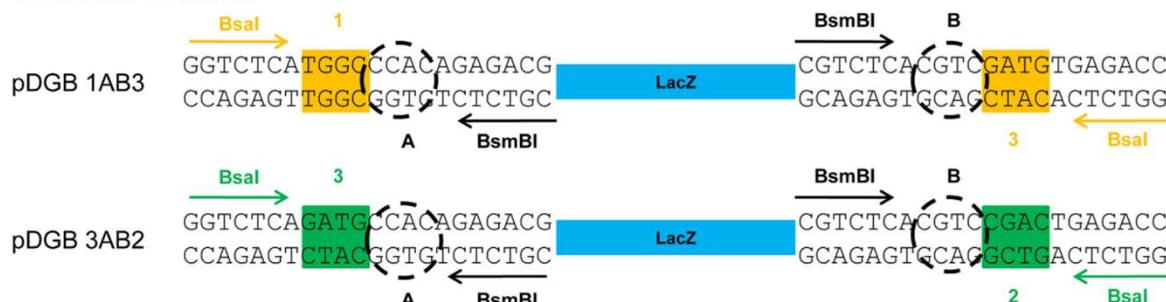
Golden Braid cloning



LEVEL α PLASMIDS

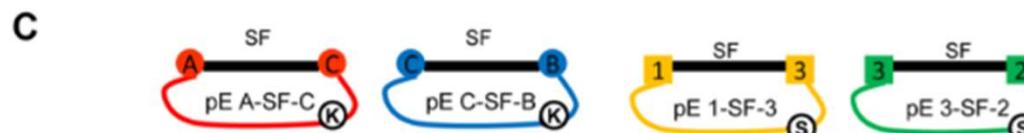
