



# Advanced Cell Biology & Biotechnology

## Biotechnology Project Lab

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& Isabella Tarulli

The lecture of November 22<sup>nd</sup> 2021 is about to begin....



## Biotechnology Project – V lesson

0 – Summary of the previous lesson

1 - Subcloning NRG1-III- $\beta$ 3 from pCR-Blunt II-TOPO into the expression vector pEGFP-C3

2 - Subcloning NRG1-III- $\beta$ 3 from pCR-Blunt II-TOPO or pEGFP-C3 into the expression vector pCMV-Tag4

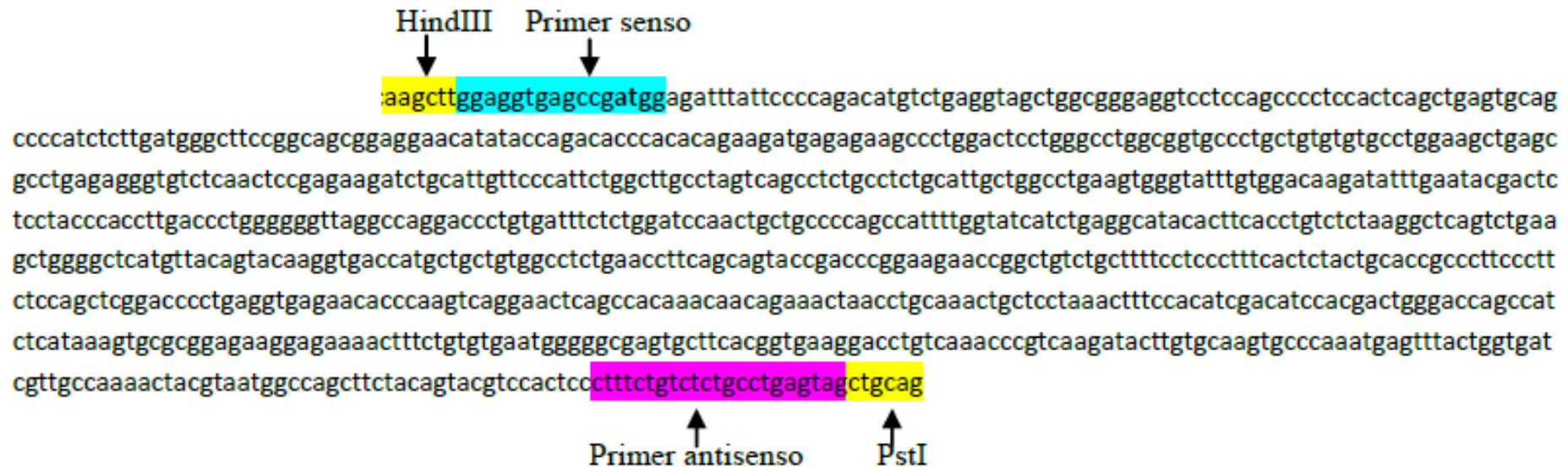
5' -CGT TAACTTG ACC**ATG**TGCATCT**TAG**CTCCATGGCATGC-3'

5' -**CGT TAACTTG**ACC**ATG**TGCATCT**TAG**CTCCATGGCATGC-3'  
3' -GCAATTGAACTGGTACACGTAGATCGAG**GTACCGTACG**-5'

Primer sense: 5' -**AAGCTTCGT TAACTTG**-3'

Primer antisense: 5' -**CTGCAGGCATGCCATG**-3'

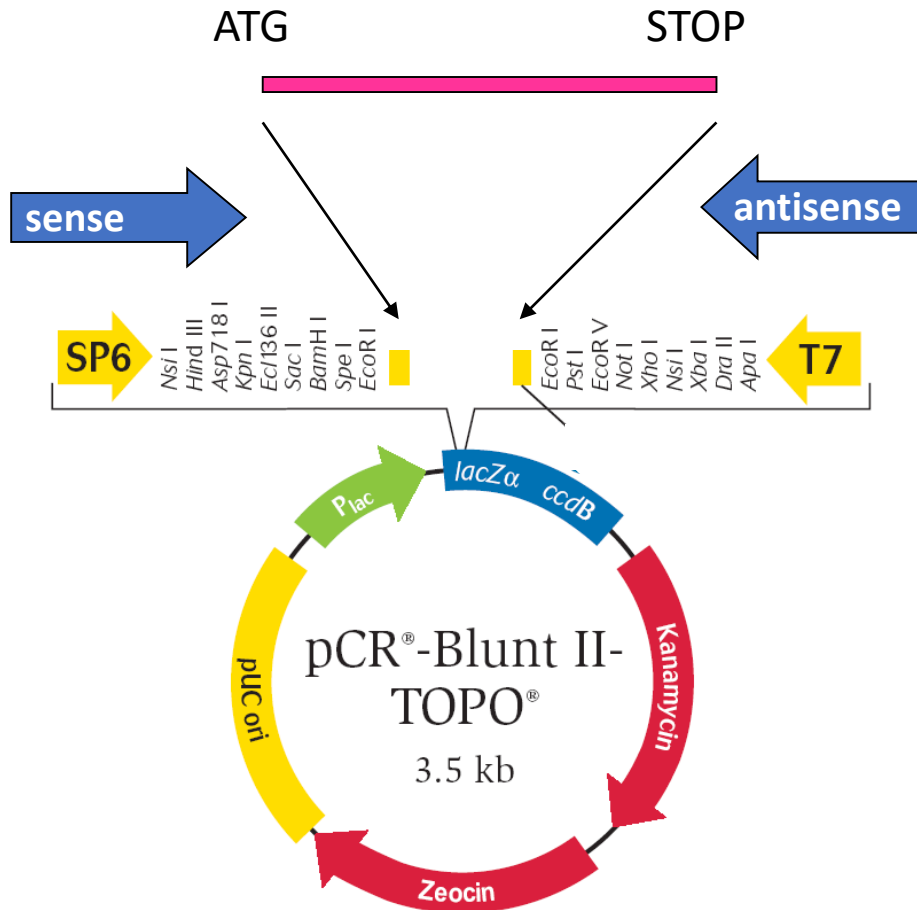
5' -**AAGCTTCGT TAACTTG**ACCATGTGCATCTAGCTCCATGGCATGC**CTGCAG**-3'  
3' -**TTCGAAGCAATTGAACT**GGTACACGTAGATCGAG**GTACCGTACGGACGTC**-5'



# Is NRG1 cloned sense or antisense within pCR-Blunt II-TOPO vector?

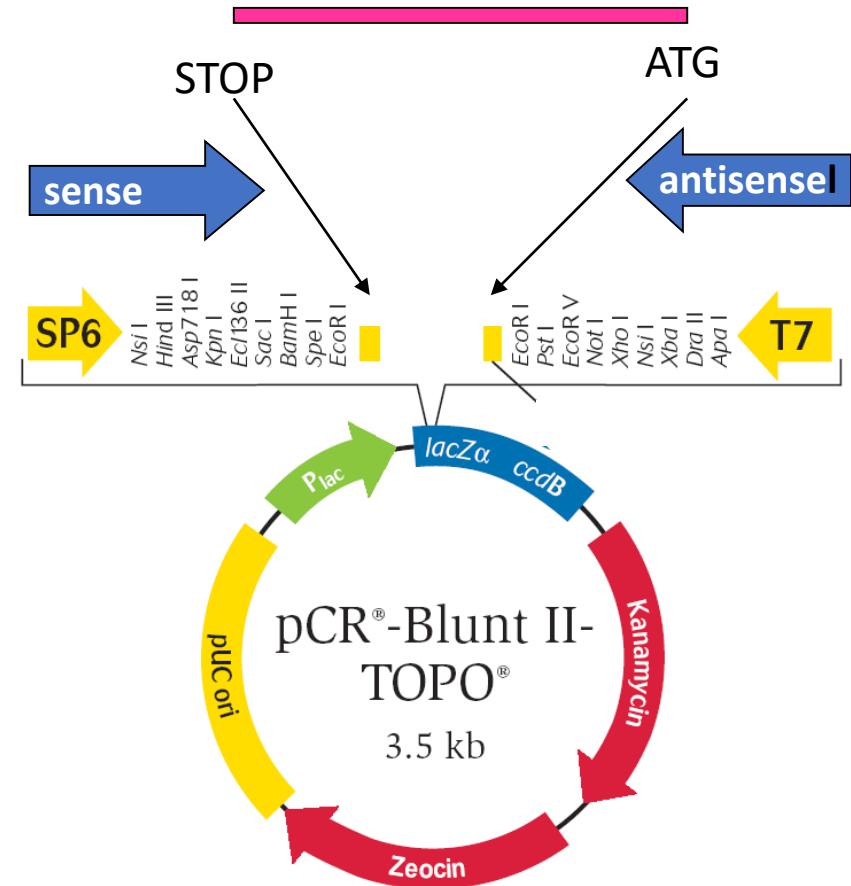
INSERT cloned in SENSE orientation

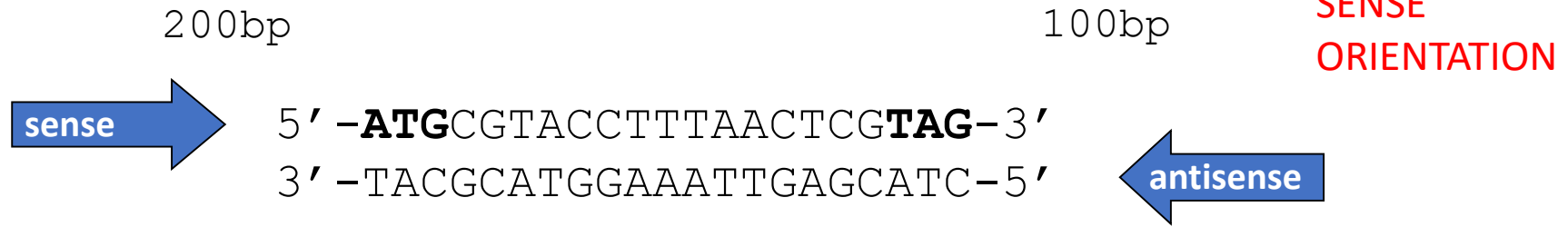
5' - **ATG**CGTACCTTTAACTCG**TAG**-3'  
 3' - TACGCATGGAAATTGAGCATC-5'



INSERT cloned in ANTISENSE orientation

5' - CTACGAGTTAAAGGTACGCAT-3'  
 3' - **GAT**GCTGAATTTCCATGCG**GTA**-5'





SENSE: NNNNNN**ATGCGTACCTTTAACTCGTAG**NNNNNN  
 ANTISENSE: NNNNNNCTACGAGTTAAAGGTACGCATNNNNNN

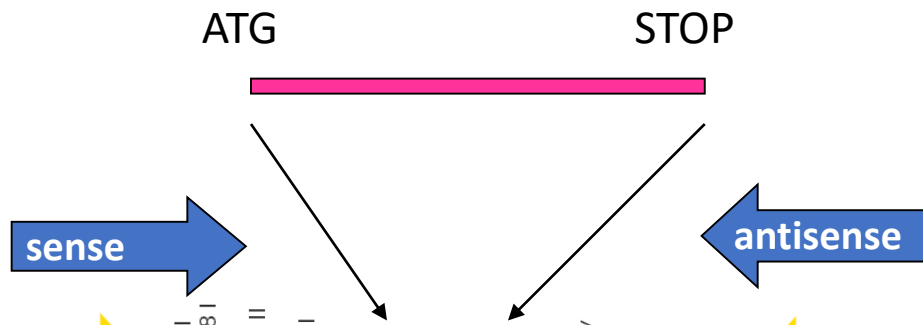
BLAST:

**Query:** 1 **ATGCGTACCTTTAACTCGTAG** 21  
 |||||

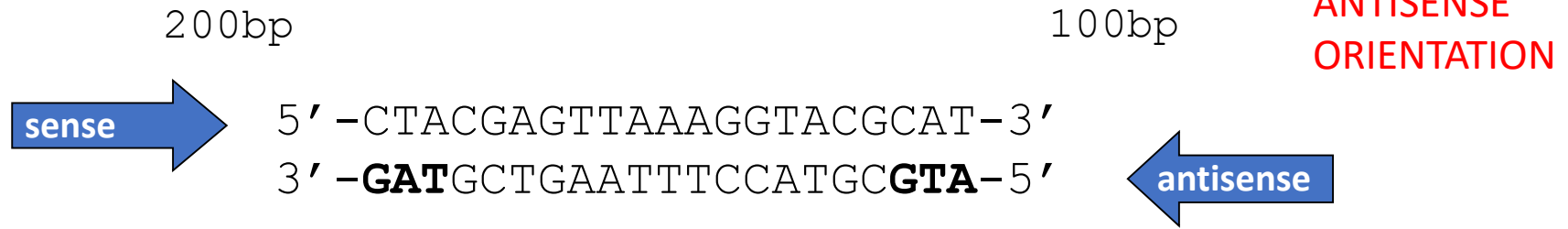
**Subjt Sense :** 201 **ATGCGTACCTTTAACTCGTAG** 221

**Query:** 1 **ATGCGTACCTTTAACTCGTAG** 21  
 |||||

**Subjt Antisense:** 121 **ATGCGTACCTTTAACTCGTAG** 101



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SENSE: NNNNNNNCTACGAGTTAAAGGTACGCATNNNNNNN

ANTISENSE: NNNNNNN**ATG**CGTACCTTTAACTCG**TAG**NNNNNNN

BLAST:

