



# MANIPULATING DNA FOR NATURAL PRODUCT APPLICATIONS



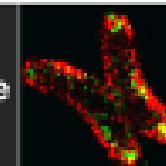
Céline AUBRY  
Researcher in I2BC

University Paris-Saclay  
M2 Fundamental Microbiology



université PARIS-SACLAY Life Sciences & Health

Master  
Biologie  
Santé



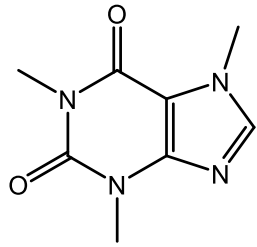
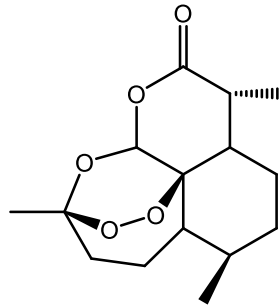
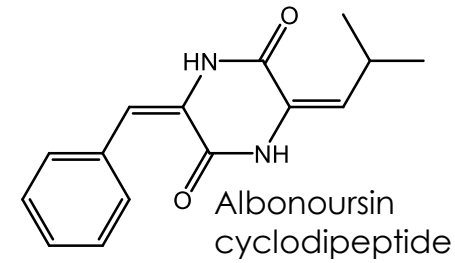
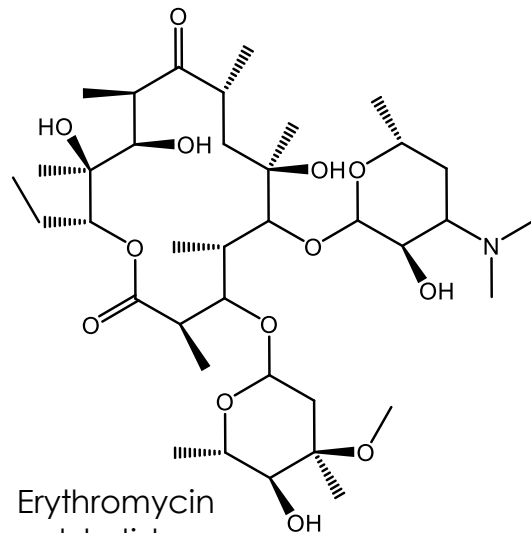
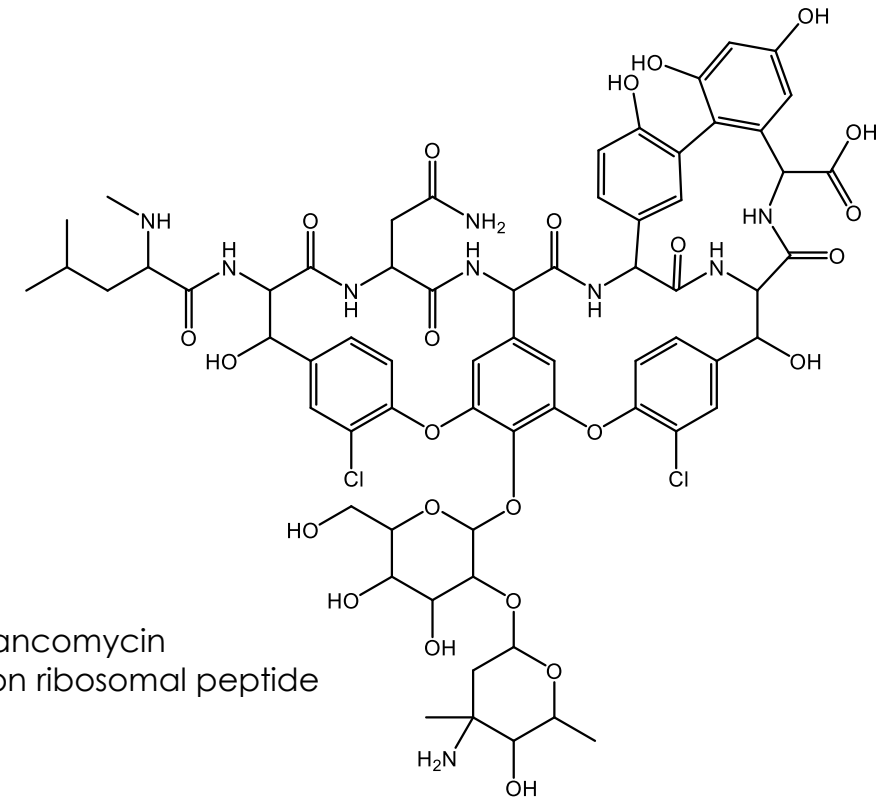
M2 Microbiologie  
fondamentale

M2 Fundamental  
Microbiology  
International Track

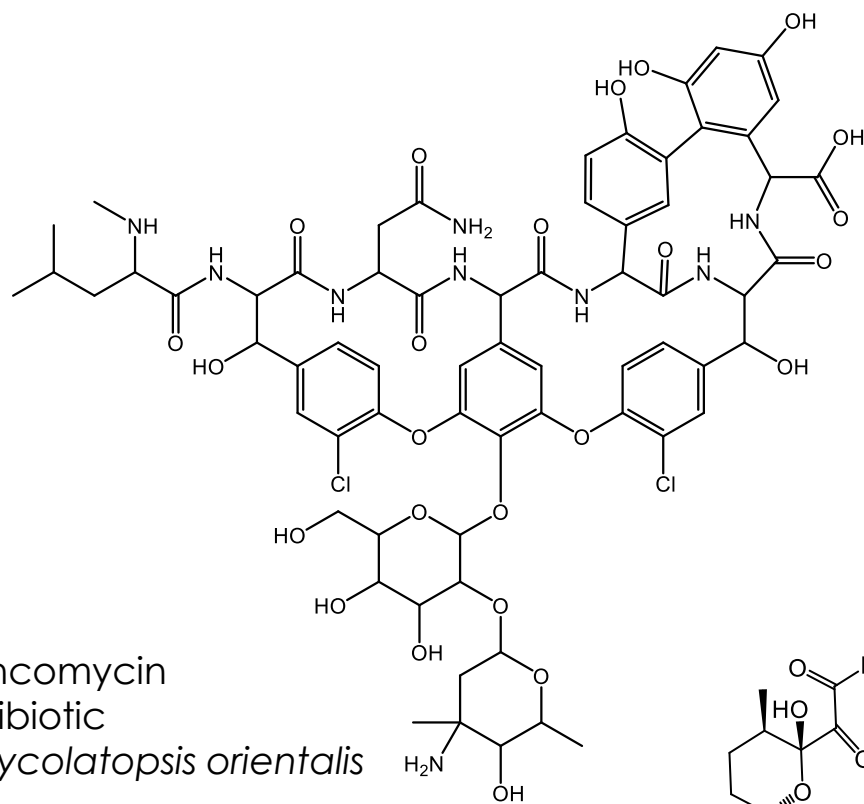
## PROGRAM OF THIS SESSION

- Some knowledge on Natural Products
  - NRPS, RiPPs
- Some DNA assembly techniques
  - Mutagenesis, LCR, PCR targeting, Biobrick assembly, SLICE
- Two examples of applications from my work
  - Refactoring congocidine biosynthetic gene cluster, producing non-natural analogs of sviceucin
- Application for non natural products, the example of adipic acid

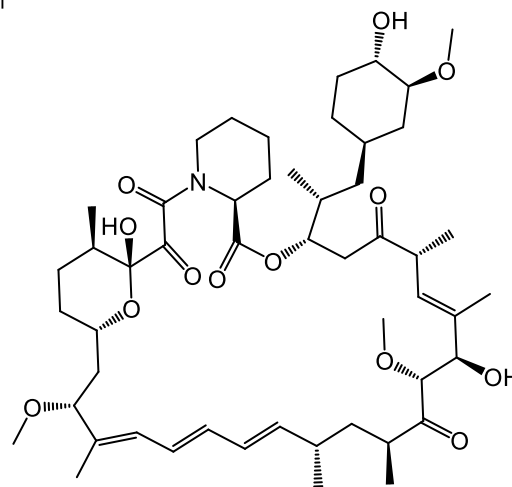
## DIFFERENT CLASSES OF NATURAL PRODUCTS

Caffeine  
alcaloïdeArtemisinin  
terpèneAlbonoursin  
cyclodipeptideErythromycin  
polyketideVancomycin  
non ribosomal peptide