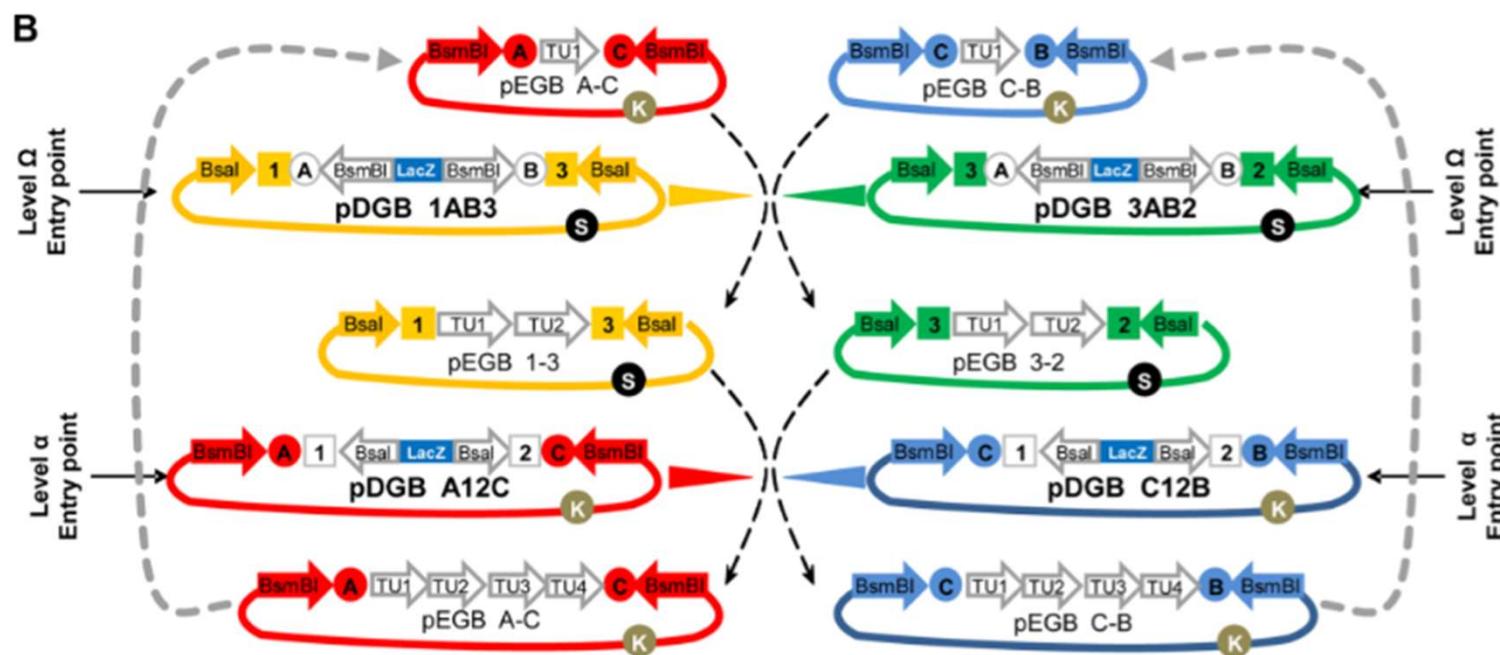
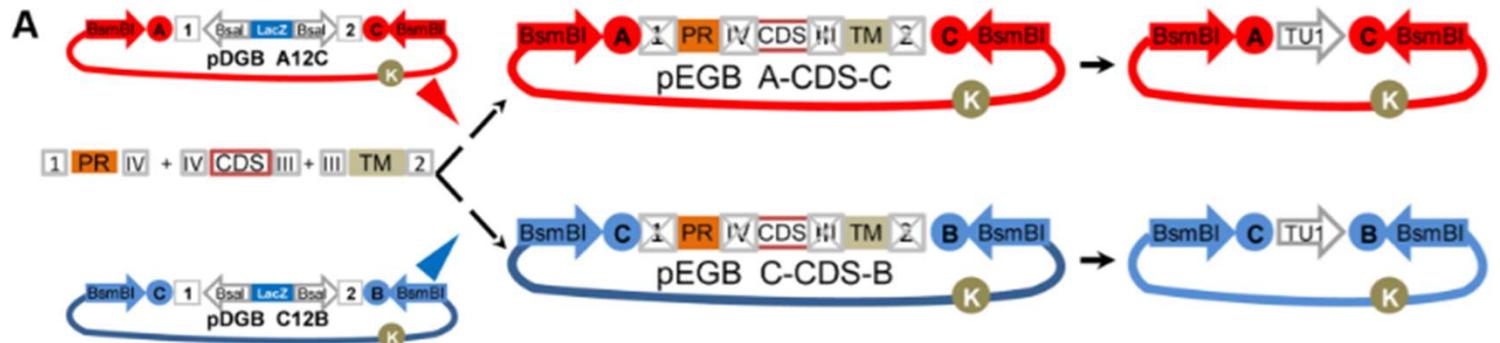