**Query:** 1 **ATGCGTACCTTTAACTCGTAG** 21

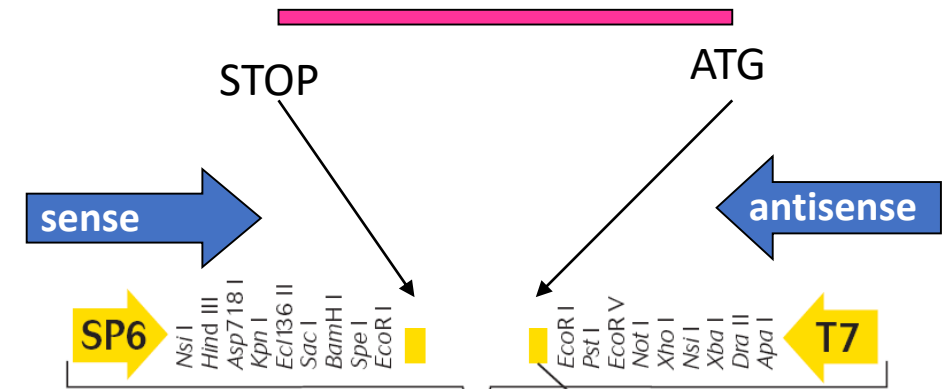
|||||

**Subjt Sense:** 221 **ATGCGTACCTTTAACTCGTAG** 201

**Query:** 1 **ATGCGTACCTTTAACTCGTAG** 21

|||||

**Subjt Antisense:** 101 **ATGCGTACCTTTAACTCGTAG** 121



Only for teaching purposes - not for reproduction or sale



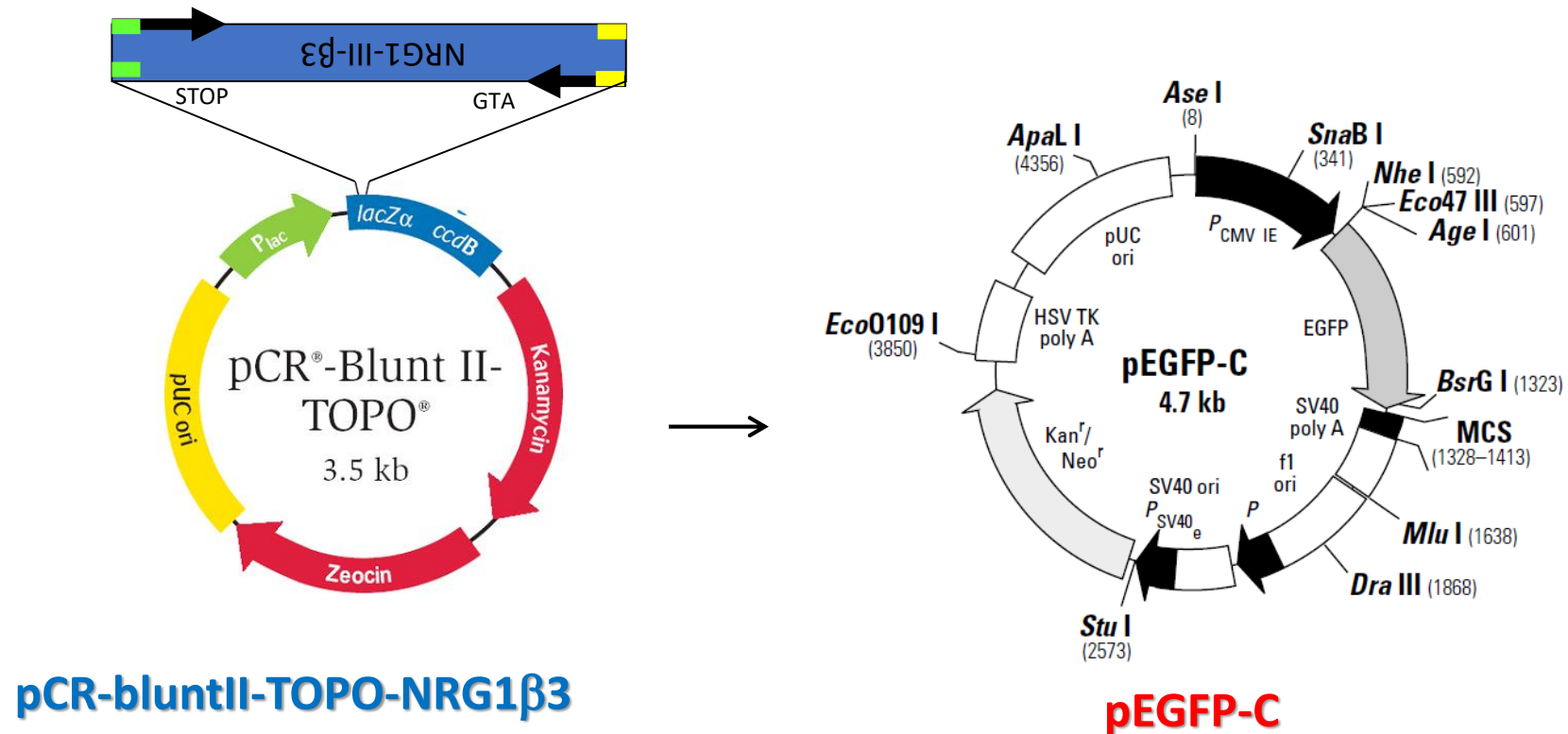
## Biotechnology Project – V lesson

0 – Summary of the previous lesson

1 - Subcloning NRG1-III- $\beta$ 3 from pCR-Blunt II-TOPO into the expression vector pEGFP-C1, 2 or 3

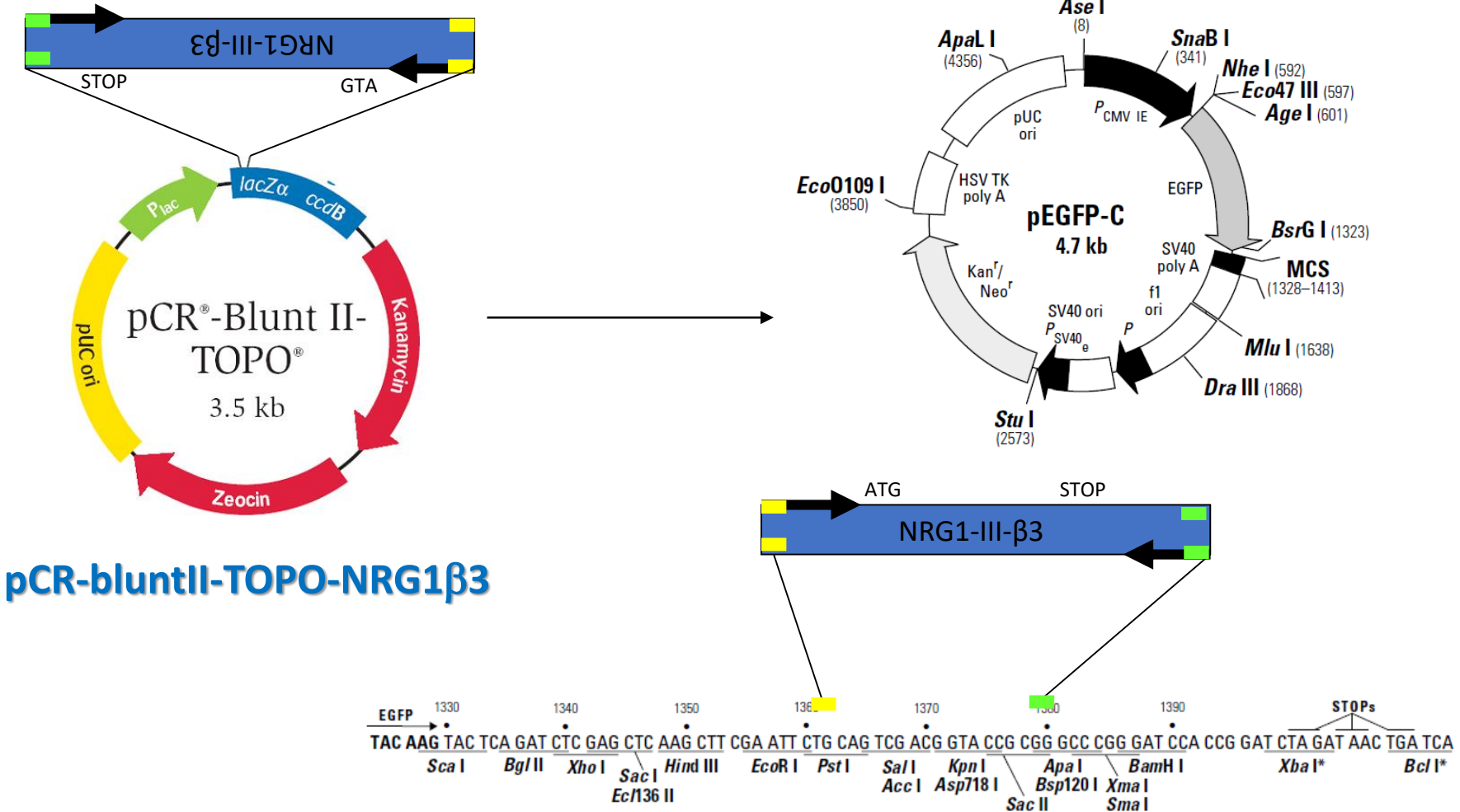
2 - Subcloning NRG1-III- $\beta$ 3 from pCR-Blunt II-TOPO or pEGFP-C3 into the expression vector pCMV-Tag4