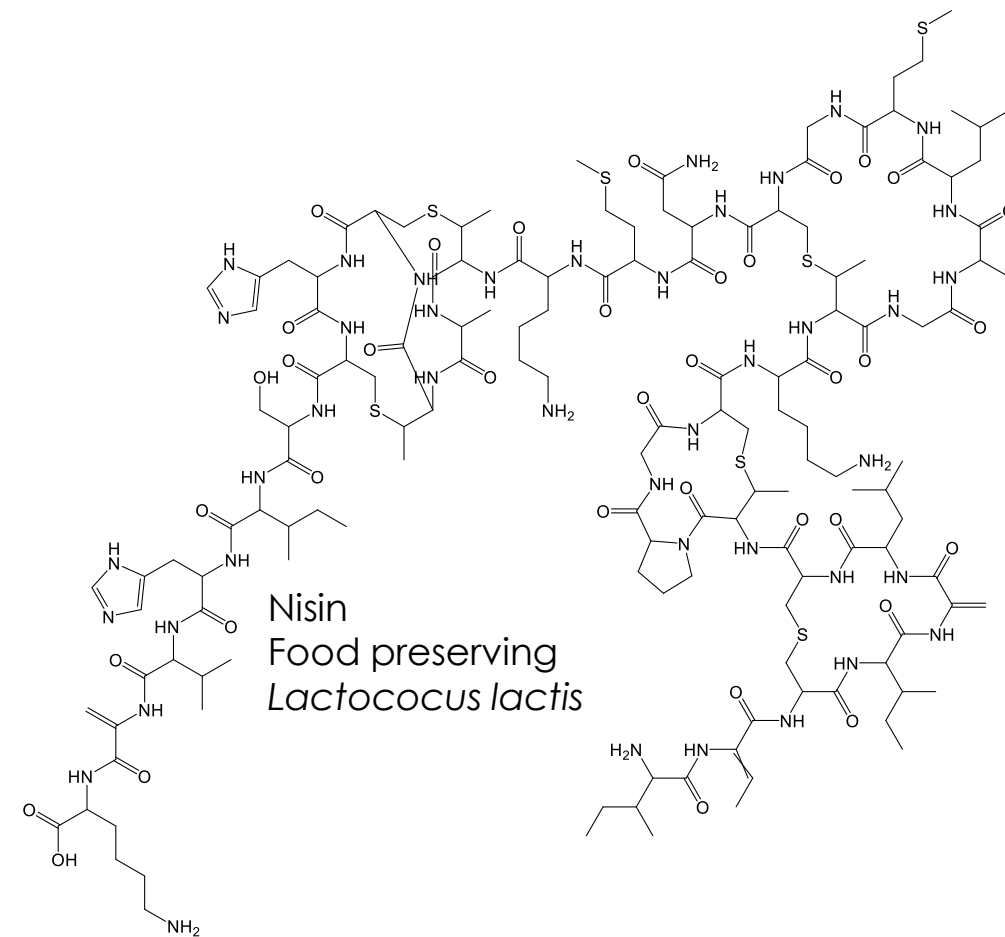
## BIOLOGICAL ACTIVITIES OF NATURAL PRODUCTS



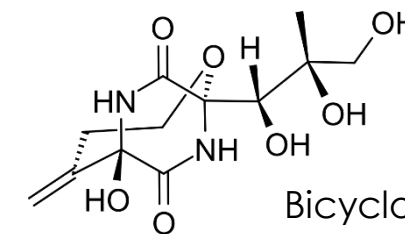
Vancomycin  
Antibiotic  
*Amycolatopsis orientalis*



Rapamycin  
Immunosuppressor  
*Streptomyces hygroscopicus*

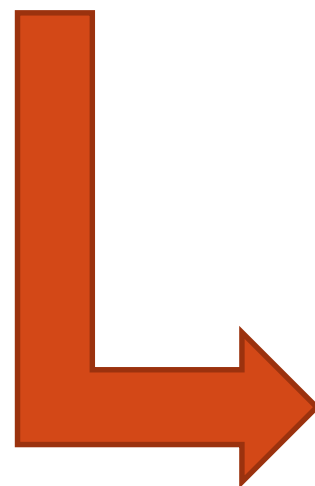
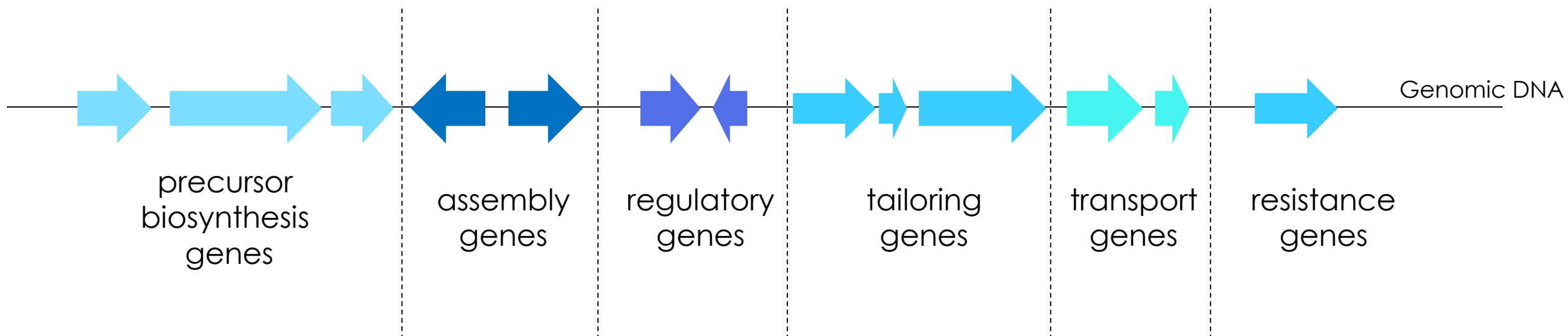


Nisin  
Food preserving  
*Lactococcus lactis*



Bicyclomycin  
Antibiotic  
*Streptomyces sapporonensis*

## ORGANISATION IN BIOSYNTHETIC GENE CLUSTERS



Production of one or several natural products

## SYNTHETIC BIOLOGY OF NATURAL PRODUCTS

- Development of tools (strains, vectors, regulatory components)
- Reconstruction of a biosynthetic gene cluster to express a compound (refactoring)
- Combinatorial biosynthesis

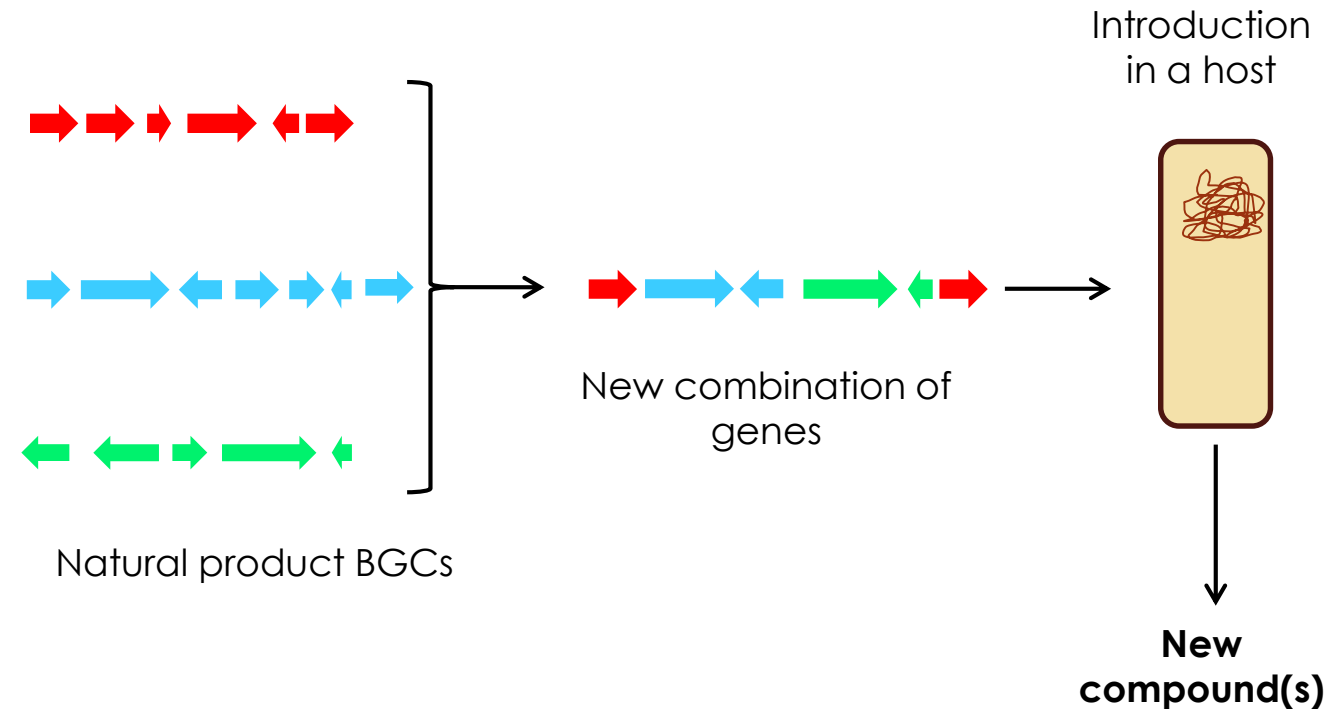
# SYNTHETIC BIOLOGY OF NATURAL PRODUCTS

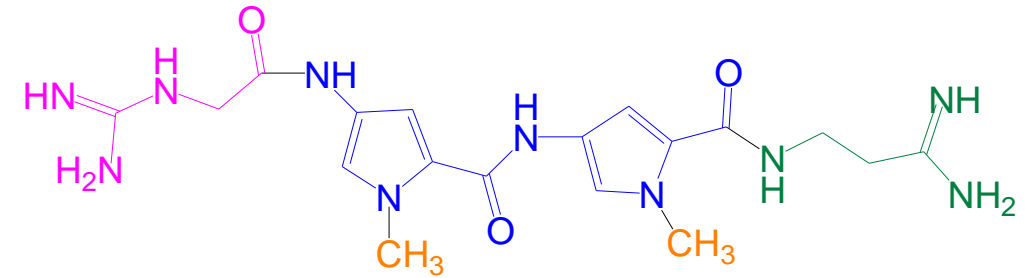
- Development of tools (strains, vectors, regulatory components)
- Reconstruction of a biosynthetic gene cluster to express a compound (refactoring)
- Combinatorial biosynthesis

Interests:

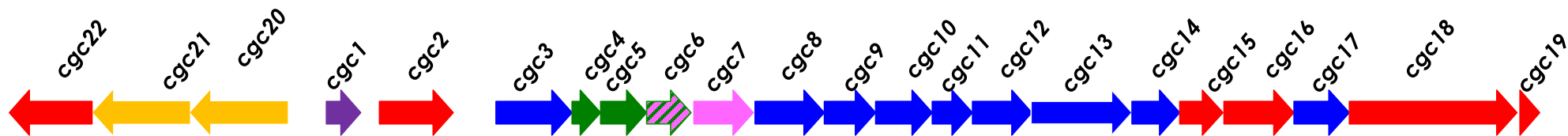
- Understanding
- Synthesis of new compounds

## Principle of Combinatorial biosynthesis



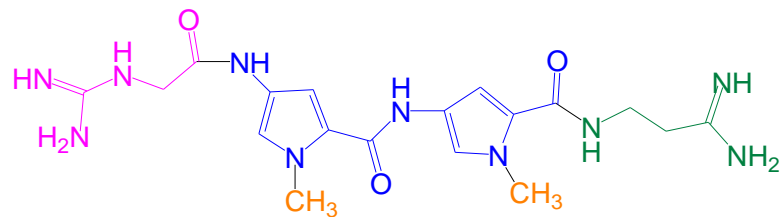
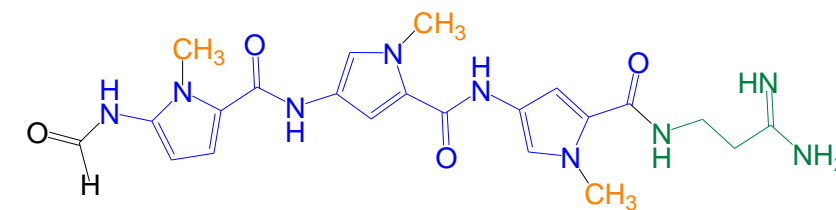
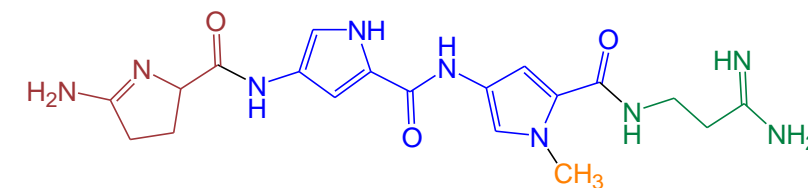
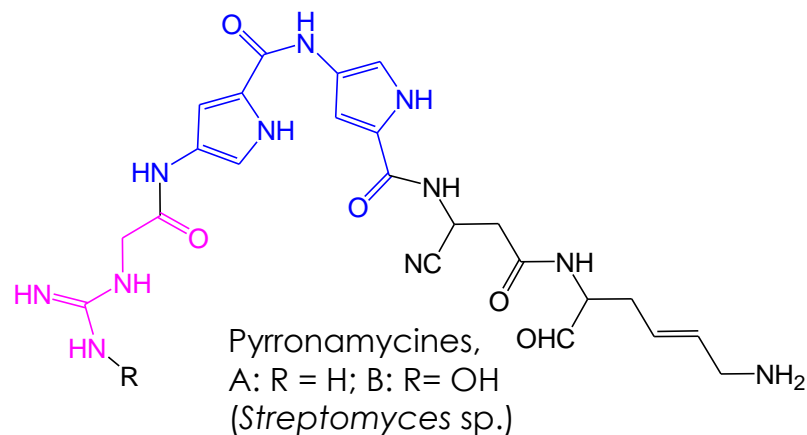
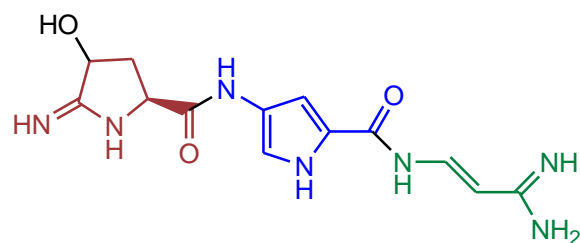
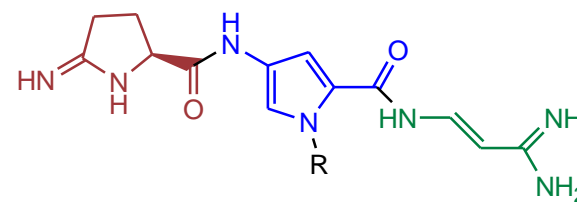
Congocidine, *S. ambofaciens*

# REFACTORING OF CONGOCIDINE BIOSYNTHETIC GENE CLUSTER

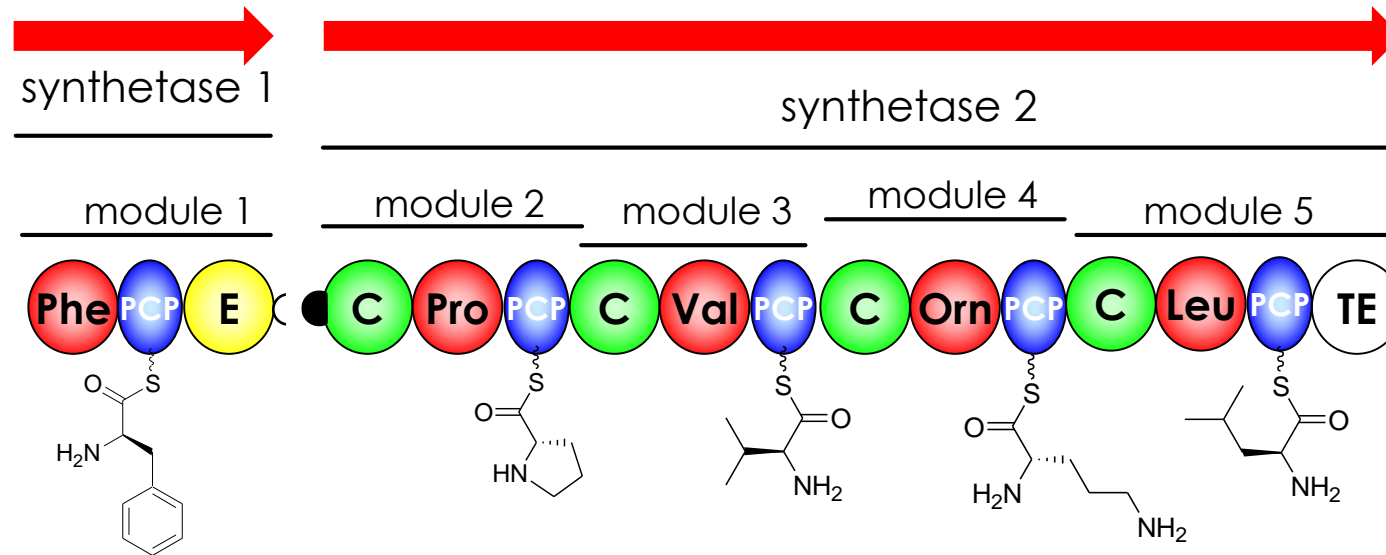




## THE PYRROLAMIDE FAMILY

Congocidine, *S. ambofaciens*Distamycine, *S. netropsis* (*S. distallicus*)Anthelvencine A, *S. venezuelae*TAN 868A, *S. idiomorphus*Kikumycines, *S. phaeochromogenes* R-719R = H kikumycine A, R = CH<sub>3</sub>, kikumycine B

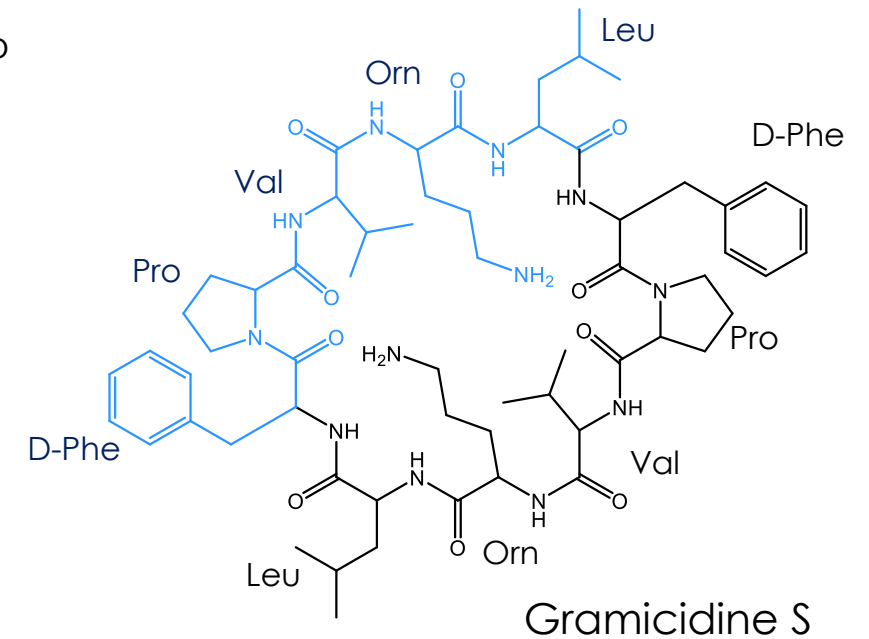
## NON RIBOSOMAL PEPTIDE SYNTHETASE (NRPS)