LEVEL Ω PLASMIDS

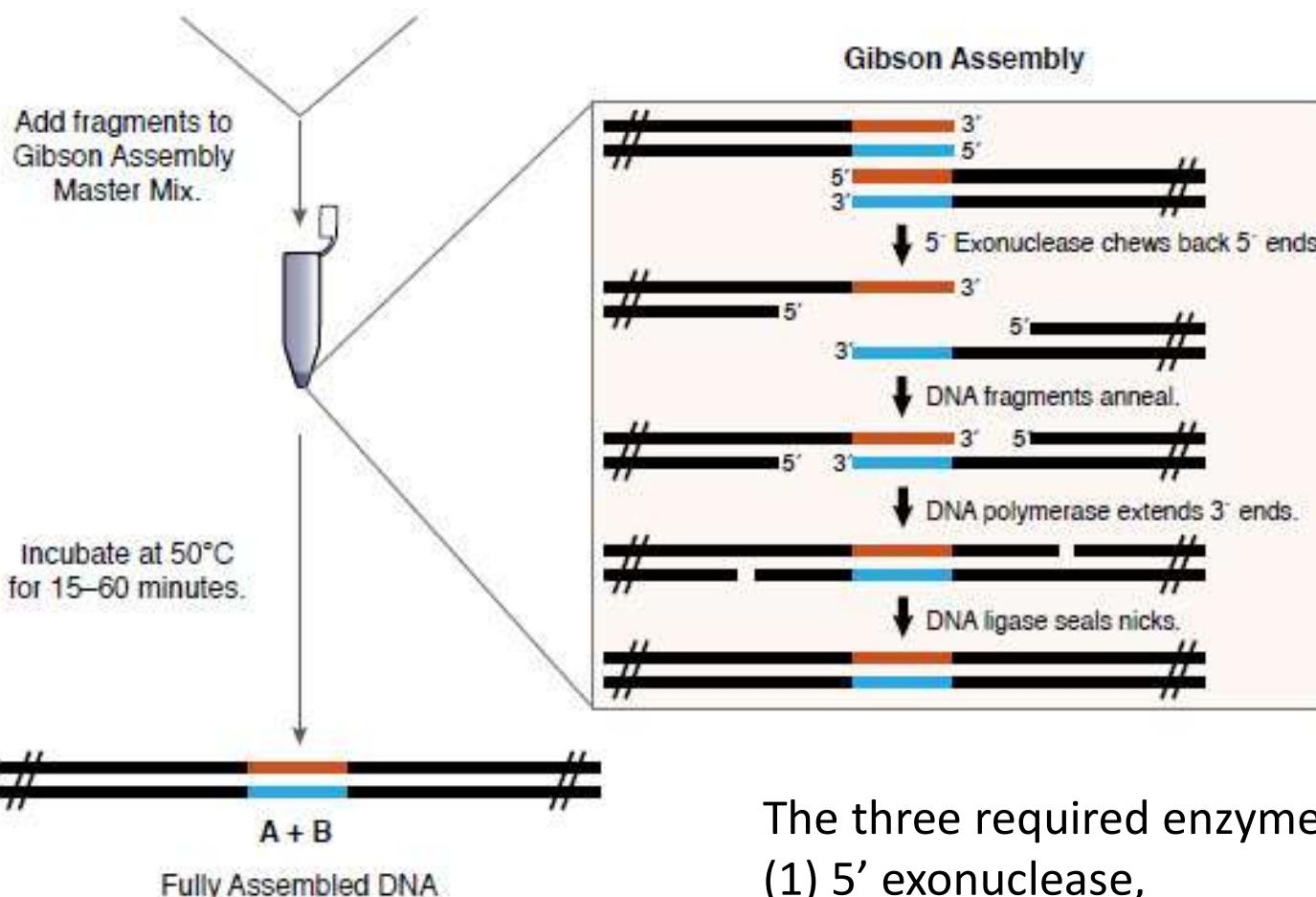
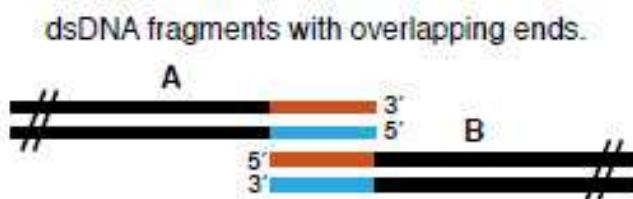


Sarrion-Perdigones *et al.*, 2011. PLoS One.