# 1-Subcloning NRG1-III- $\beta$ from pCR-Blunt II-TOPO into pEGFP-C



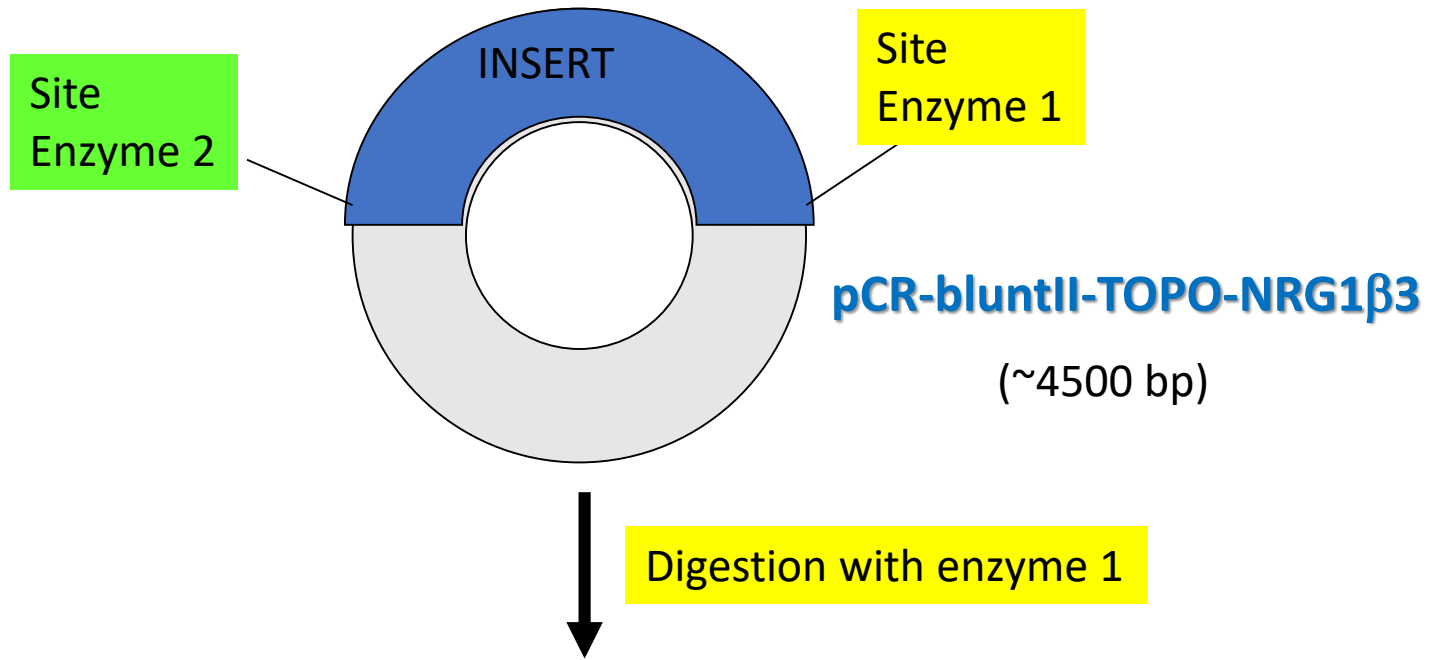


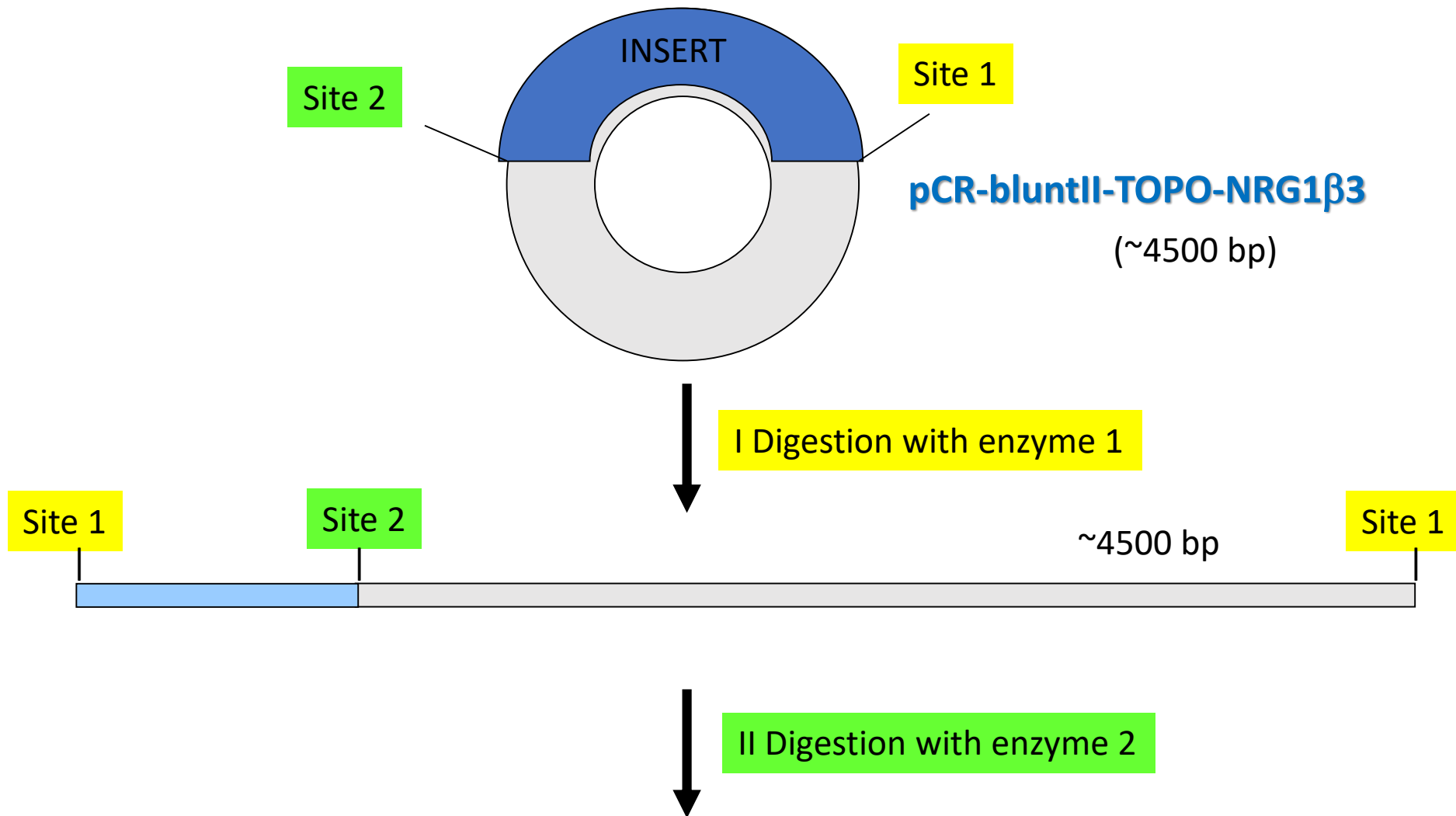
both c/d and g/h were cloned antisense

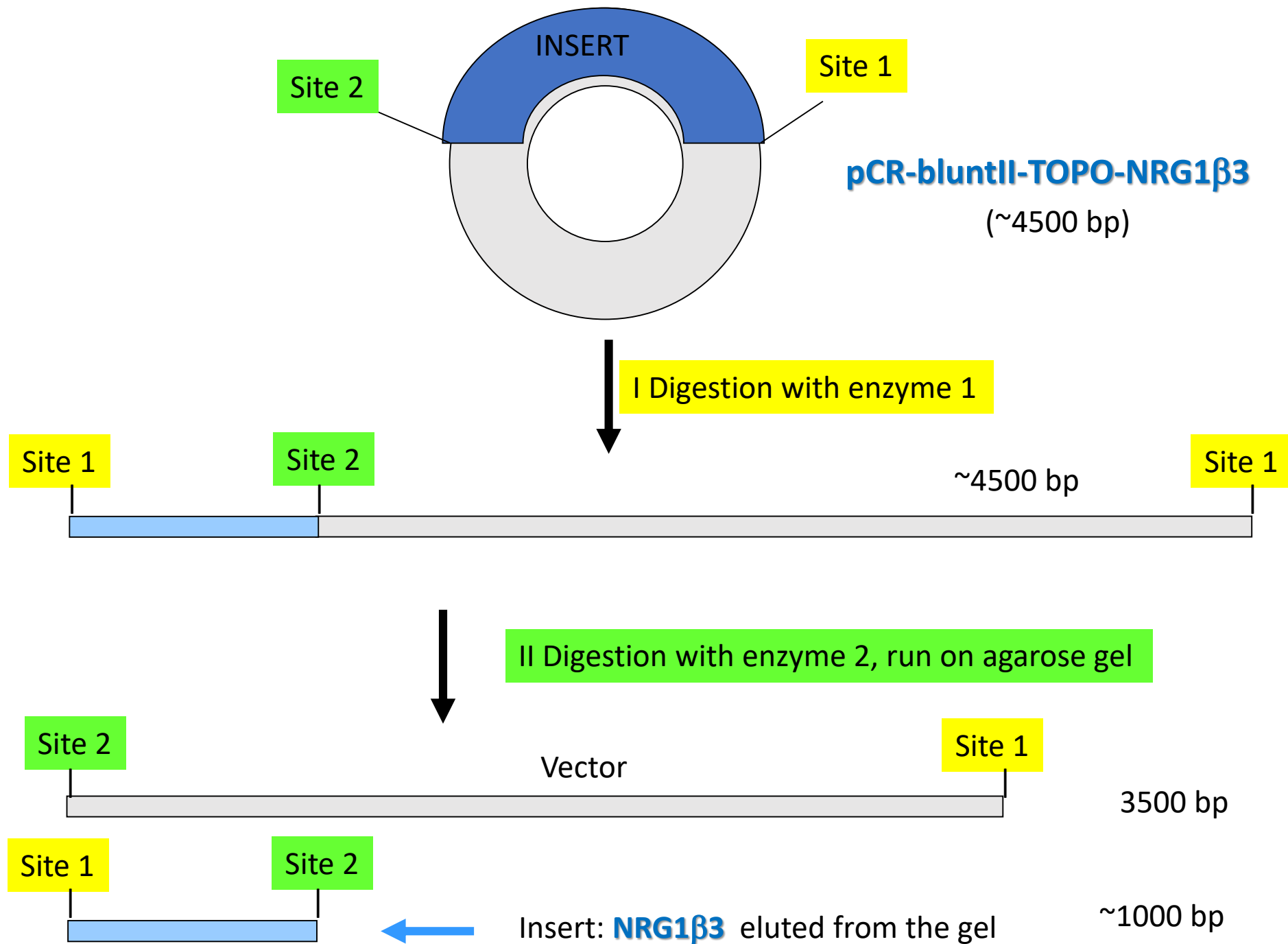


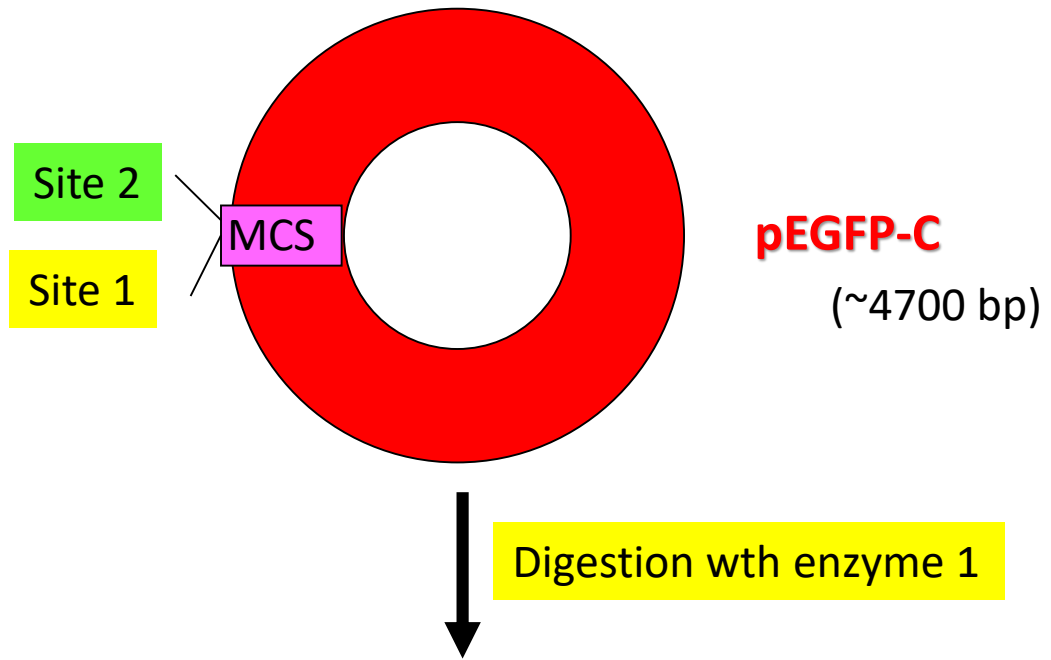
To transfer the insert (cDNA coding NRG1IIIβ3) from the vector **pCR-blunt II TOPO** into the new vector **pEGFP-C** you have to digest both vectors:

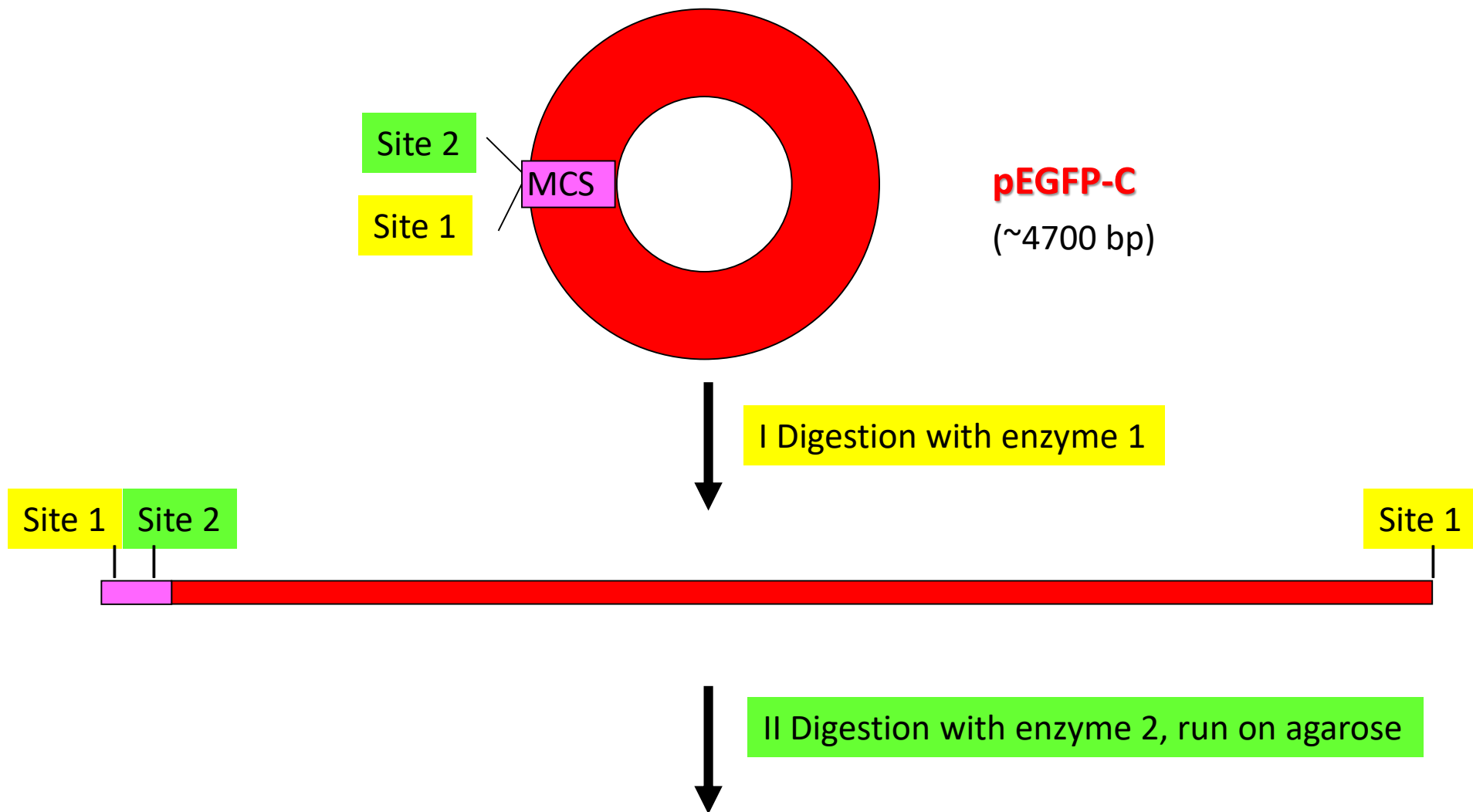
- 1- with the restriction enzyme that cuts on the upstream primer (**yellow**);
- 2- with the restriction enzyme that cuts on the downstream primer (**green**).

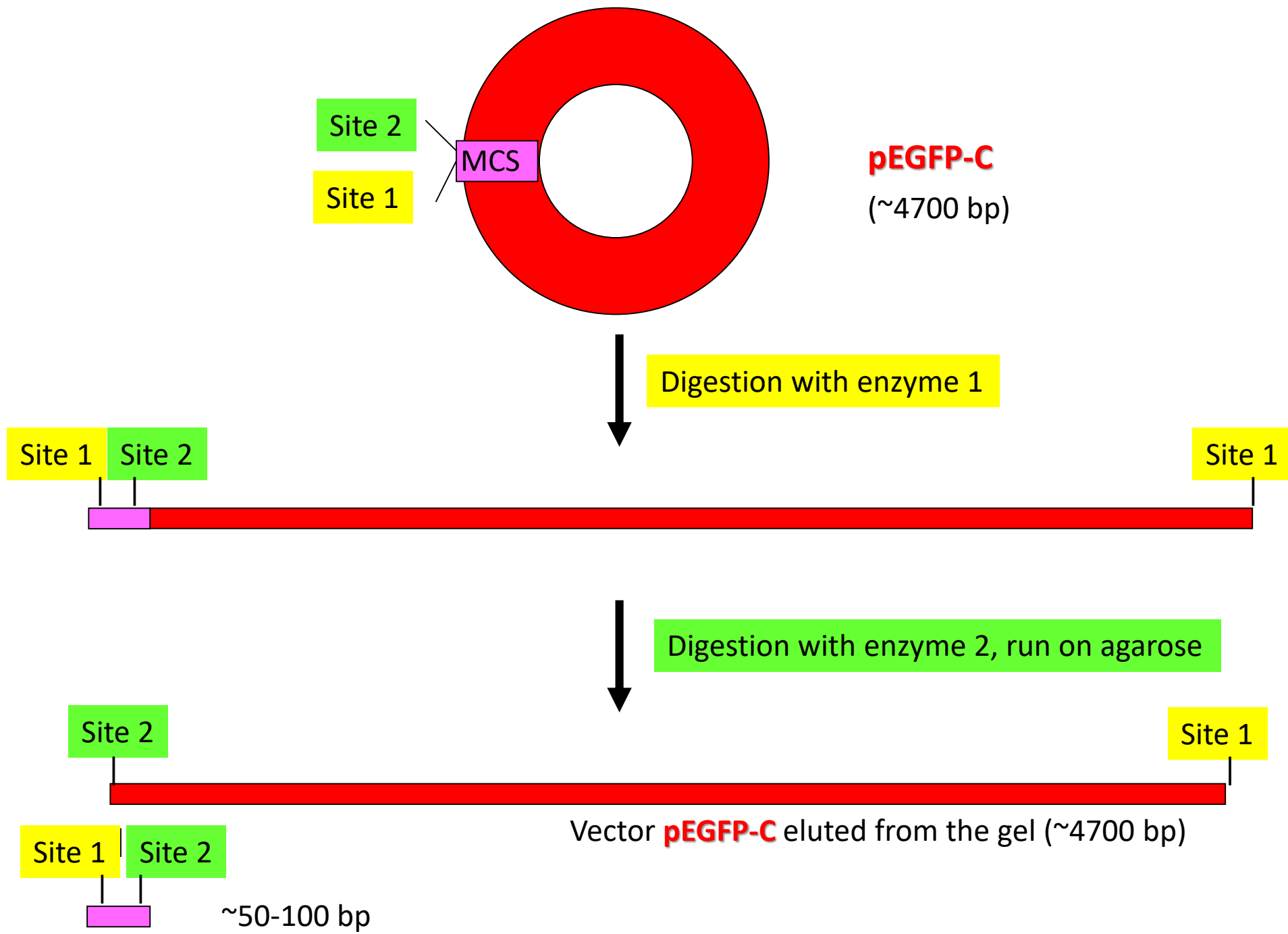




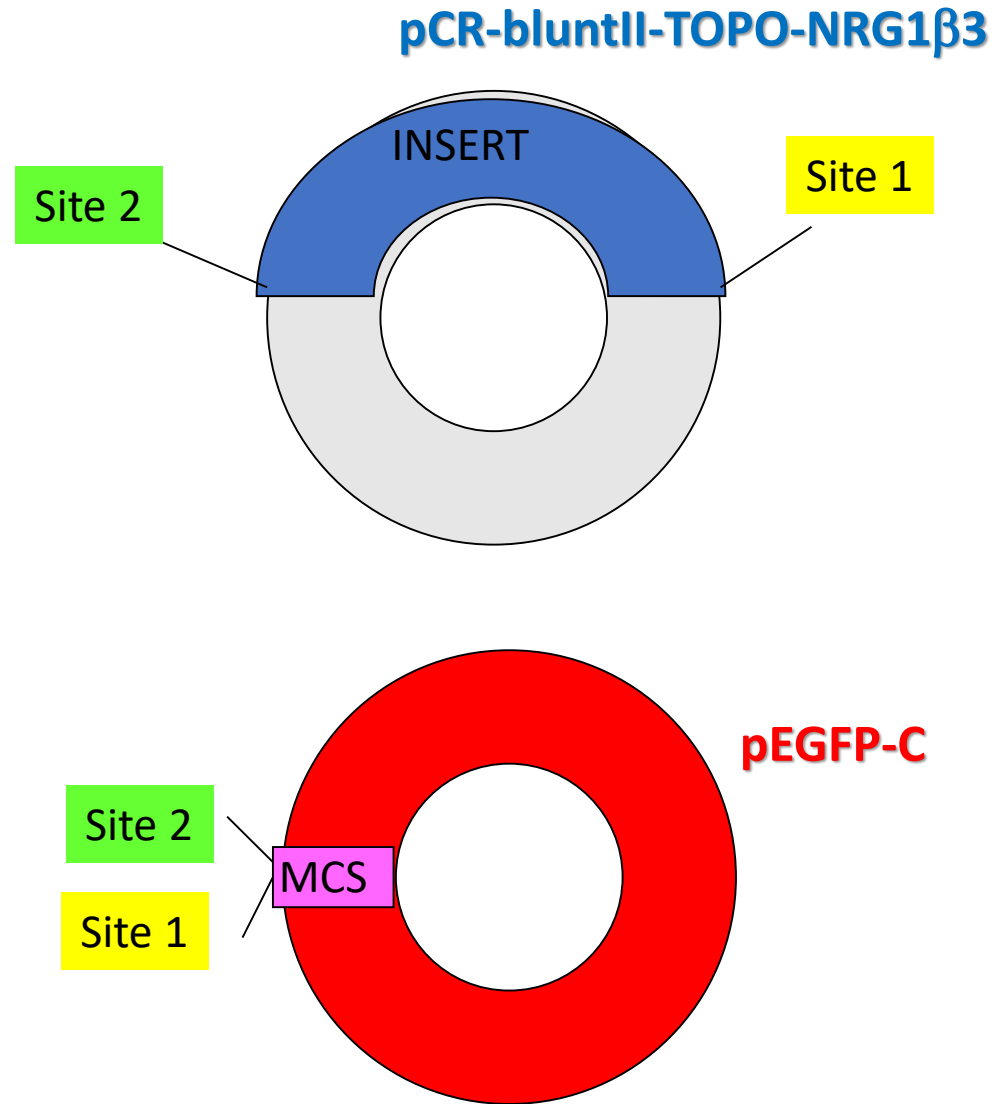
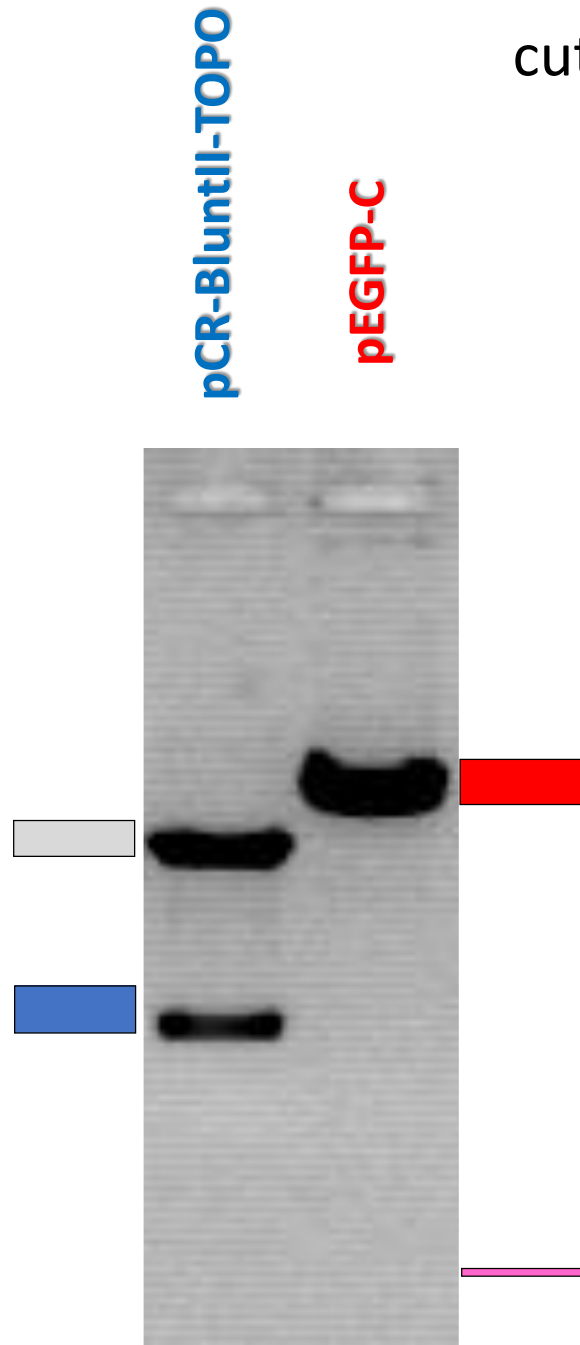