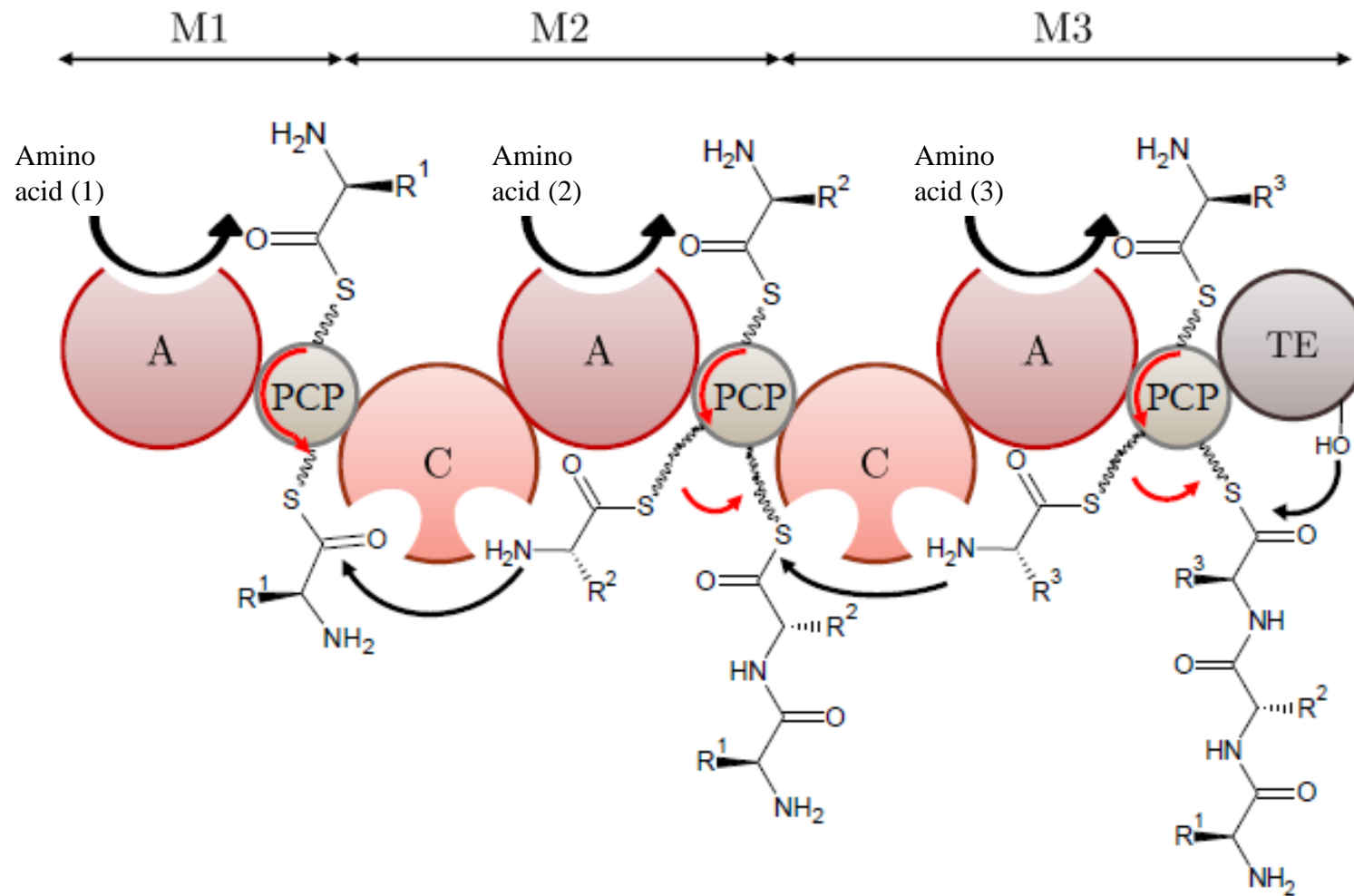
**Adenylation domain (A)**

**Peptidyl-Carrier Protein (PCP)**

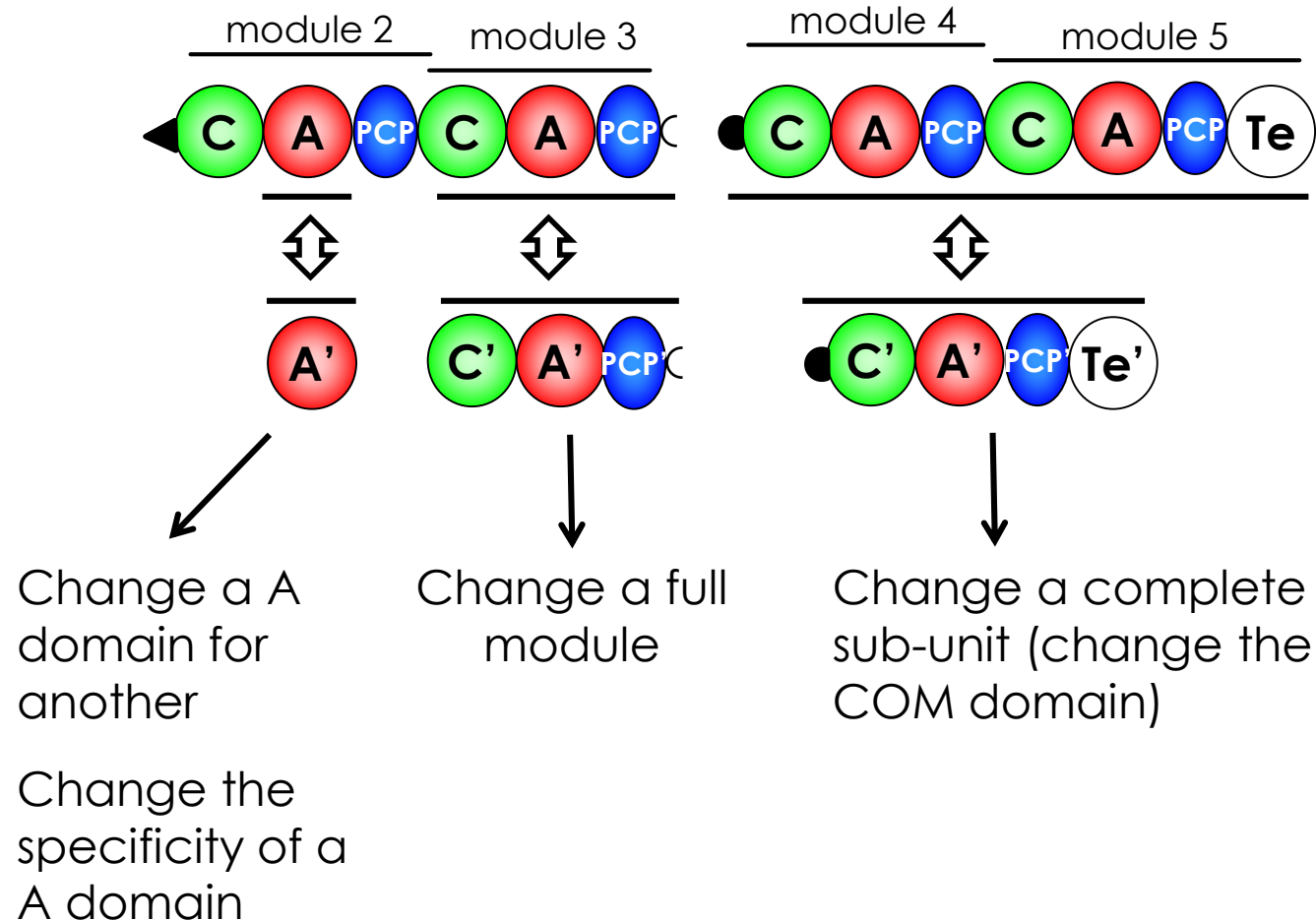
**Condensation domain (C)**



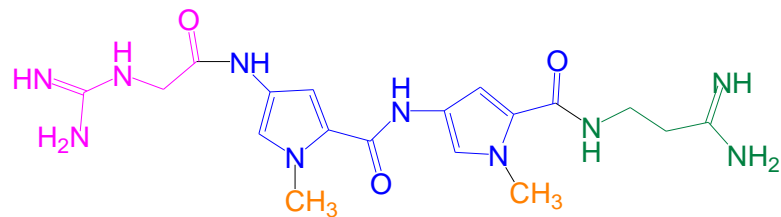
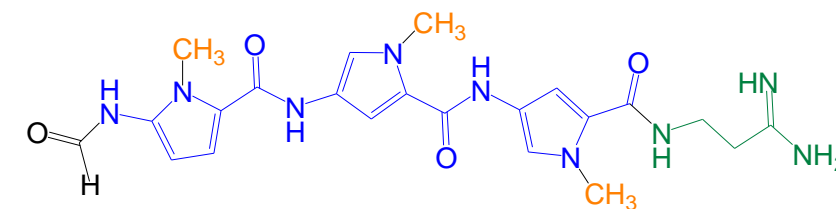
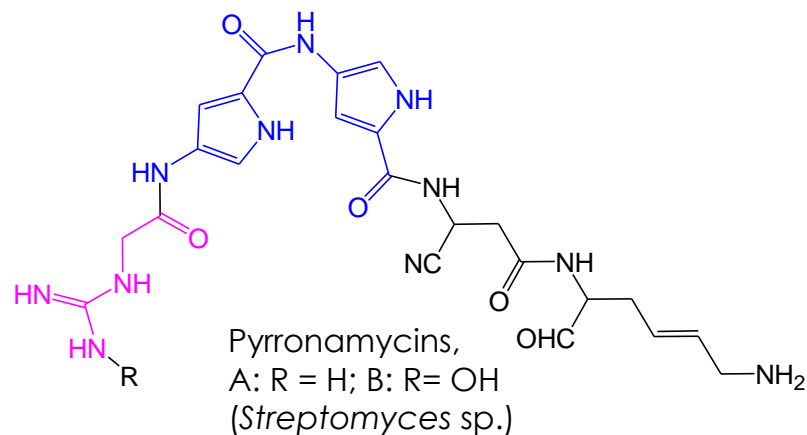
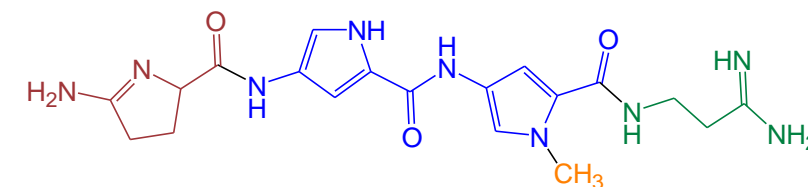
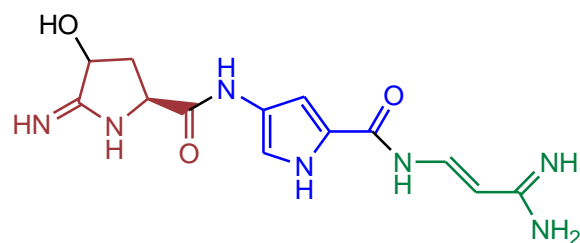
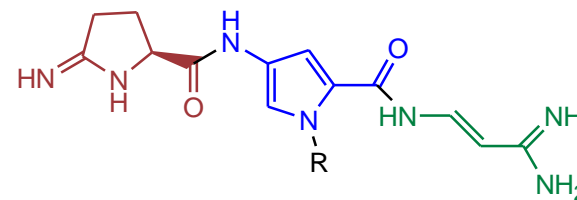
## NON RIBOSOMAL PEPTIDE BIOSYNTHESIS MODEL