Golden Braid cloning



Gibson cloning



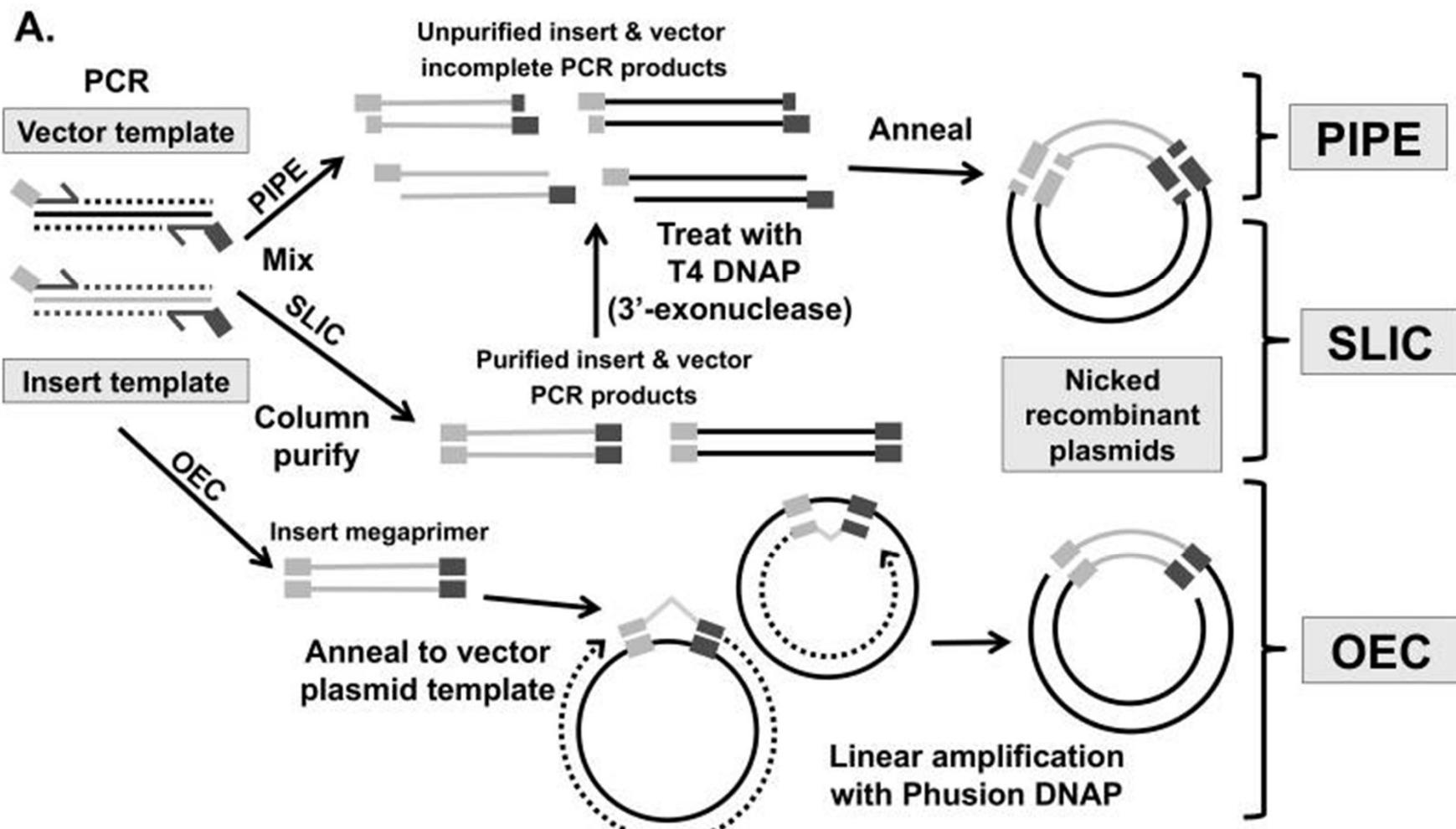
- Chew Back and Anneal Assembly (CBA)
- Isothermal Assembly (50 °C)

Gibson, D.G. et.al (2009). Nature Methods. 343-345.