**pCR-Blunt II-TOPO & pEGFP-C**  
cut with the enzyme 1 and enzyme 2





# I digestion

**pCR-BluntII-TOPO-NRG1-III-β3 (2,5 µg/µl)**

buffer 10x (which?)

Enzyme I (which?)

BSA 10x (1 µg/µl)

H<sub>2</sub>O

µl -> 20 µg

µl -> 1x

µl -> 1u/µg

µl -> 1x (0,1 µg/µl)

---

total

50 µl

**pEGFP-C (1, 5 µg/µl)**

buffer 10x (which?)

Enzyme I (which?)

BSA 10x (1 µg/µl)

H<sub>2</sub>O

µl -> 5 µg

µl -> 1x

µl -> 1u/µg

µl -> 1x (0,1 µg/µl)

---

total

50 µl

- after digestion with the first enzyme, verify that digestion is complete by running 5  $\mu$ l on agarose gel
- purify DNA by loading it on a column
- elute purified DNA in 50 $\mu$ l water
- proceed with the second digestion

# II digestion

## pCR-BluntII-TOPO-NRG1-III-β3

(already digested with enzyme I)

buffer 10x (which?)

Enzyme II (which?)

BSA 10x (1 μg/μl)

H<sub>2</sub>O

μl (how many μl?)

μl -> 1x

μl -> 1u/μg

μl -> 1x (0,1 μg/μl)

---

total

μl (how many μl?)

## pEGFP-C

(already digested with enzyme I)

buffer 10x (which?)

enzyme II (which?)

BSA 10x (1 μg/μl)

H<sub>2</sub>O

μl (how many μl?)

μl -> 1x

μl -> 1u/μg

μl -> 1x (0,1 μg/μl)

---

total

μl (how many μl?)

- after digestion with the second enzyme, verify that digestion is complete by running 5  $\mu$ l on agarose gel
- run the digestion on an agarose gel and purify the insert and the vector for the following ligase reaction

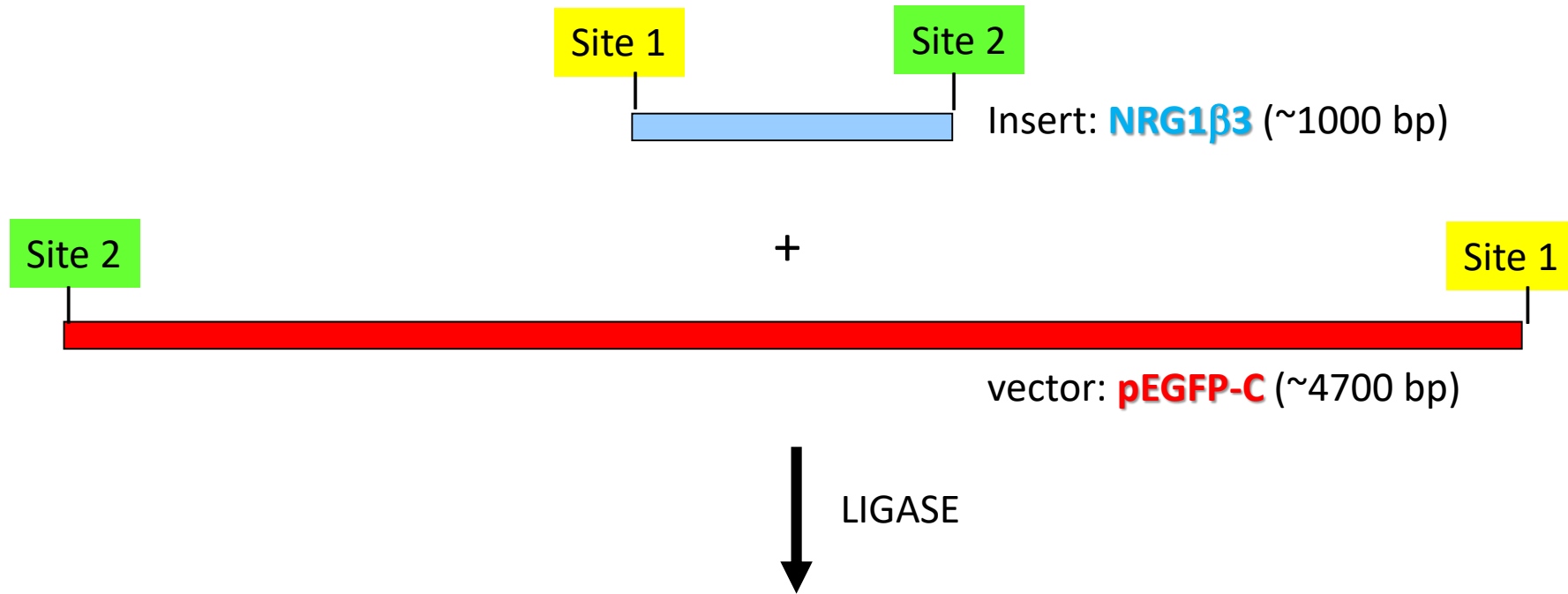
If the two enzymes cut DNA in the same buffer,  
you can digest DNA with both enzymes together

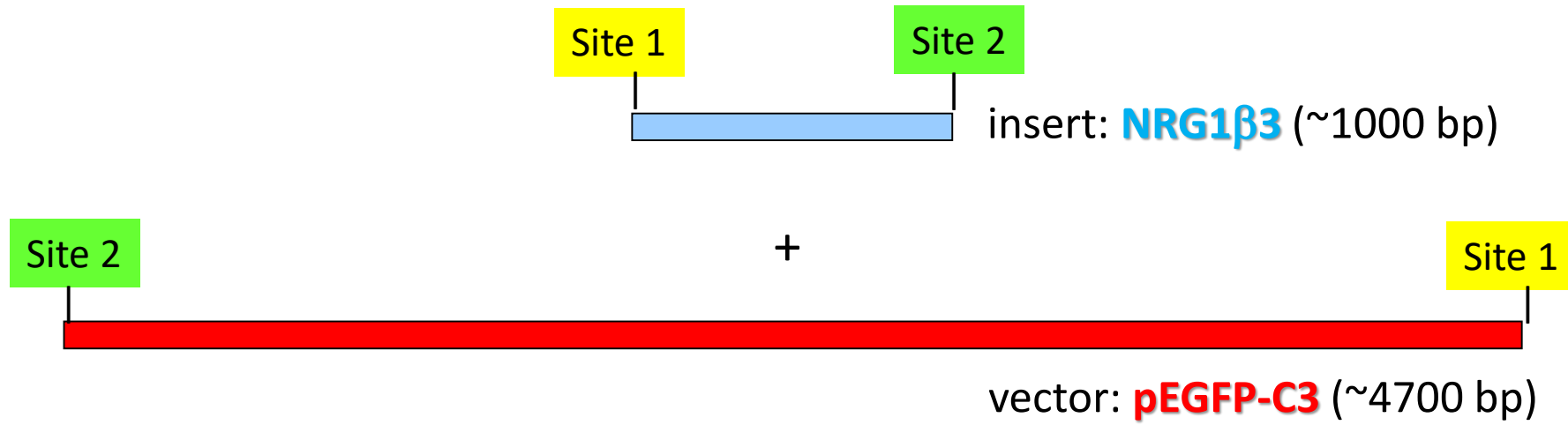
## Single digestion (enzyme I + enzyme II)

<b>pCR-BluntII-TOPO-NRG1-III-β3</b> (2,5 µg/µl)	µl	-> 20 µg
buffer 10x (which?)	µl	-> 1x
Enzyme I (which?)	µl	-> 1u/µg
Enzyme II (which?)	µl	-> 1u/µg
BSA 10x (1 µg/µl)	µl	-> 1x (0,1 µg/µl)
H2O		
<hr/>		
total	50 µl	

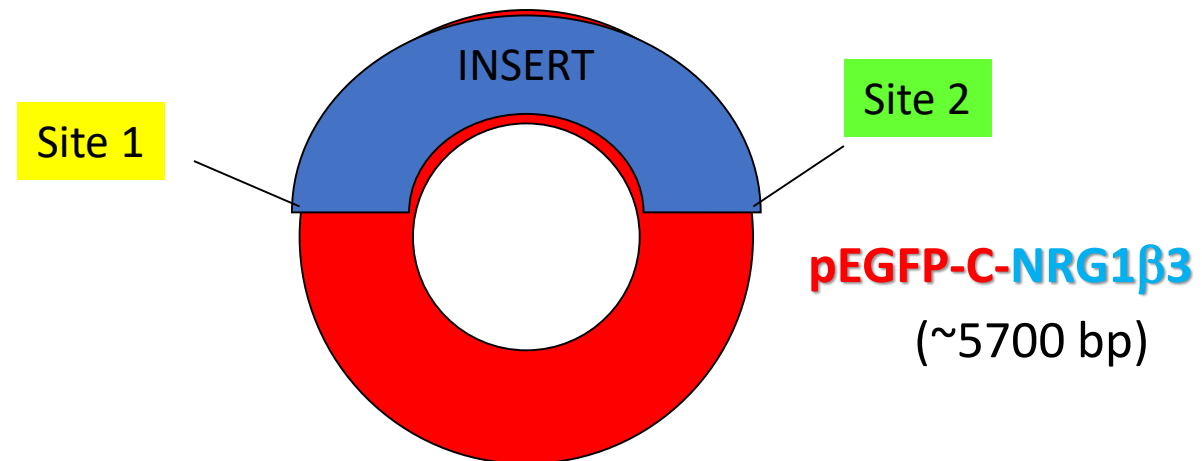
Use about 1 unit (u) enzyme/µg DNA

<b>pEGFP-C</b> (1,5 µg/µl)	µl	-> 5 µg
buffer 10x (which?)	µl	-> 1x
Enzyme I (which?)	µl	-> 1u/µg
Enzyme II (which?)	µl	-> 1u/µg
BSA 10x (1 µg/µl)	µl	-> 1x (0,1 µg/µl)
H2O		
<hr/>		
total	50 µl	





↓  
LIGASE





## I Exercise:

- identify the buffers to digest with enzyme 1 and enzyme 2 the vector with the insert (**pCR-bluntII-TOPO**) and the vector for the following subcloning (**pEGFP-C**)

As we do in the in notebook in the lab, write the protocol for all necessary passages to digest the vector with the insert (pCR-bluntII-TOPO) and the vector for the following subcloning (pEGFP-C3):

- first digestion (write all ingredients of the first reaction)
- purification of the DNA?
- second digestion (write all ingredients of the second reaction)

OR

- first & second digestion together (write all ingredients of the reaction)