# COMBINATORIAL BIOSYNTHESIS POSSIBILITIES OF NON RIBOSOMAL PEPTIDE SYNTHETASES (NRPS)

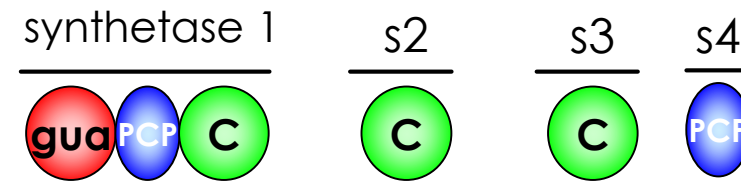


## THE PYRROLAMIDE FAMILY

Congocidine, *S. ambofaciens*Distamycine, *S. netropsis* (*S. distallicus*)Pyrronamycins,  
A: R = H; B: R = OH  
(*Streptomyces* sp.)Anthelvencin A, *S. venezuelae*TAN 868A, *S. idiomorphus*Kikumycins, *S. phaeochromogenes* R-719R = H kikumycin A, R = CH<sub>3</sub>, kikumycin B

# NON-RIBOSOMAL PEPTIDE SYNTHETASE (NRPS) OF CONGOCIDINE

## Congocidine NRPS

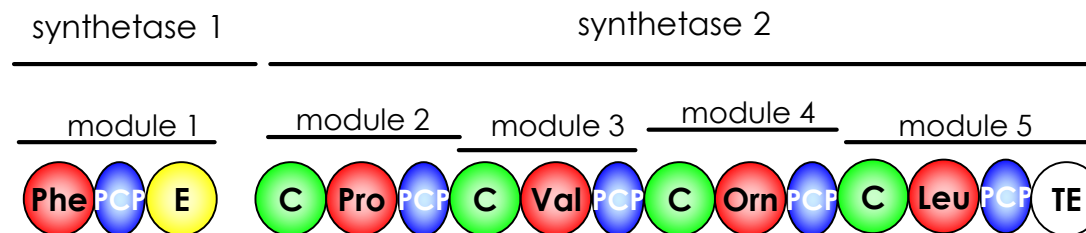


**Adenylation domain (A)**

**Peptidyl Carrier Protein (PCP)**

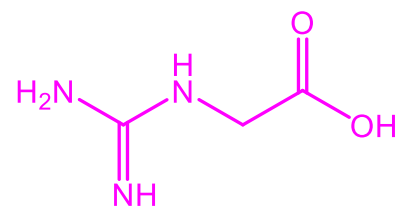
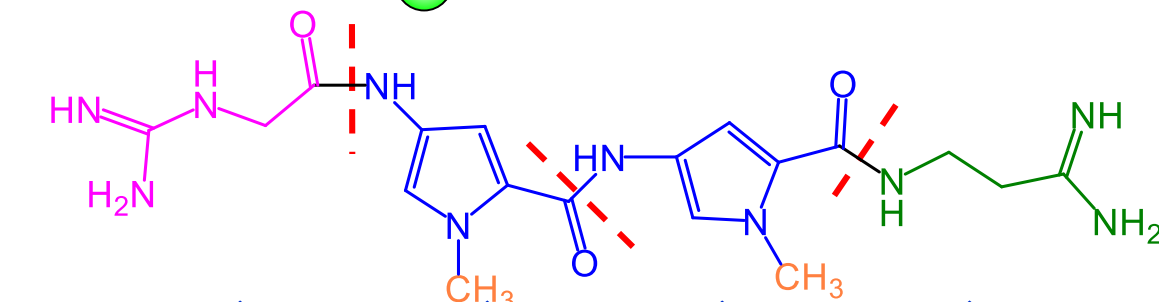
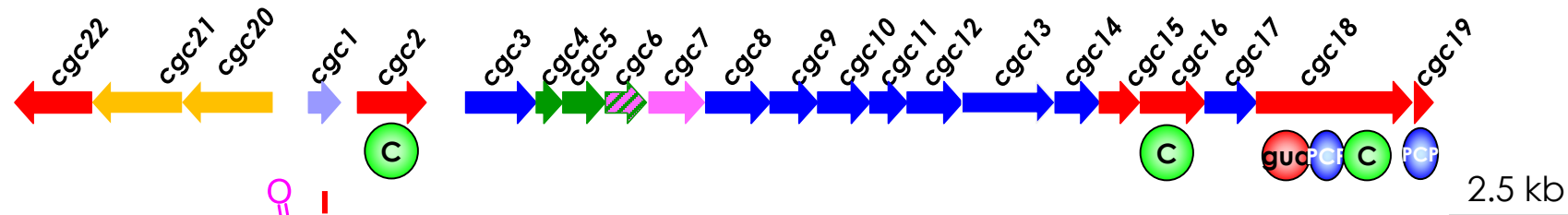
**Condensation domain (C)**