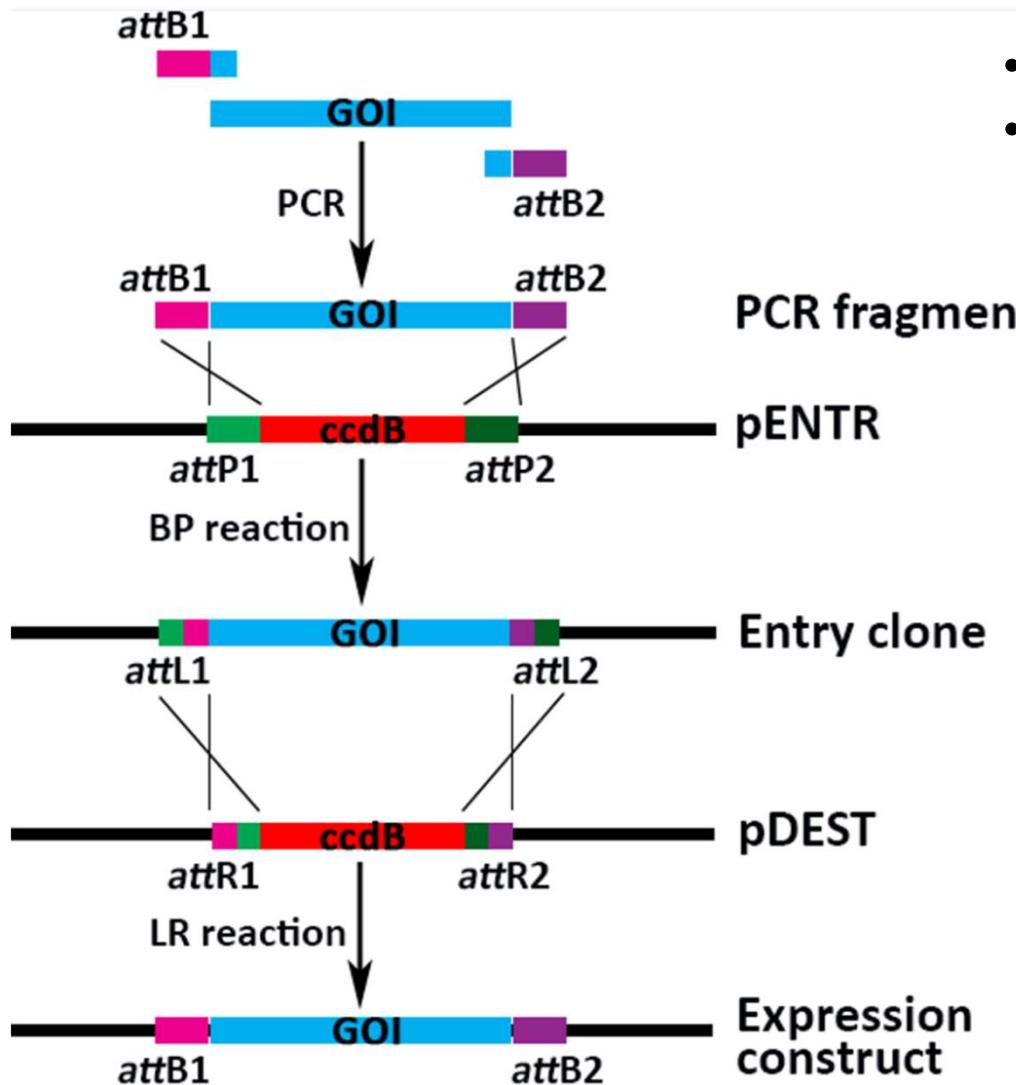
The three required enzyme activities are:

- (1) 5' exonuclease,
- (2) DNA polymerase (Phusion), and
- (3) DNA ligase (Taq ligase)