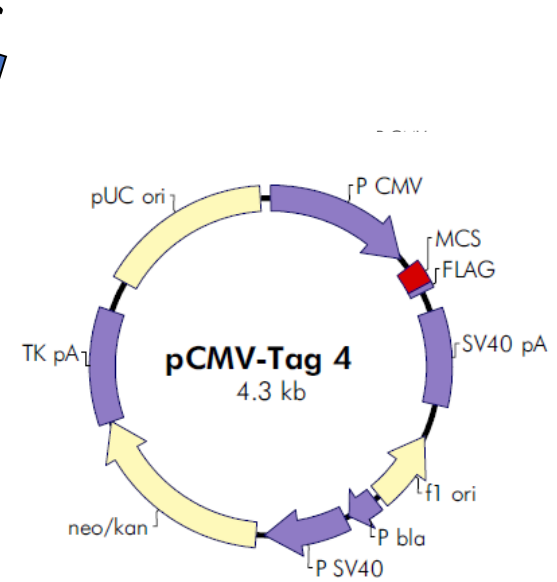
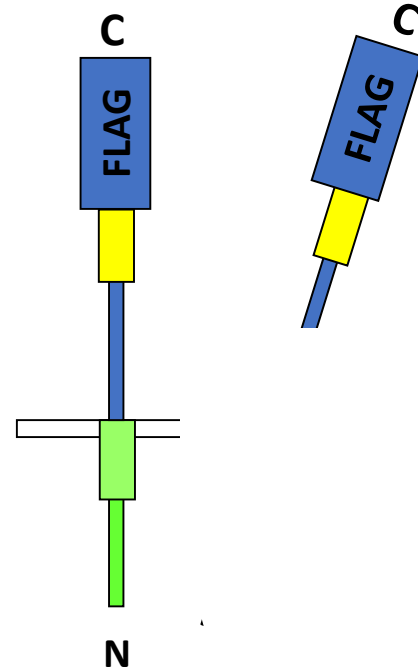
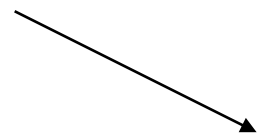
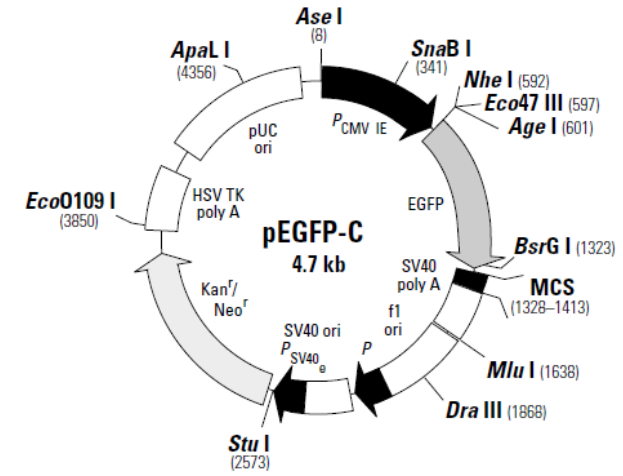
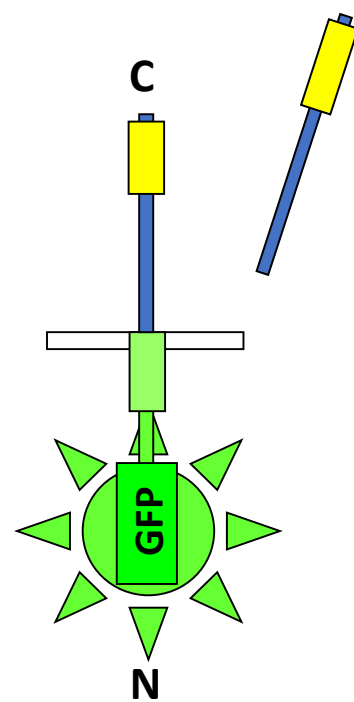
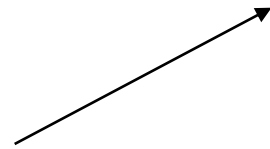
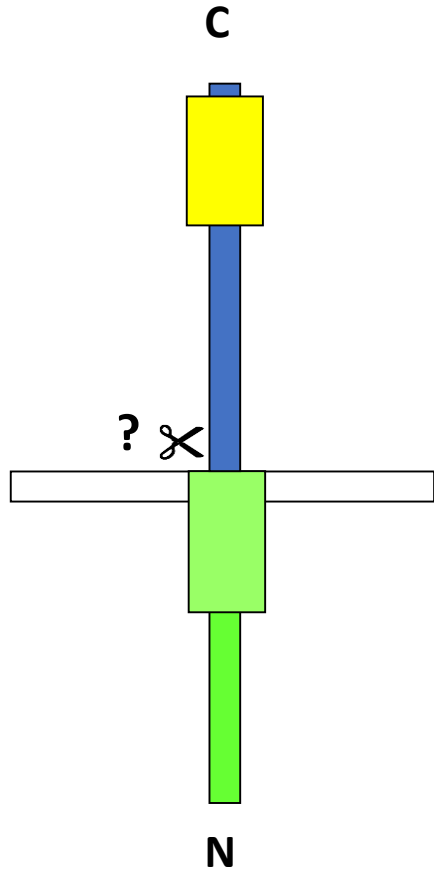


## Biotechnology Project – V lesson

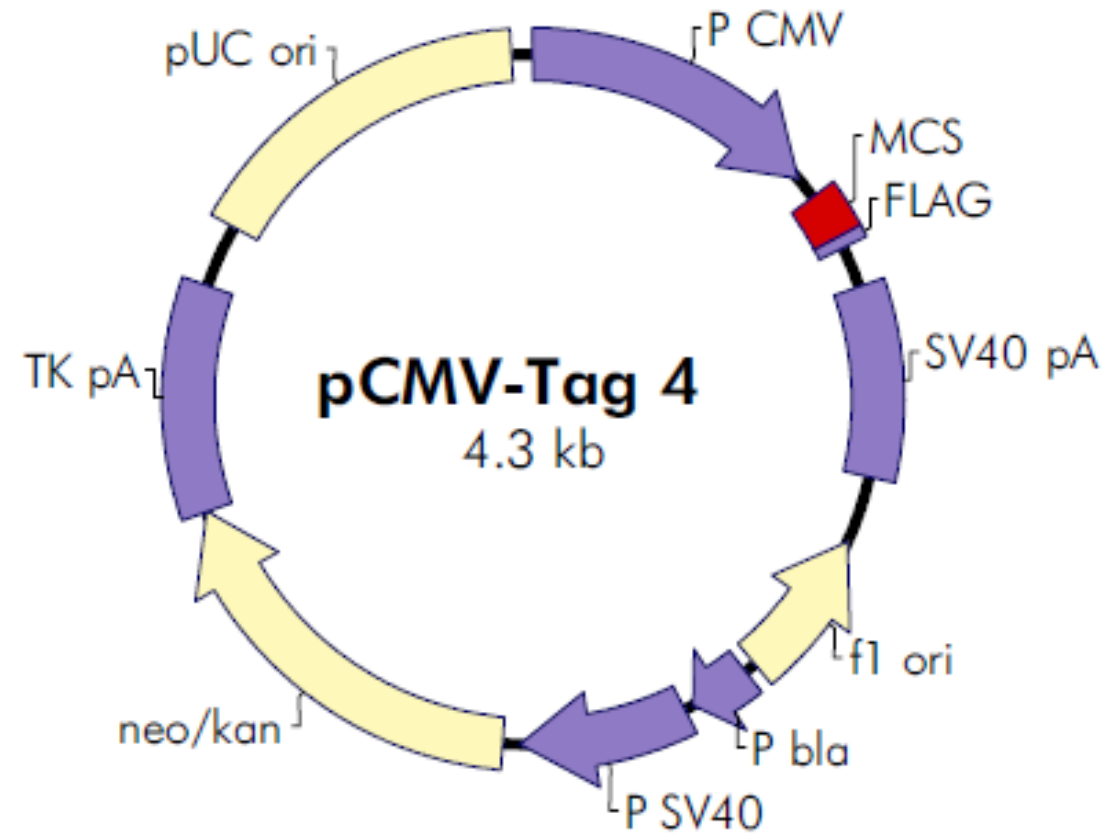
0 – Summary of the previous lesson

1 - Subcloning NRG1-III- $\beta$ 3 from pCR-Blunt II-TOPO into the expression vector pEGFP-C3

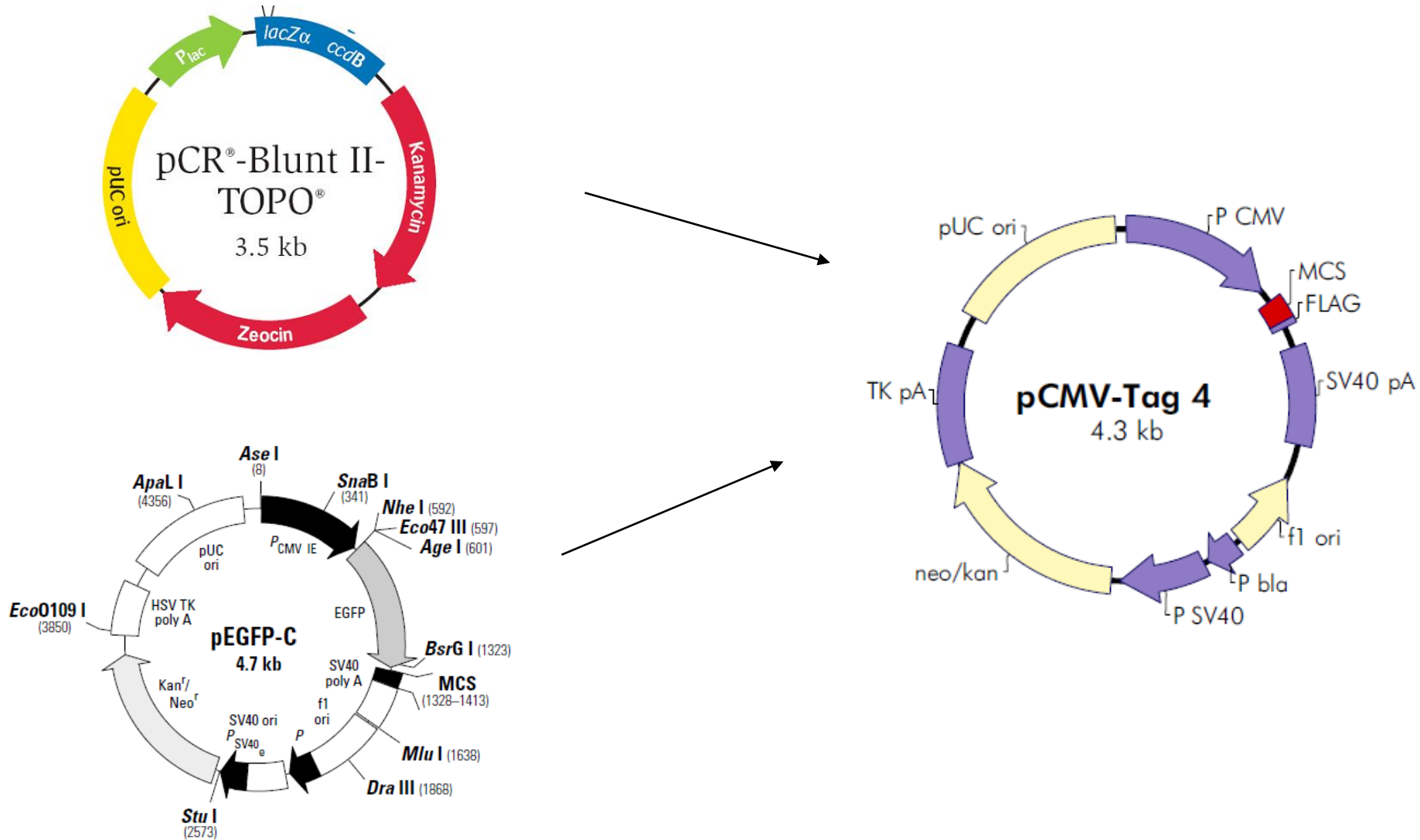
2 - Subcloning NRG1-III- $\beta$ 3 from **pCR-Blunt II-TOPO** or **pEGFP-C** into the expression vector **pCMV-Tag4**

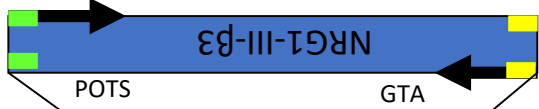


## 2-Subcloning into the expression vector **pCMV-Tag4**

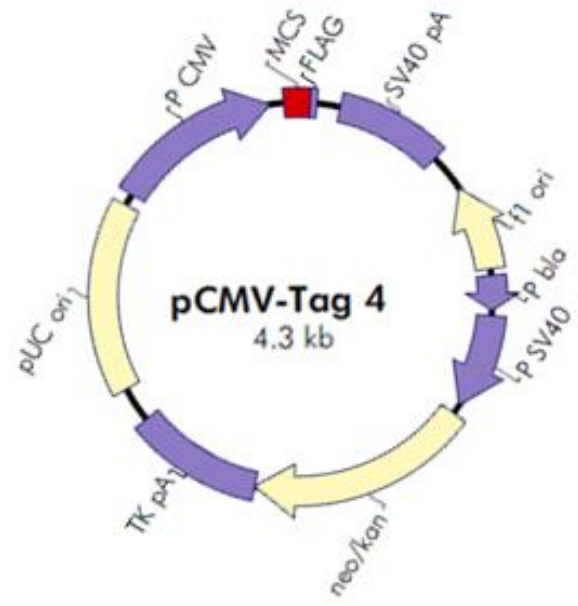
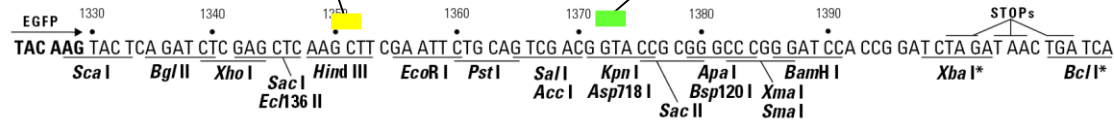
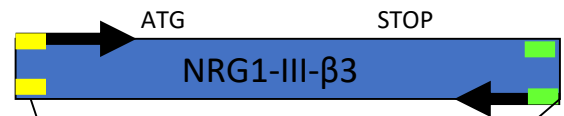
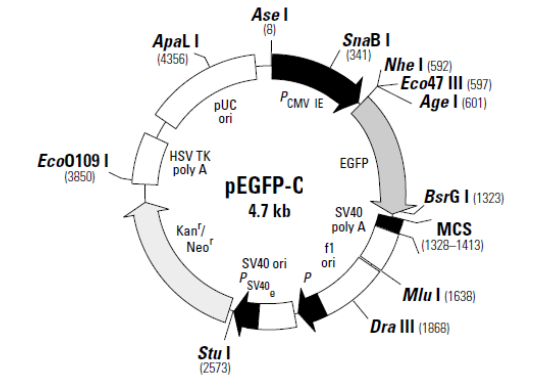


# Subcloning into the expression vector **pCMV-Tag4**

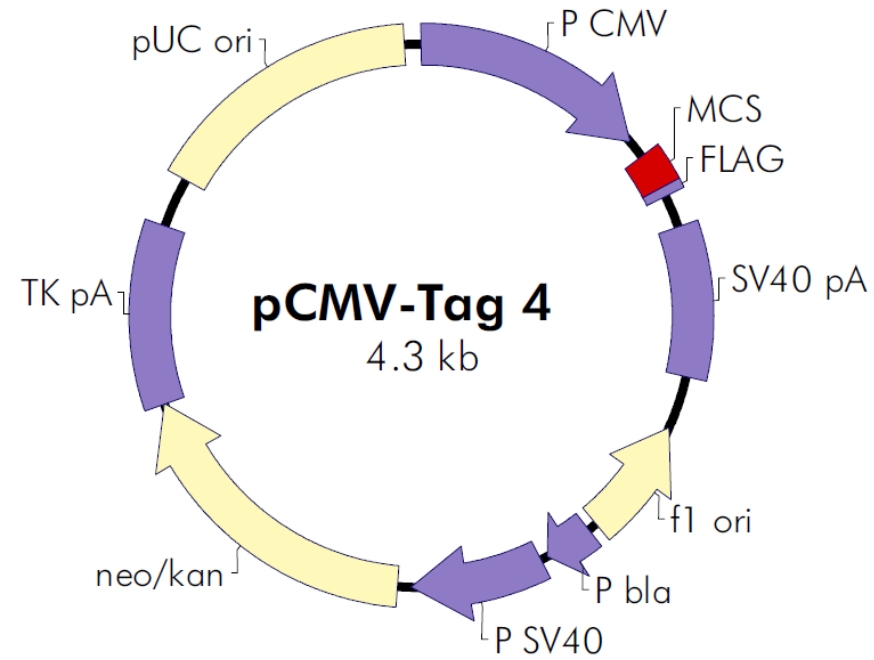




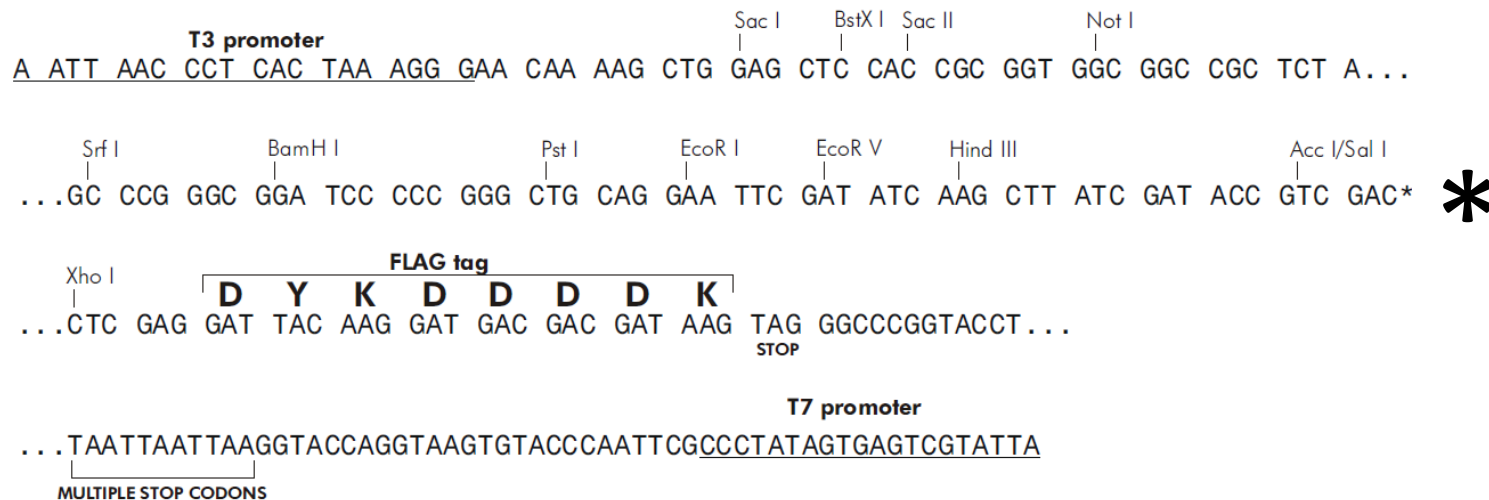
- Nsi I
- Hind III
- Asp718 I
- Kpn I
- Ecl136 II
- Sac I
- BamH I
- Spe I
- EcoR I
- EcoR I
- EcoR V
- Pst I
- Not I
- Xho I
- Nsi I
- Xba I
- Dra II
- Apa I