## Gramicidine NRPS

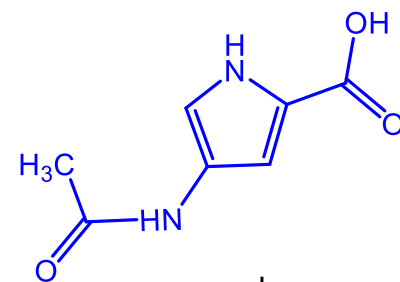


# BIOSYNTHETIC GENE CLUSTER OF CONGOCIDINE FROM *STREPTOMYCES AMBOFACIENS*

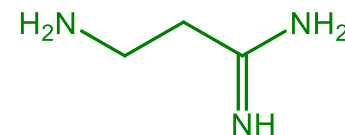
## *S. ambofaciens* cgc cluster



guanidino  
acétate  
precursor



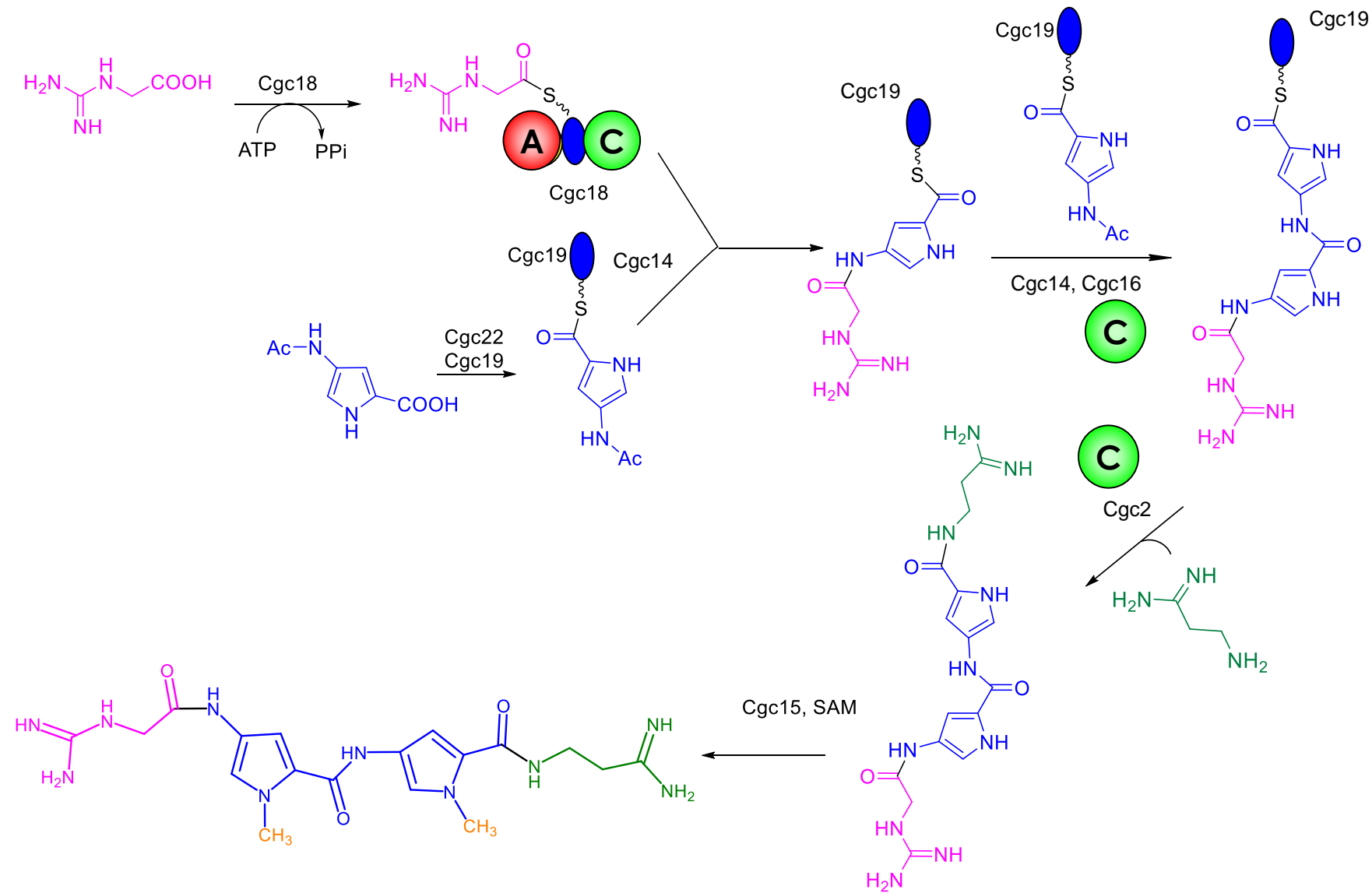
pyrrole  
precursors



3-Amino  
propionamide  
precursor

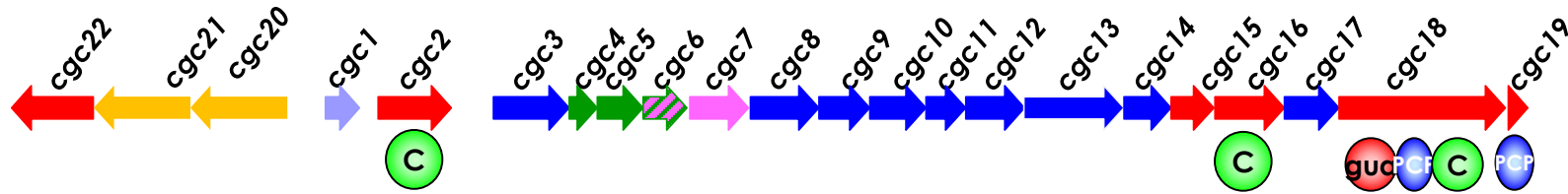
- Regulation
- Resistance
- Assembly
- Pyrroles
- Guanidinoacetate
- 3-Aminopropionamide

# MODELE OF ASSEMBLY OF CONGOCIDINE



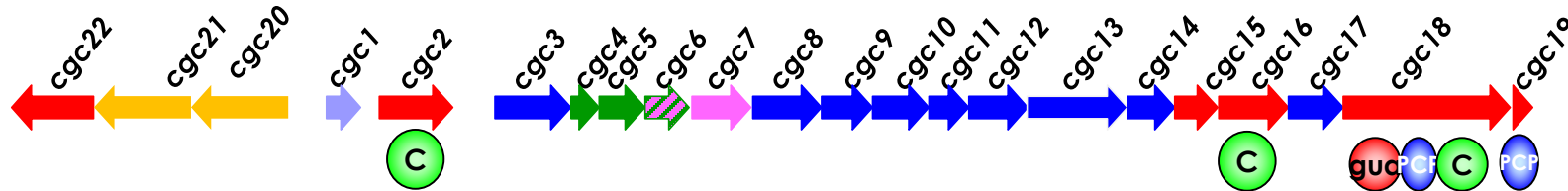


## MODIFICATION OF A BGC: PRELIMINARY QUESTIONS

*S. ambifaciens* cgc cluster

# MODIFICATION OF A BGC: PRELIMINARY QUESTIONS

## *S. ambifaciens* cgc cluster

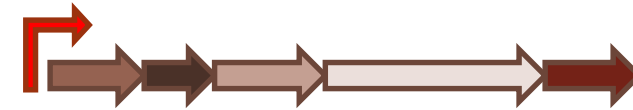
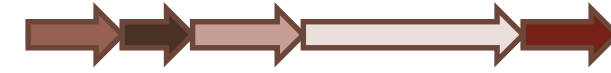


- How does the regulation work ?
- What are the limits of the genes ?
- Where are the operons ?

Decision to refactor the cluster to have a reconstructed cluster with exchangeable elements

# PRINCIPLE OF REFACTORIZING OF A BIOSYNTHETIC GENE CLUSTER

- Different levels of refactorizing
  - Addition of a **promoter** upstream of the operon



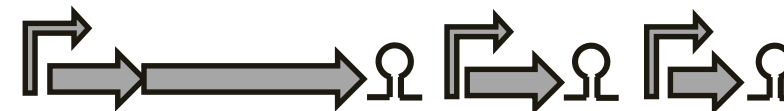
- **Selection** of some genes, in order to evade natural transcriptional regulation



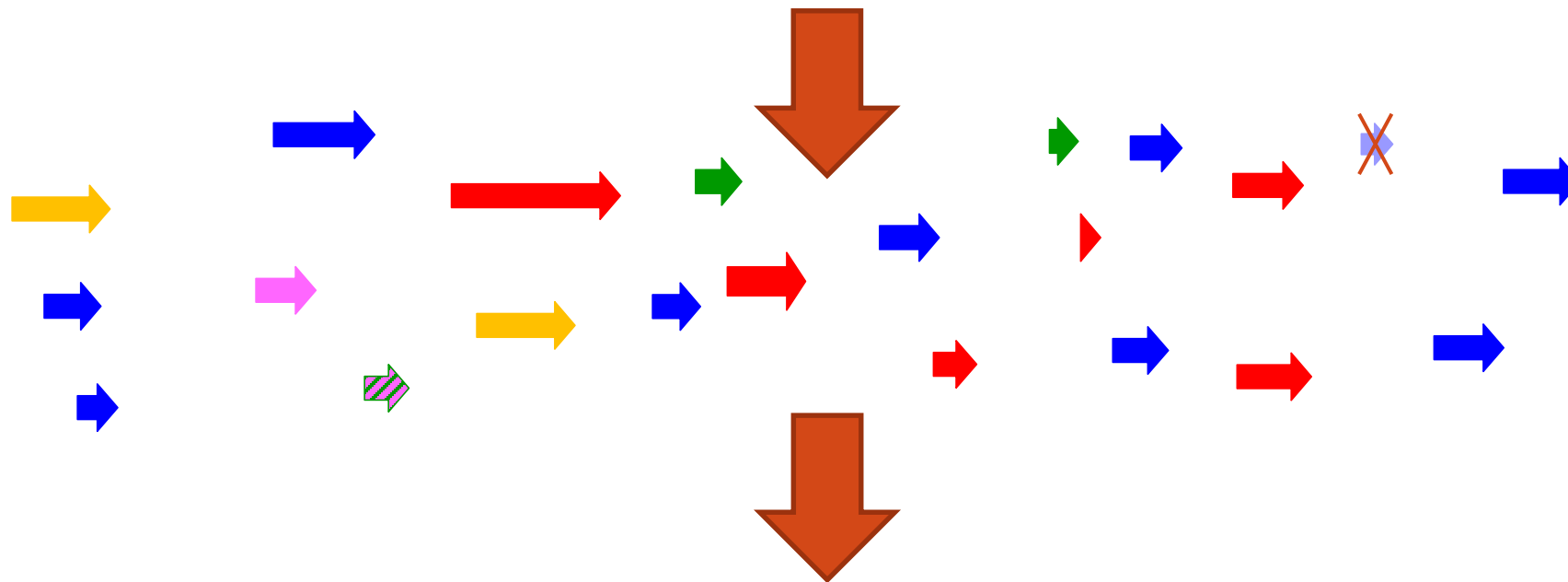
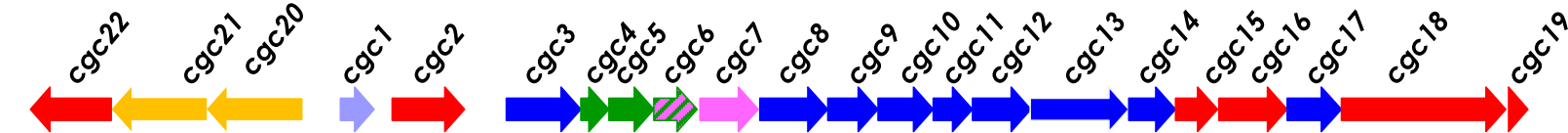
- **Reorganisation** of the group of genes



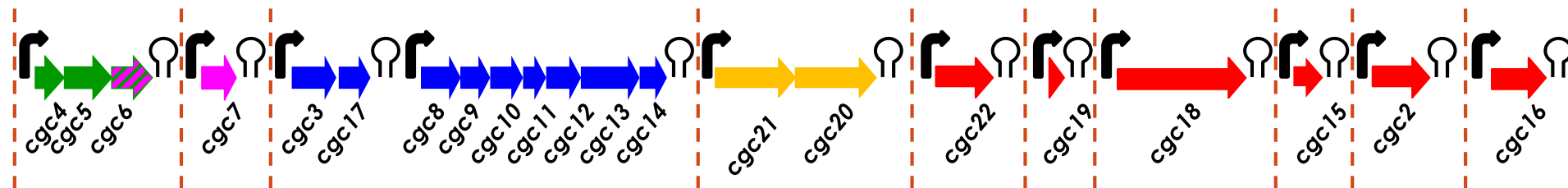
- **Synthesis** of a totally synthetic construct