Other “Ligation Independent” Cloning methods



Recombination based cloning

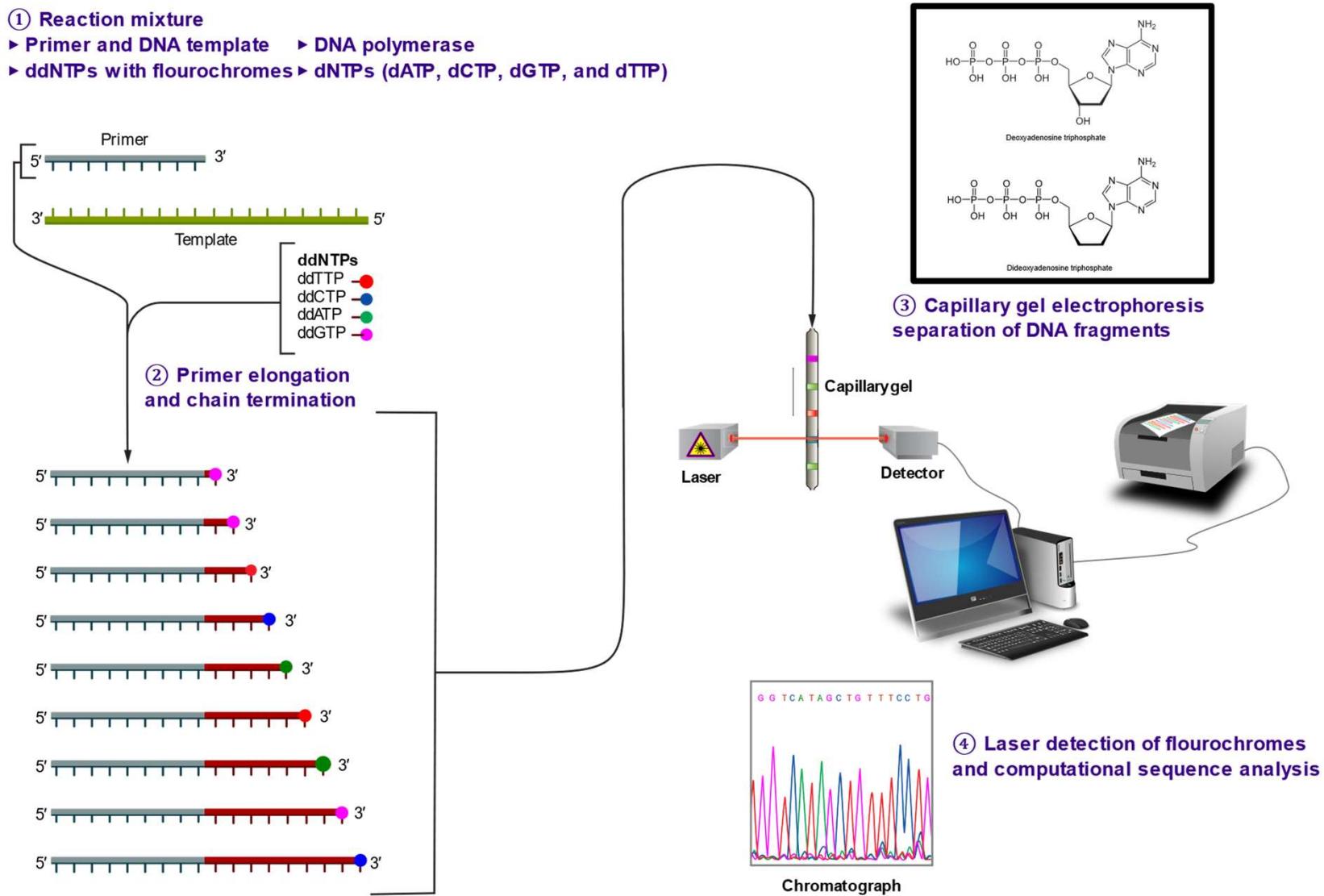


- Gateway cloning
- Phage lambda (λ) recombination system

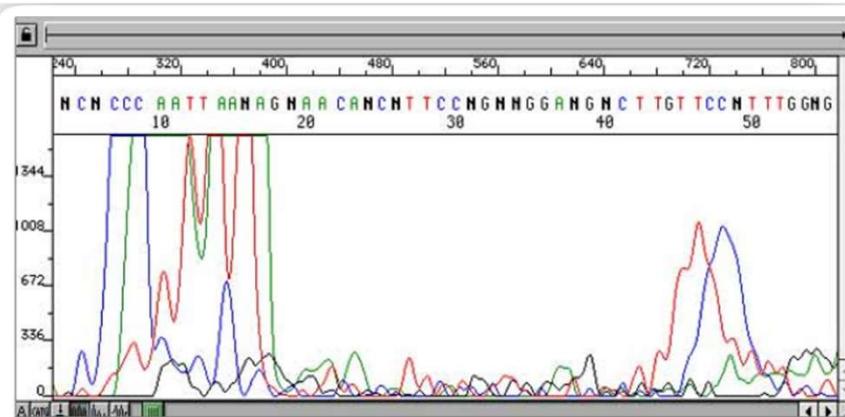
DNA Sequencing

- **Sanger sequencing:** the most common sequencing method after cloning: (di-deoxy method)