# pCMV-Tag 4A

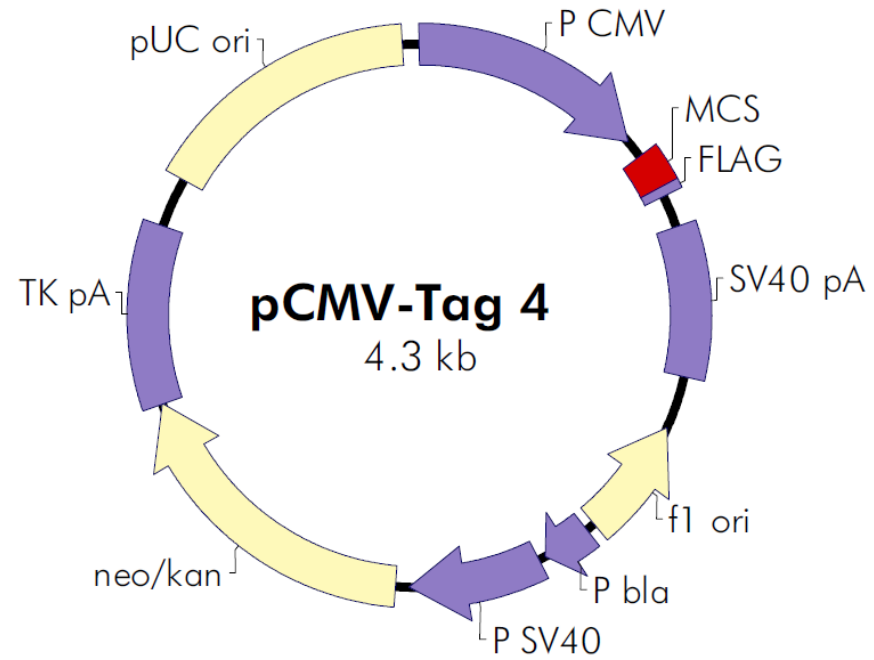


## pCMV-Tag 4 Multiple Cloning Site Region (sequence shown 620–839)

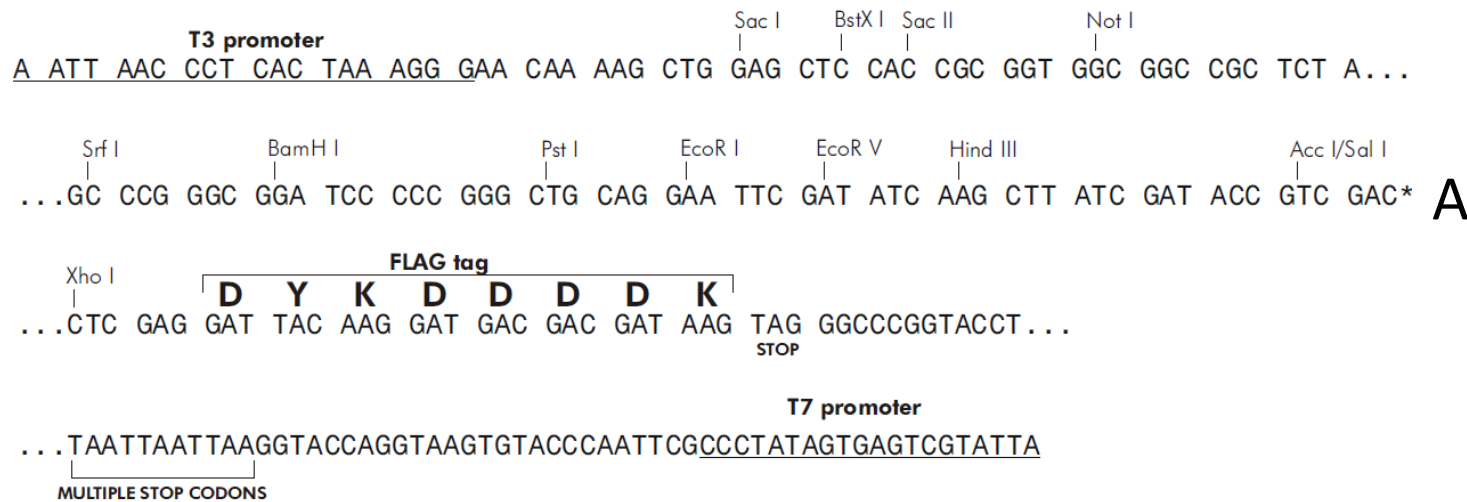


\* In pCMV-Tag 4A, no bases inserted; in pCMV-Tag 4B, A inserted; in pCMV-Tag 4C, AA inserted

# pCMV-Tag 4B



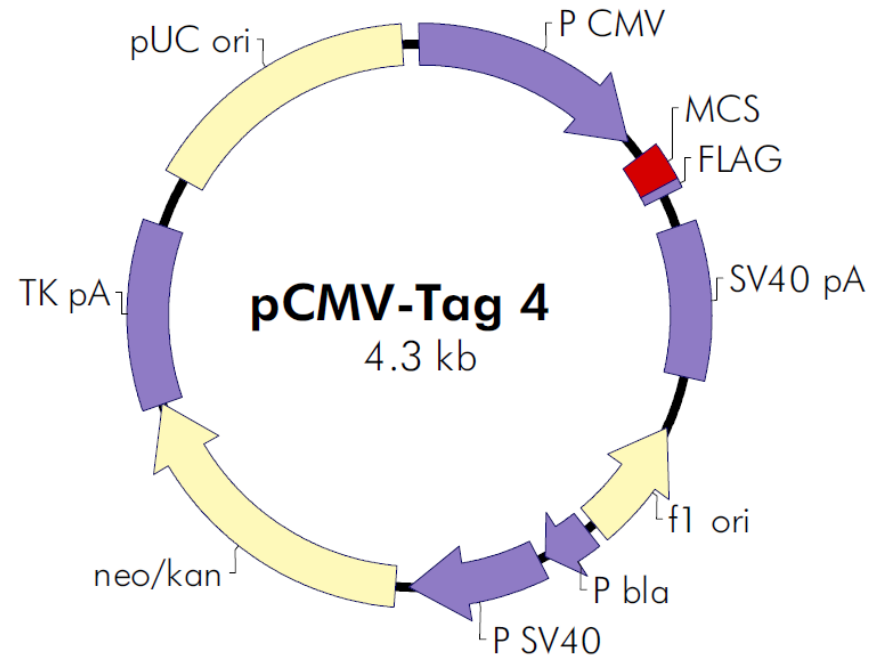
## pCMV-Tag 4 Multiple Cloning Site Region (sequence shown 620–839)



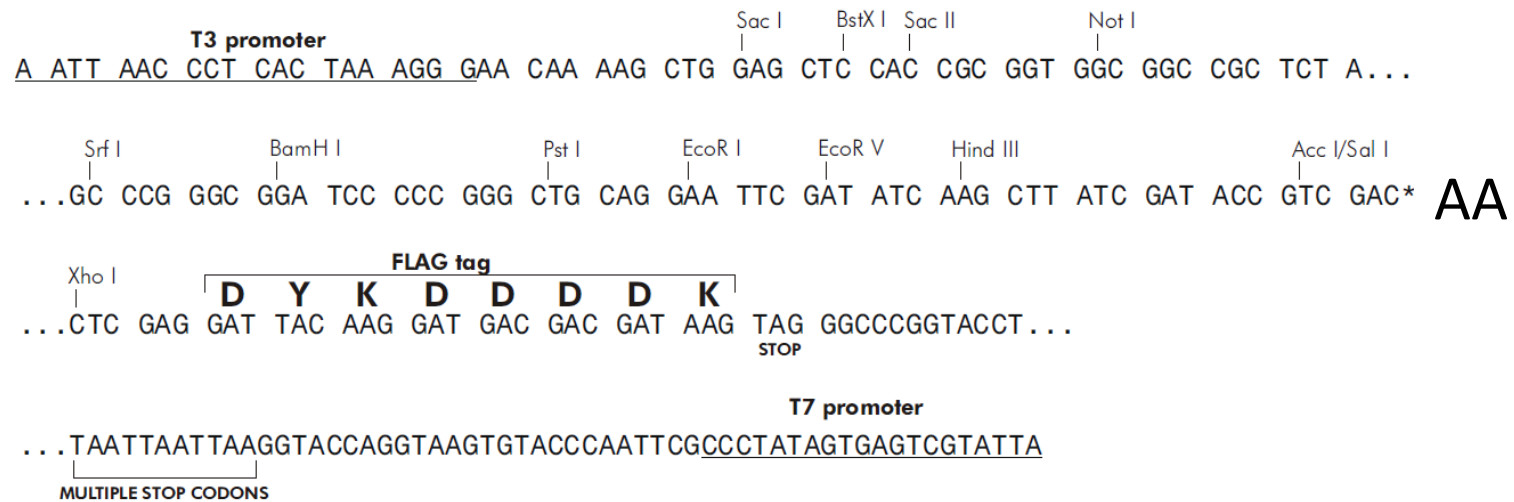
\* In pCMV-Tag 4A, no bases inserted; in pCMV-Tag 4B, A inserted; in pCMV-Tag 4C, AA inserted



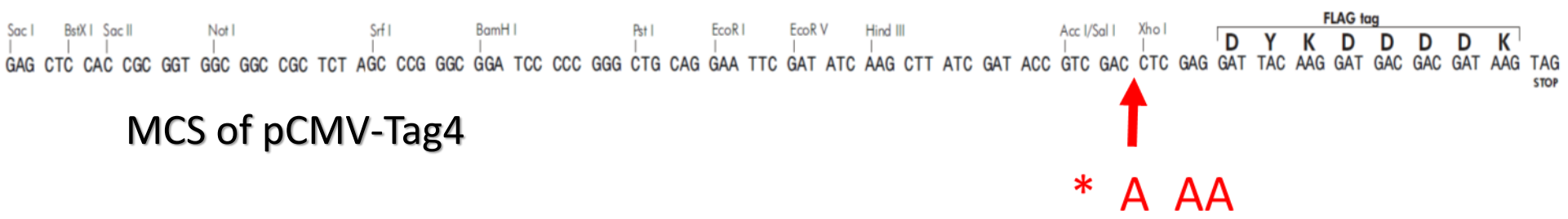
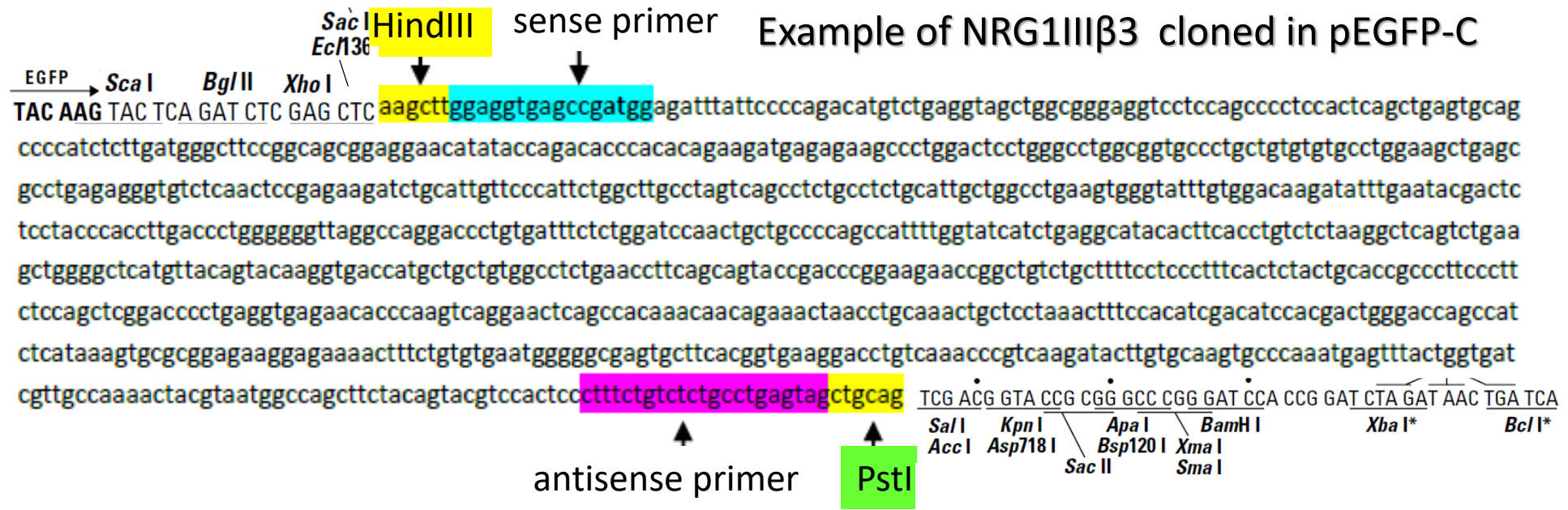
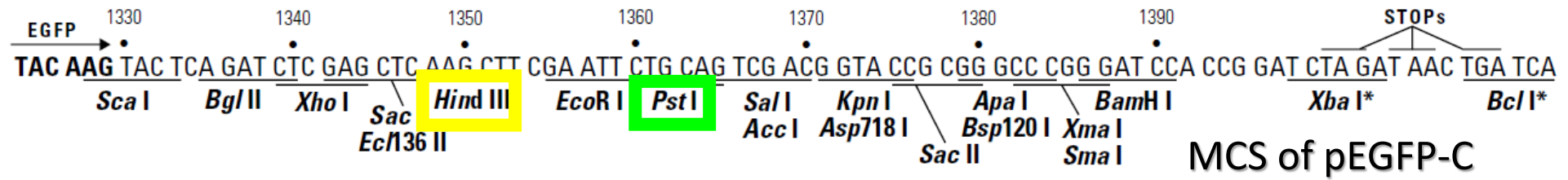
# pCMV-Tag 4C



## pCMV-Tag 4 Multiple Cloning Site Region (sequence shown 620–839)



\* In pCMV-Tag 4A, no bases inserted; in pCMV-Tag 4B, A inserted; in pCMV-Tag 4C, AA inserted