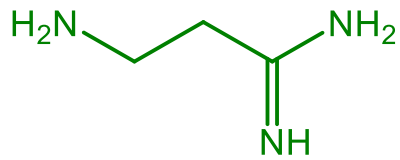
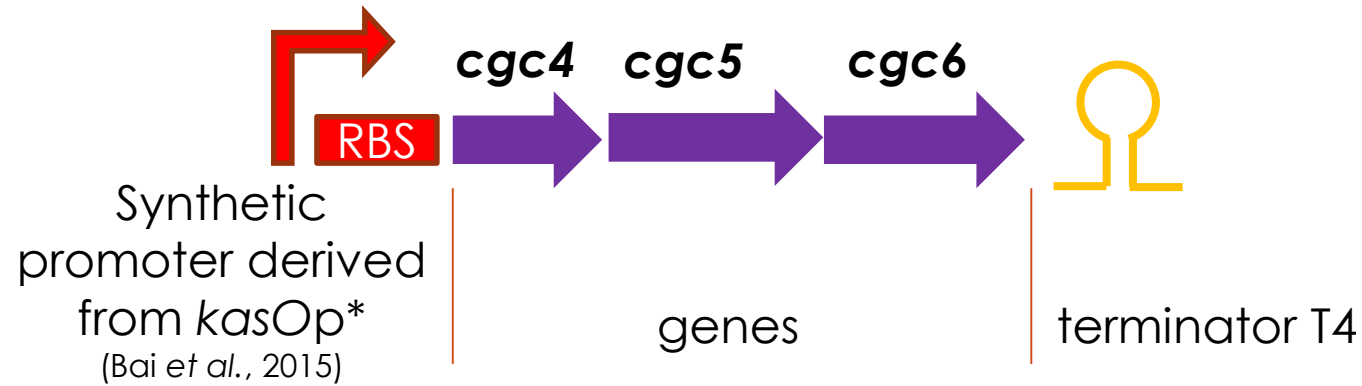
## REFACTORING OF THE CONGOCIDINE BGC

*S. ambofaciens* *cgc* cluster

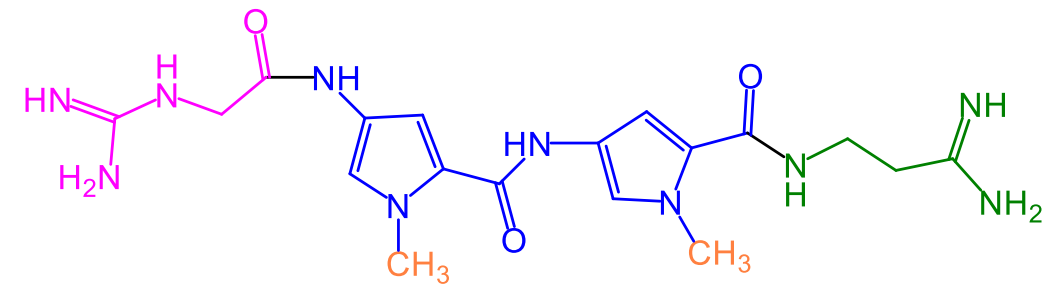
How do we get there ??



## EXAMPLE OF THE SYNTHETIC CASSETTE

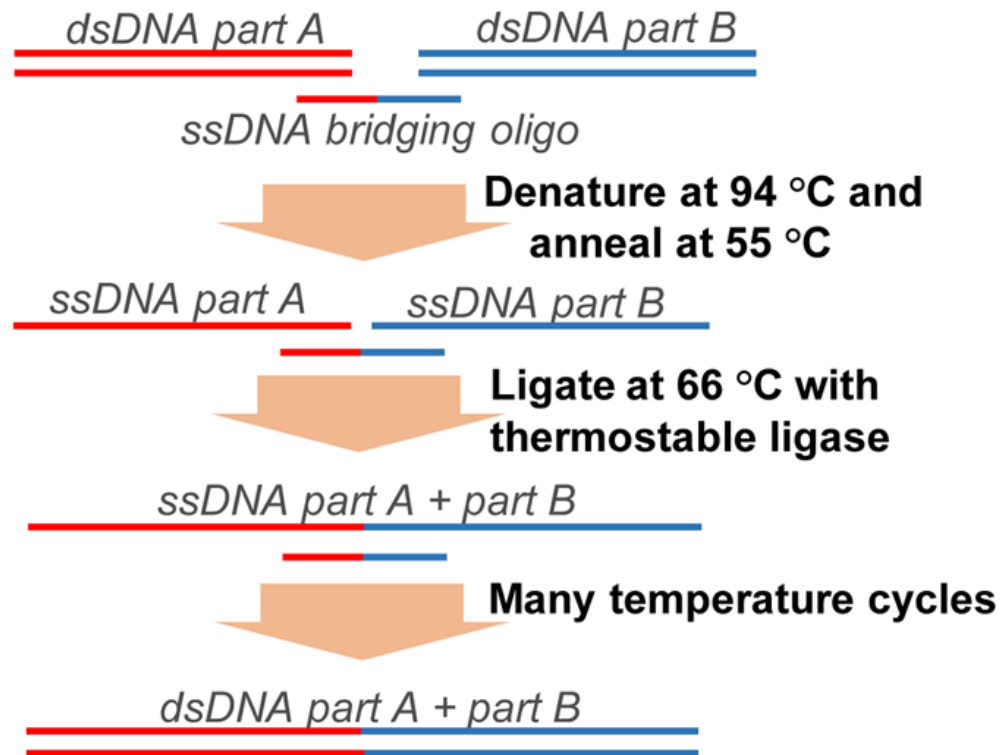


*cgc4*, *cgc5*, *cgc6* :  
Biosynthetic genes of the precursor  
3-Aminopropionamidine



congocidine

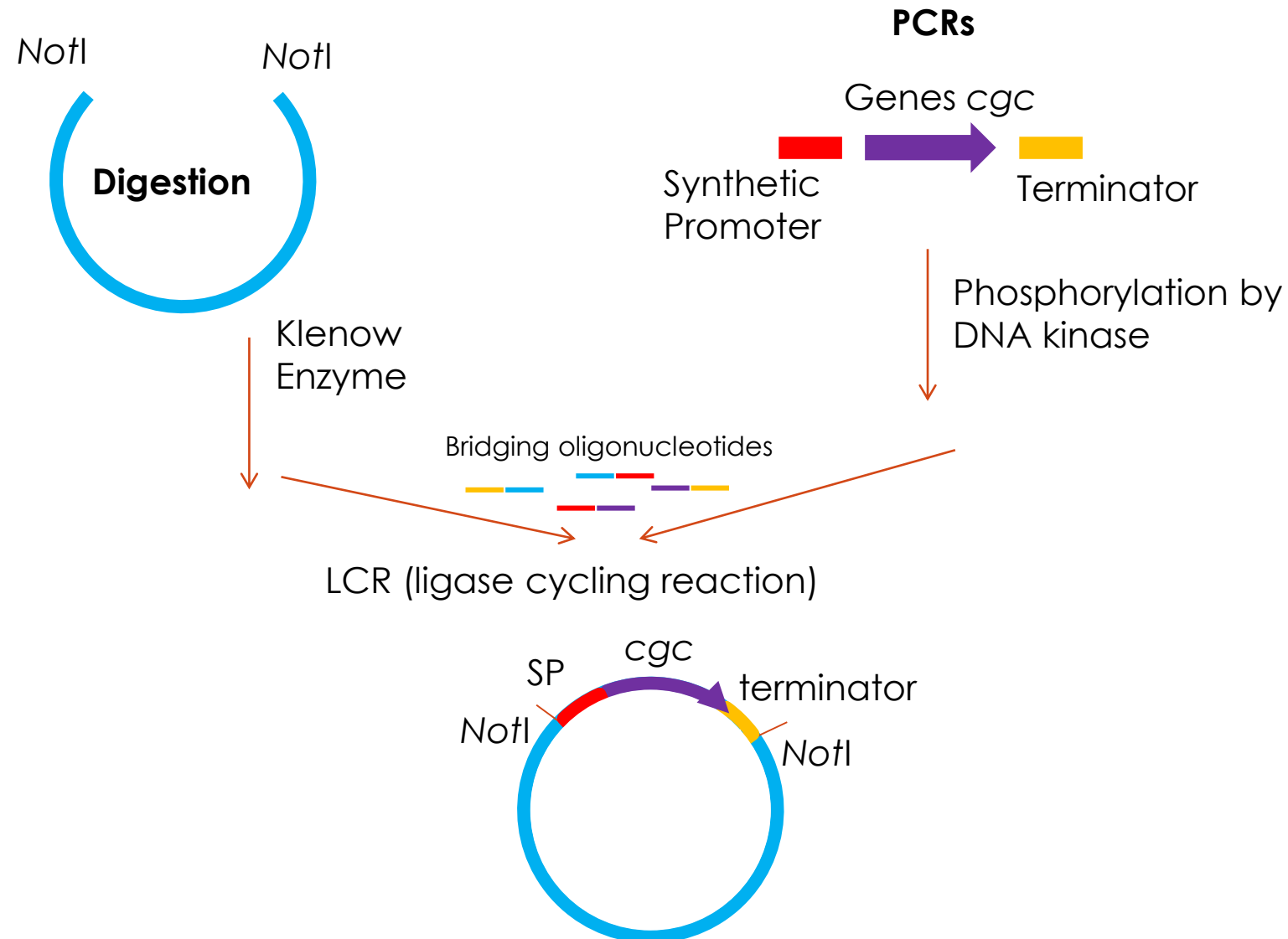
# LCR ligase cycling reaction



- single-stranded bridging oligos complementary to the ends of neighboring DNA parts,
- thermostable ligase to join DNA backbones,
- multiple denaturation–annealing–ligation temperature cycles