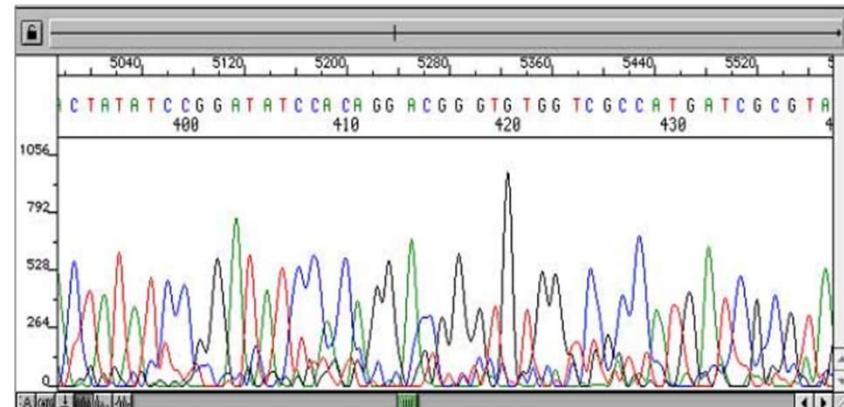
https://en.wikipedia.org/wiki/Sanger_sequencing



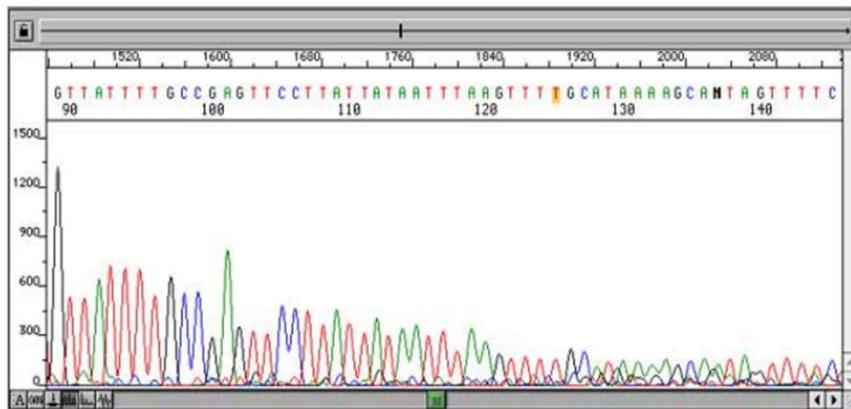
Sanger Sequencing Troubleshooting



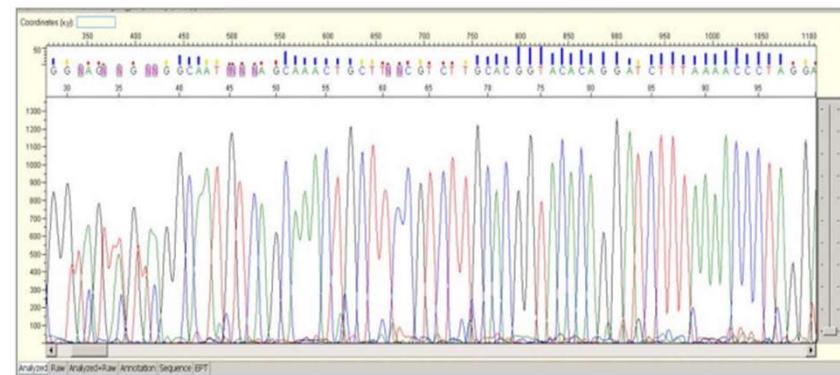
Poor quality template or primer,
missing binding site



Multiple priming, mixed templates



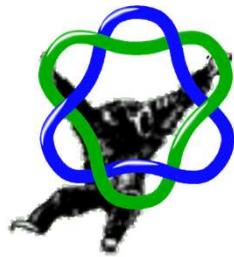
Low template/ primer concentrations,
poor primer design/ binding



Too much template

Preparing for the Practical Exercise

(1) Download and install: A Plasmid Editor (ApE)



ApE plasmid editor

Download: <https://jorgensen.biology.utah.edu/wayned/ape/>

Tutorials: [https://www.youtube.com/channel/UC - pObWrnUZRhsO8YbIX6gQ](https://www.youtube.com/channel/UC-pObWrnUZRhsO8YbIX6gQ)



Benchling

Starting Tutorial: <https://benchling.com/tutorials/49/nav-redesign-overview>

Molecular Biology: <https://www.youtube.com/watch?v=rhamB8liWxA>

(3) Make an account on: DeNovoDNA / RBS calculator

- <https://www.denovodna.com/software/login>
- Use academic email ID (.edu, universite-paris-saclay.fr, inra.fr)

Questions welcome.

manish.kushwaha@inrae.fr