### pCMV-Tag 4A Multiple Cloning Site Region

(sequence shown 620–839)

ATT AAC CCT CAC TAA AGG GAA CAA AAG CTG **GAG CTC** CAC **CGC** **GGT** GGC  
GGC CGC TCT AGC CCG GGC **GGA TCC** CCC GGG **CTG CAG** **GAA TTC** **GAT ATC**  
**AAG CTT** ATC GAT ACC GTC GAC\*CTC GAG **GAT TAC AAG GAT GAC GAC GAT**  
**AAG** TAG GGC CCG GTA CCT TAA TTA ATT AAG GTA CCA GGT AAG TGT ACC  
CAA TTC GCC CTA TAG TGA GTC GTA TTA

<b>EcoRI</b>	<b>PstI</b>	<b>SacII</b>
<b>EcoRV</b>	<b>BamHI</b>	
<b>HindIII</b>	<b>SacI</b>	<b>FLAG</b>

### pCMV-Tag 4B Multiple Cloning Site Region

(sequence shown 621–840)

TTA ACC CTC ACT AAA GGG AAC AAA AGC TGG **AGC TCC** ACC **GCG** **GTG** GCG  
GCC GCT CTA GCC CGG GCG **GAT CCC** CCG GGC **TGC AGG** **AAT TCG** **ATA TCA**  
**AGC TTA** TCG ATA CCG TCG ACA CTC GAG **GAT TAC AAG GAT GAC GAC GAT**  
**AAG** TAG GGC CCG GTA CCT TAA TTA ATT AAG GTA CCA GGT AAG TGT ACC  
CAA TTC GCC CTA TAG TGA GTC GTA TTA

### pCMV-Tag 4C Multiple Cloning Site Region

(sequence shown 622–841)

TAA CCC TCA CTA AAG GGA ACA AAA GCT **GGA GCT** CCA **CCG CGG** TGG CGG  
CCG CTC TAG CCC GGG **CGG ATC CCC** CGG **GCT GCA GGA** **ATT CGA TAT CAA**  
**GCT TAT** CGA TAC CGT CGA **CAA** CTC GAG **GAT TAC AAG GAT GAC GAC GAT**  
**AAG** TAG GGC CCG GTA CCT TAA TTA ATT AAG GTA CCA GGT AAG TGT ACC  
CAA TTC GCC CTA TAG TGA GTC GTA TTA

## II Exercise

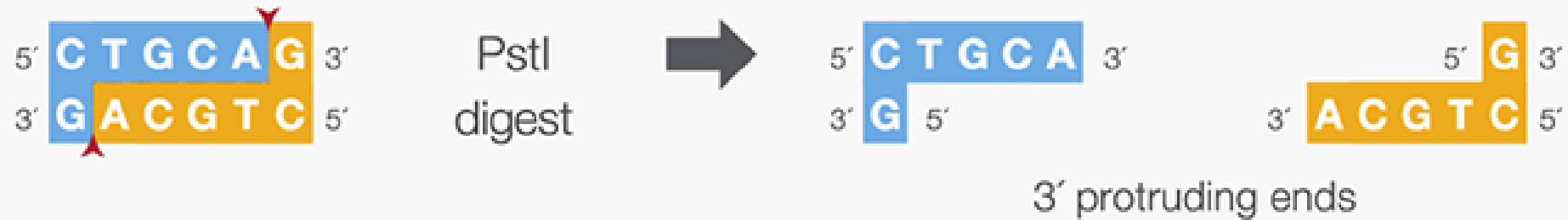
- find a cloning strategy to subclone the NRG1-III beta3 from the vector **pCR-bluntII-topo** **OR** from the vector **pEGFP-C** into the vector **pCMV-Tag4**
- identify which restriction sites can be used to recover the insert from one vector and which can be used to clone the insert
- identify which of the three plasmids (4A, 4B or 4C) do you have to use to maintain the frame between the NRG1 and the FLAG

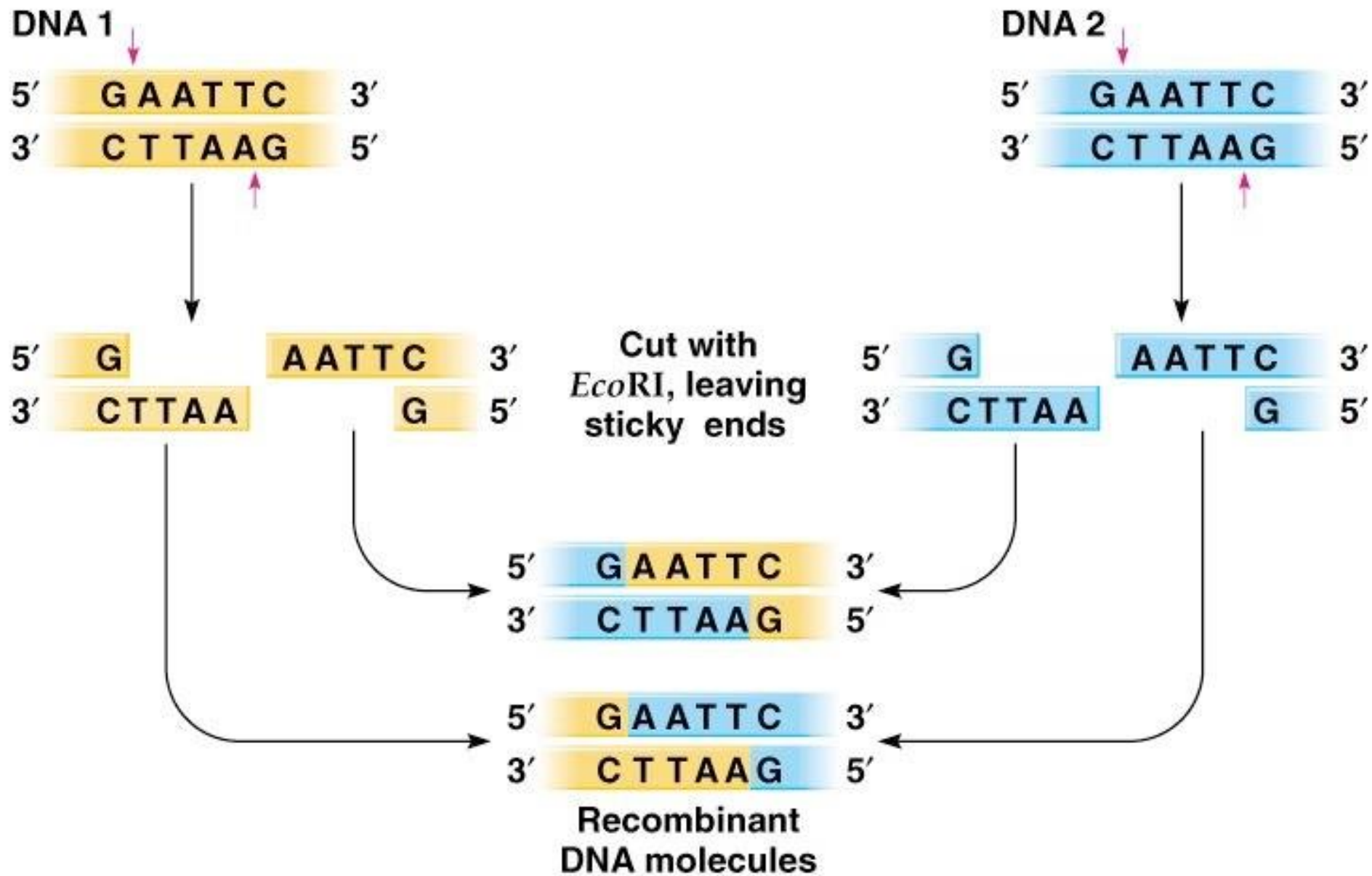
-> Translate the protein that you obtain after the cloning:  
if you have the correct frame you will obtain the NRG1 followed by the **FLAG:**  
**DYKDDDDK**

- if using plasmid 4A protein NRG1 is NOT in frame with the FLAG,  
try the other two plasmids: 4B and 4C,  
(you have to add A to obtain plasmid 4B or AA to obtain plasmid 4C to the  
multiple cloning site where there is an asterisk \*)

- prepare a sequence containing the multiple cloning site of the vector and NRG1 and, using neb-cutter, translate it to verify that NRG1 is in frame with the FLAG
- in a slide show the translation of NRG1 + flag (DYKDDDDK), with the information about the restriction enzymes you used to clone it
- if your insert can enter either sense or antisense, **please find** a restriction enzyme digestion to determine the insert orientation and write in the slide the name of the enzyme and the length of the fragments that you obtain when the insert is sense or antisense
- you can up-load the slide with map and cloning information on moodle
- **Please, up-load a single slide with all information!**

# Ends after restriction enzyme digestion





A microscopic image showing several cells with a complex network of green filaments (likely cytoskeleton) and prominent purple nuclei. The cells are set against a dark background. A white rectangular box is overlaid on the image, containing the text "Suggestions for the cloning strategy".

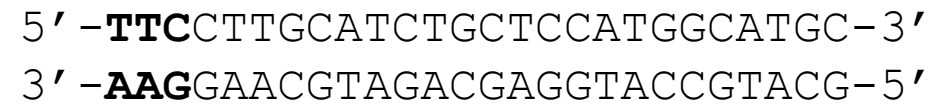
Suggestions for the cloning strategy



If the ends are both blunt you can ligate them,  
even if you used different restriction enzymes



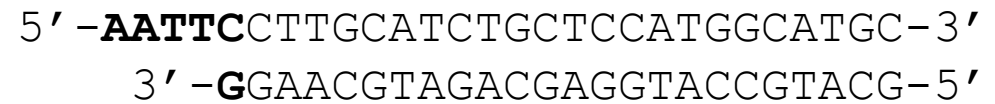
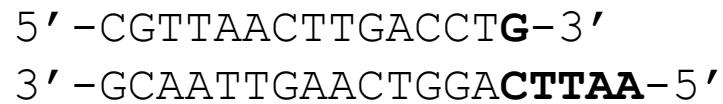
If the ends are both blunt you can ligate them,  
even if you used different restriction enzymes



- if you do not find suitable enzymes, you can blunt the ends obtained after restriction enzyme digestion with different enzymes, so they will become compatible



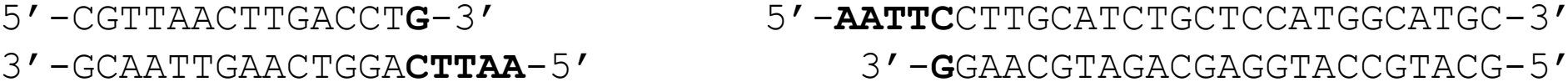
TYPE I ↓



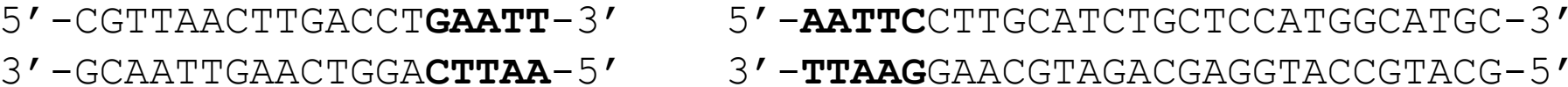
?



# BLUNTING TYPE I (5' PROTRUDING)



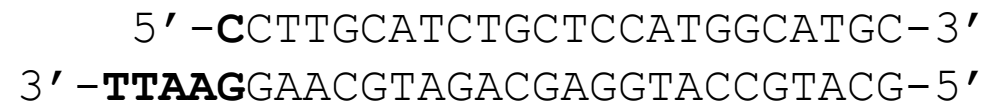
DNA polimerase (klenow)



- if you do not find suitable enzymes, you can blunt the ends obtained after restriction enzyme digestion with different enzymes, so they will become compatible



TYPE II ↓



?



## BLUNTING TYPE II (3' PROTRUDING)

5' -CGT TAACTTGACCT **GAATTC** CTTGCATCTGCTCCATGGCATGC -3'  
3' -GCAATTGAACTGGAC **CTTAAG** GAACGTAGACGAGGTACCGTACG -5'



5' -CGT TAACTTGACCT **GAATT** -3'  
3' -GCAATTGAACTGGAC -5'

5' -**C**CTTGCATCTGCTCCATGGCATGC -3'  
3' -**TTAAG**GAACGTAGACGAGGTACCGTACG -5'

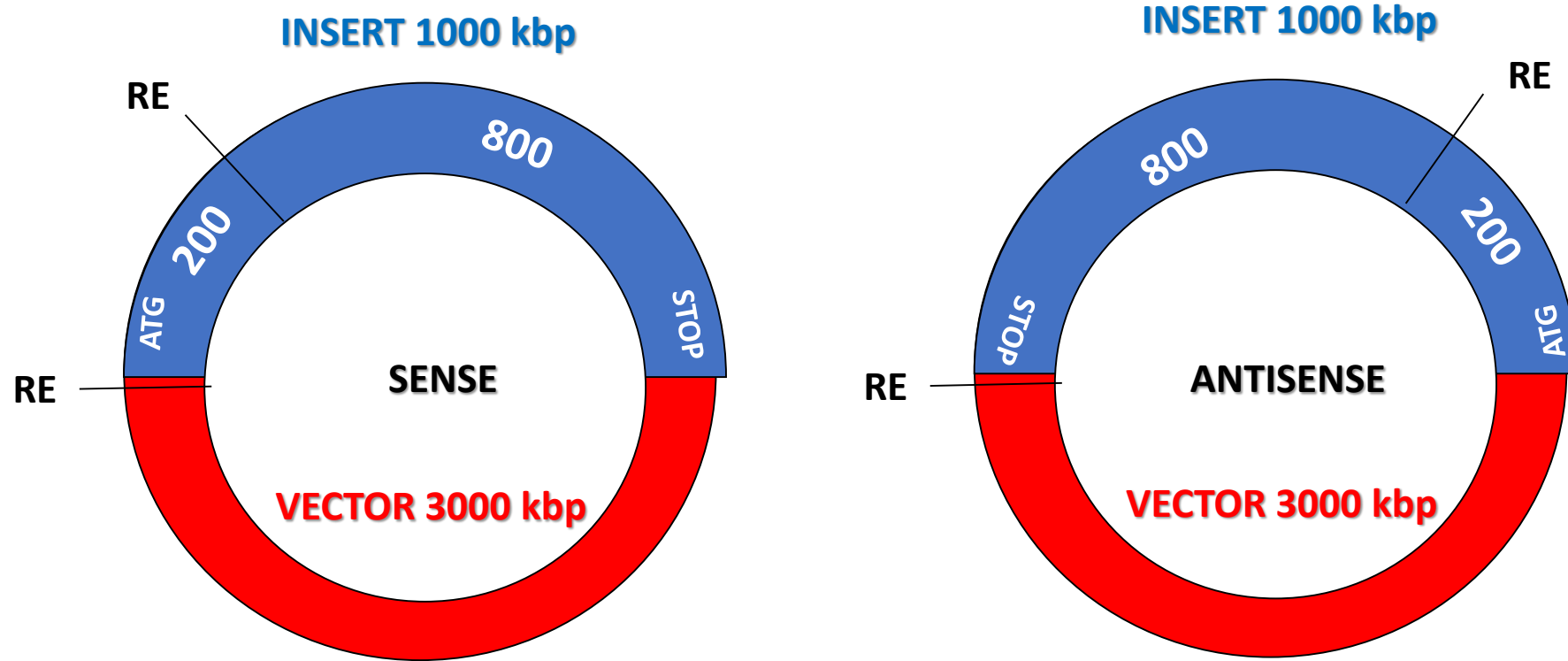


3'-DNA exonuclease

5' -CGT TAACTTGACCT **G** -3'  
3' -GCAATTGAACTGGAC -5'

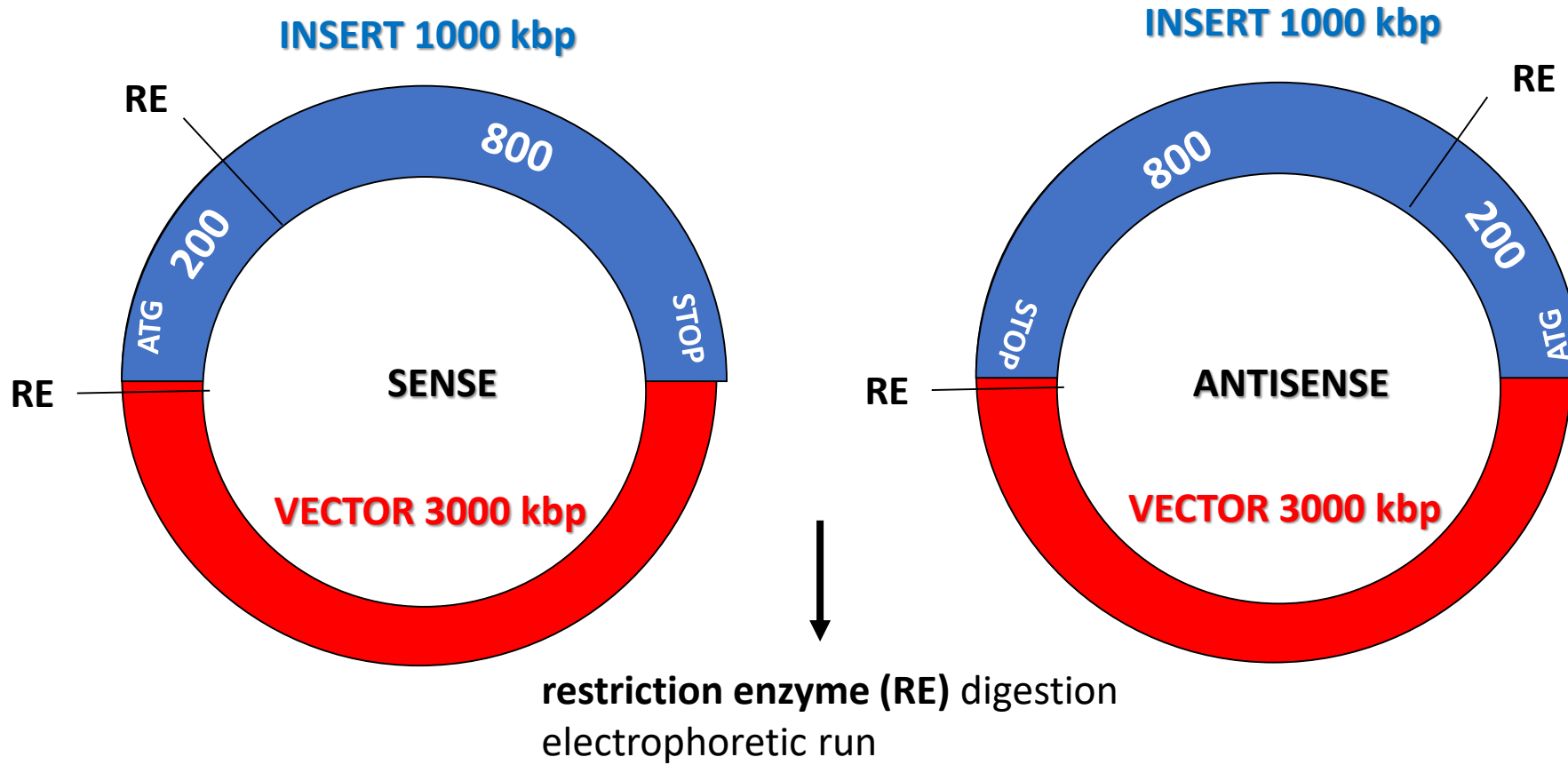
5' -**C**CTTGCATCTGCTCCATGGCATGC -3'  
3' -**G**GAACGTAGACGAGGTACCGTACG -5'

- if you do not find suitable enzymes, you can blunt the ends obtained after restriction enzyme digestion with different enzymes, so they will become compatible
- in this case, your insert can be cloned sense or antisense, and then you will have to design a digestion to verify the orientation of the insert



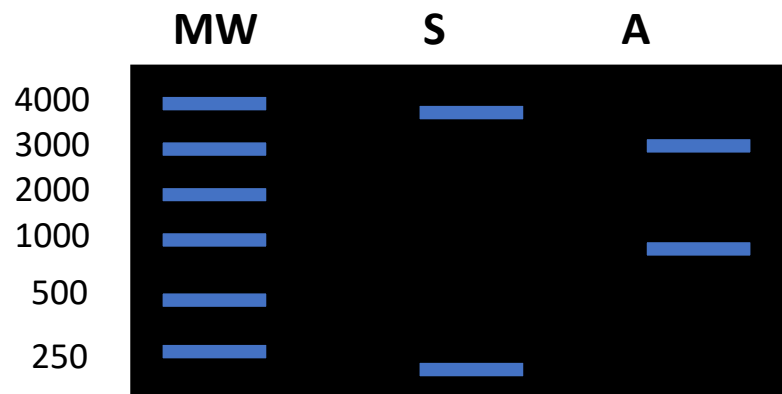
- if you design a sub-cloning using blunt ends at both ends of the insert or the same restriction enzyme at both ends of the insert, the insert can be sub-cloned sense or antisense.
- therefore you have to identify a **restriction enzyme (RE)** that will enable you to verify the correct orientation of the insert into the new vector.





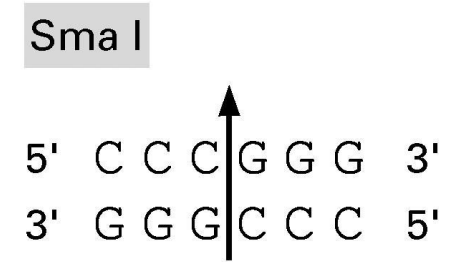
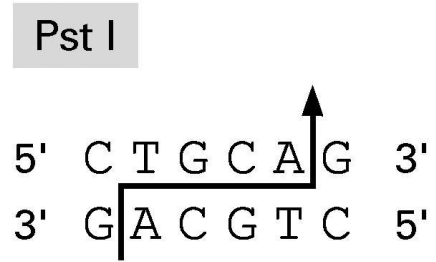
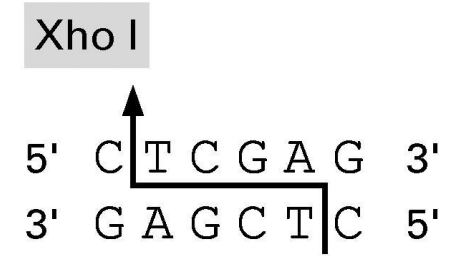
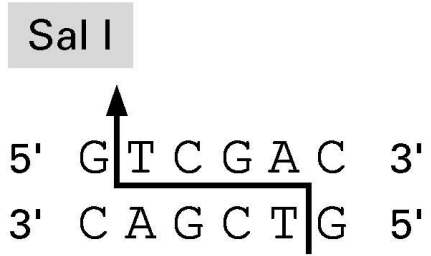
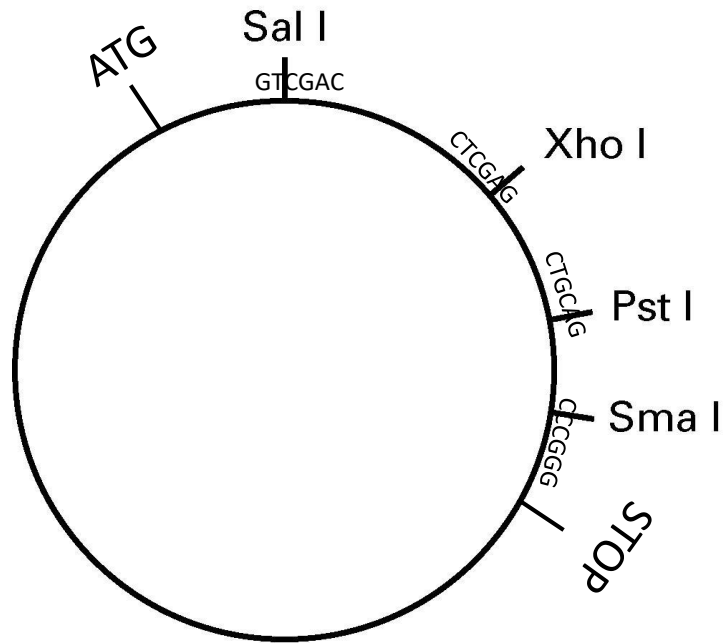
**SENSE**

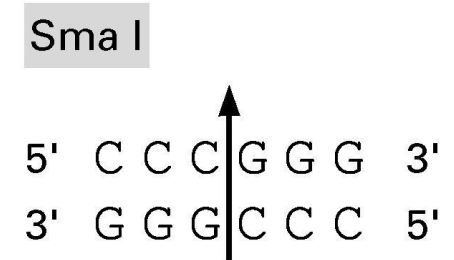
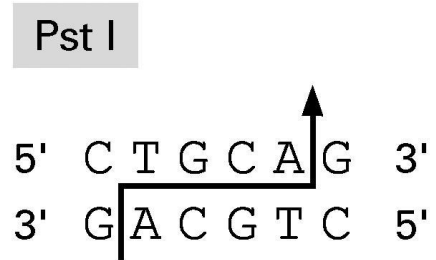
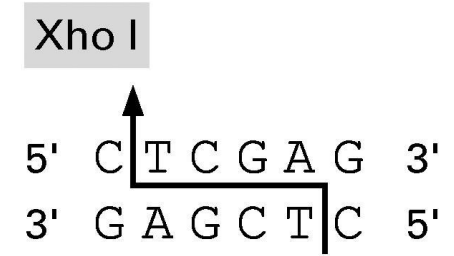
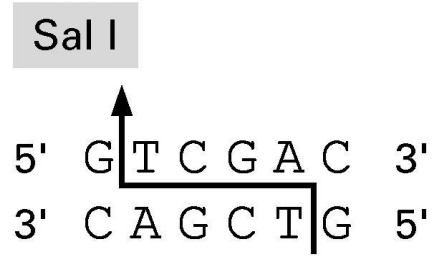
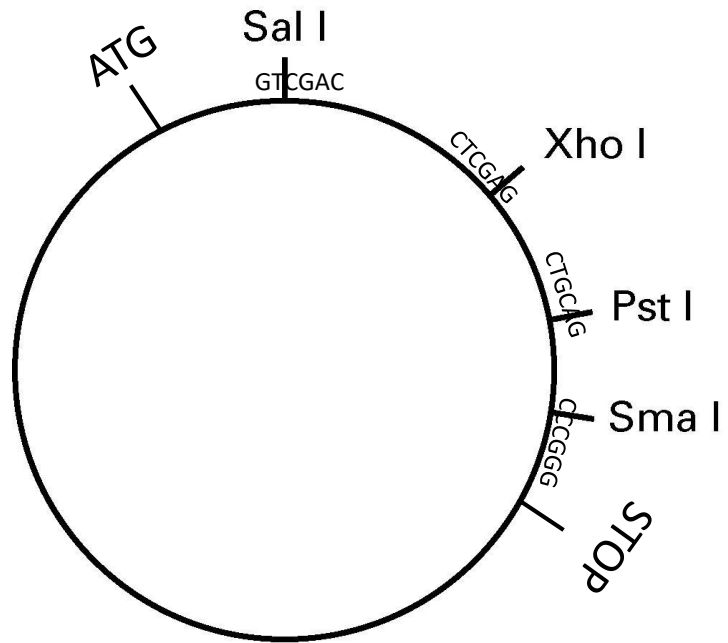
3800 + 200



**ANTISENSE**

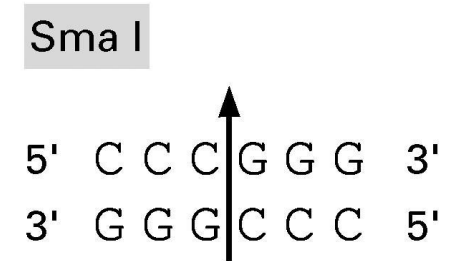
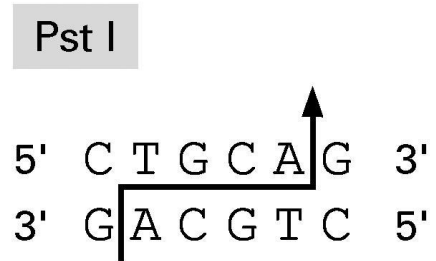
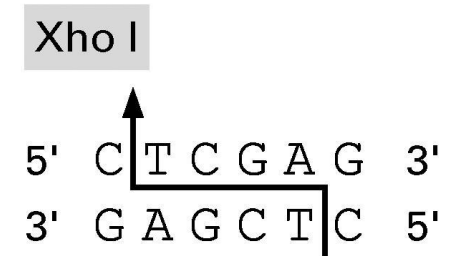
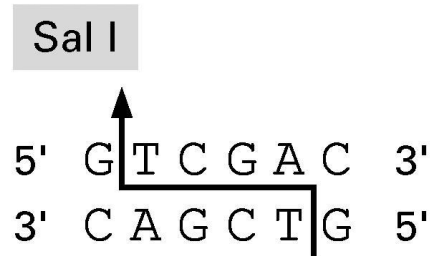
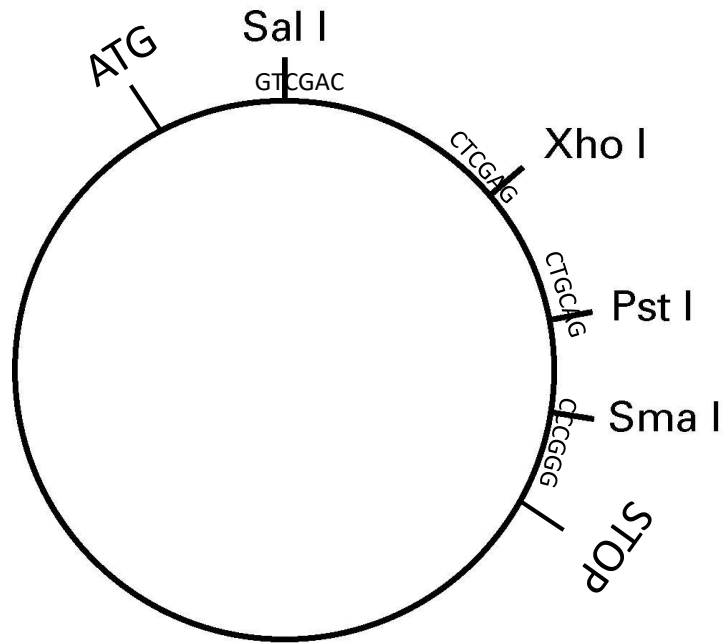
3200 + 800





*Exercise:*

-How can you ligate **Sal I** with **Xho I**?



*Exercise:*

- How can you ligate **Sal I** with **Xho I**? 5'-**GTCGAG**-3' (compatible)  
5'-**GTCGATCGAG**-3' (blunted)
- How can you ligate **Sal I** with **Pst I**? 5'-.....-3'
- How can you ligate **Sal I** with **Sma I**? 5'-.....-3'
- How can you ligate **Xho I** with **Pst I**? 5'-.....-3'
- How can you ligate **Xho I** with **Sma I**? 5'-.....-3'
- How can you ligate **Pst I** with **Sma I**? 5'-.....-3'