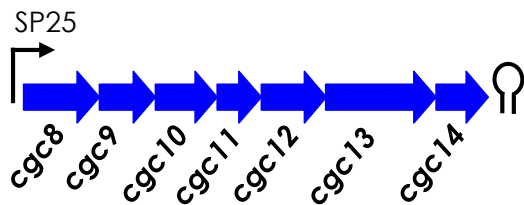
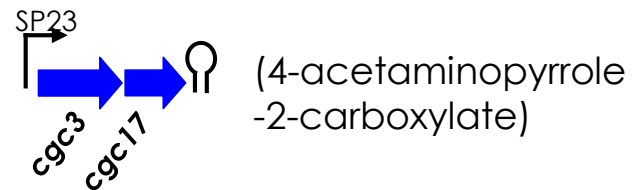
Up to 20 kb and up to 20 parts in *E. coli*

## GENERAL PRINCIPLE OF A CASSETTE CONSTRUCTION

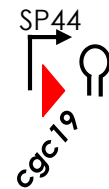
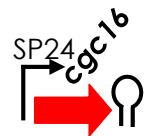
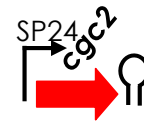
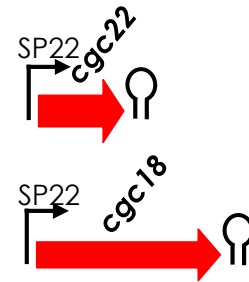


# CONGOCIDINE GENE CASSETTES

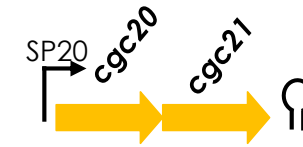
## Precursor biosynthesis genes



## Assembly



## Resistance gene

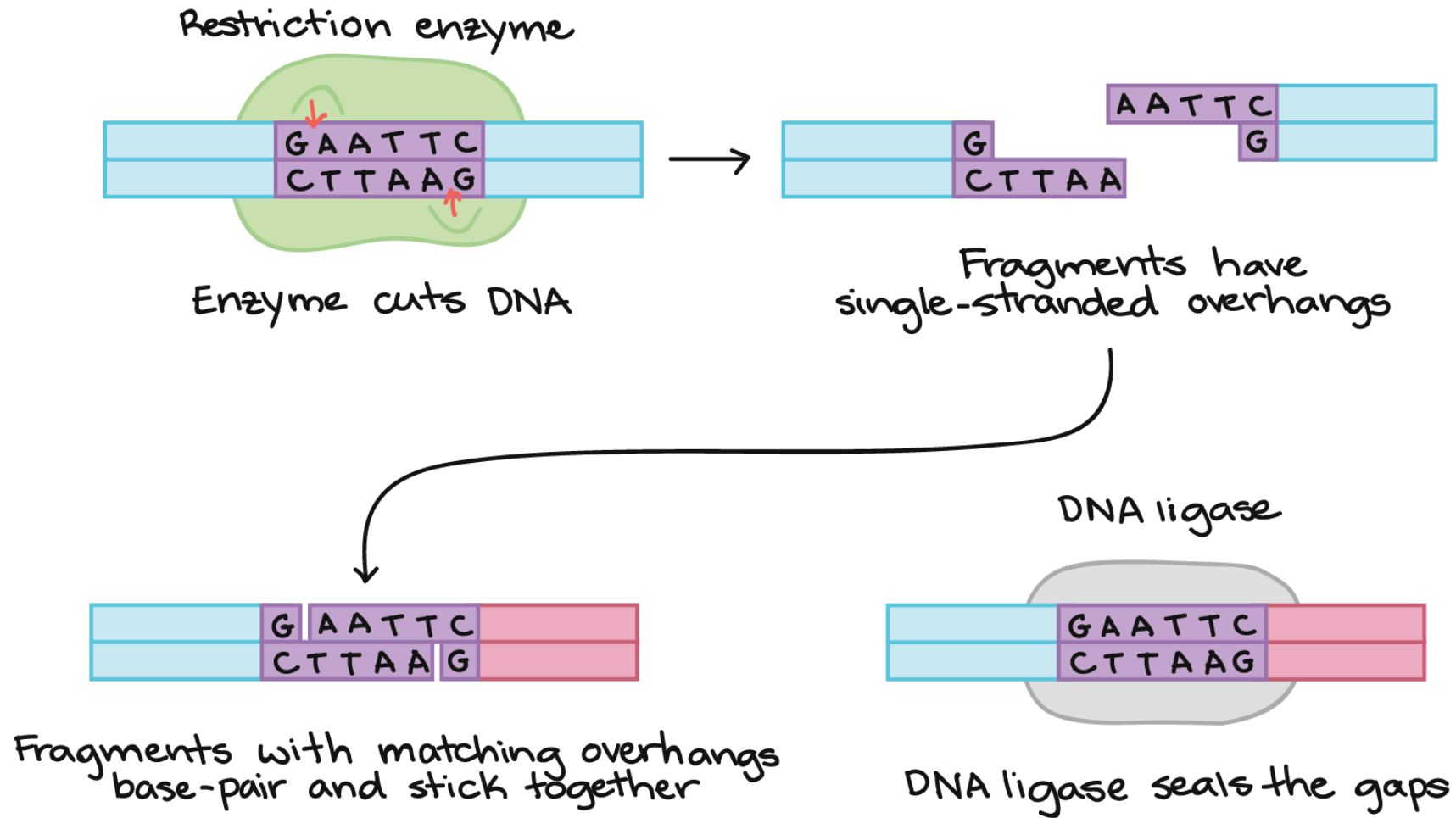


## Tailoring gene

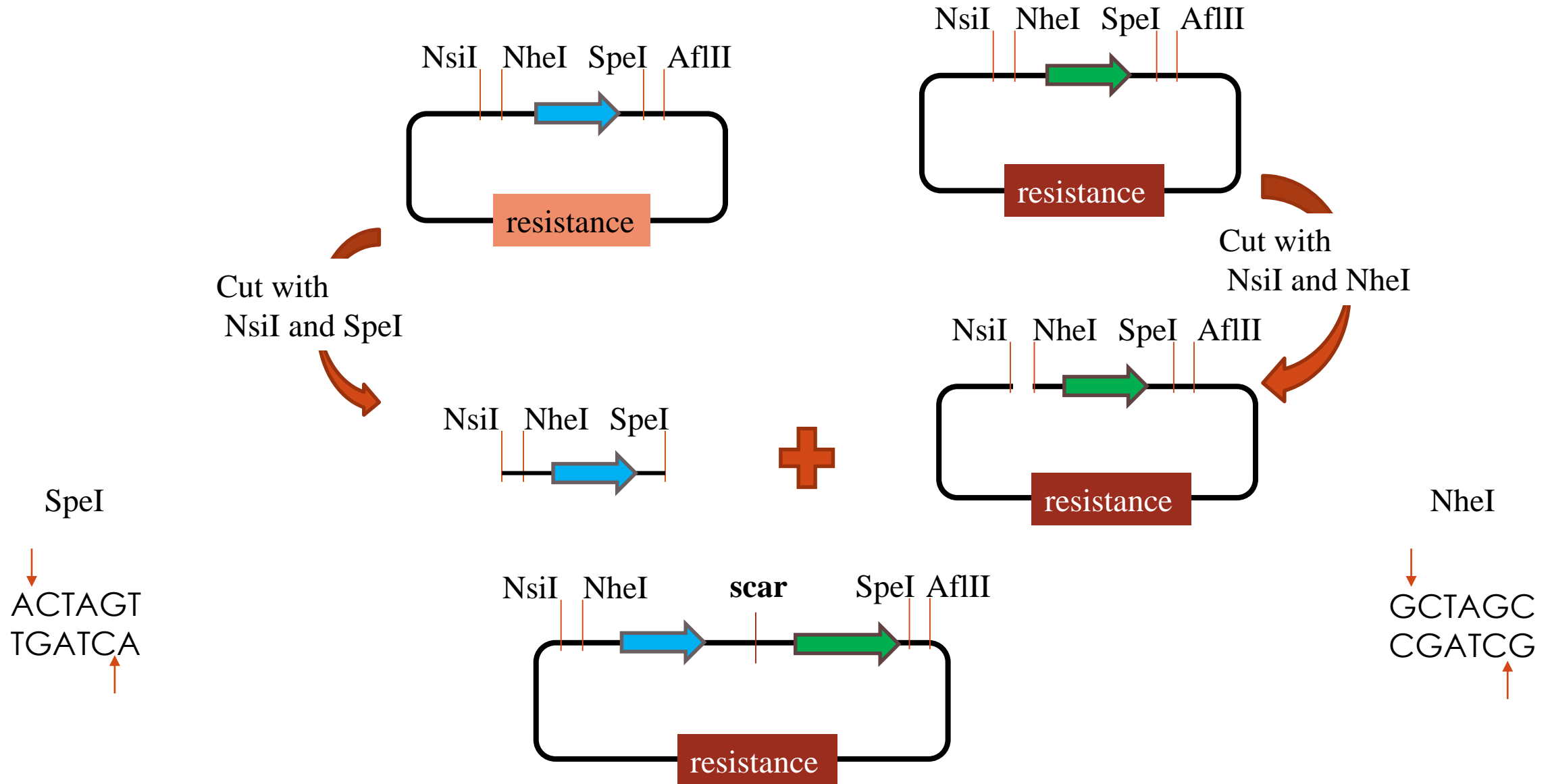


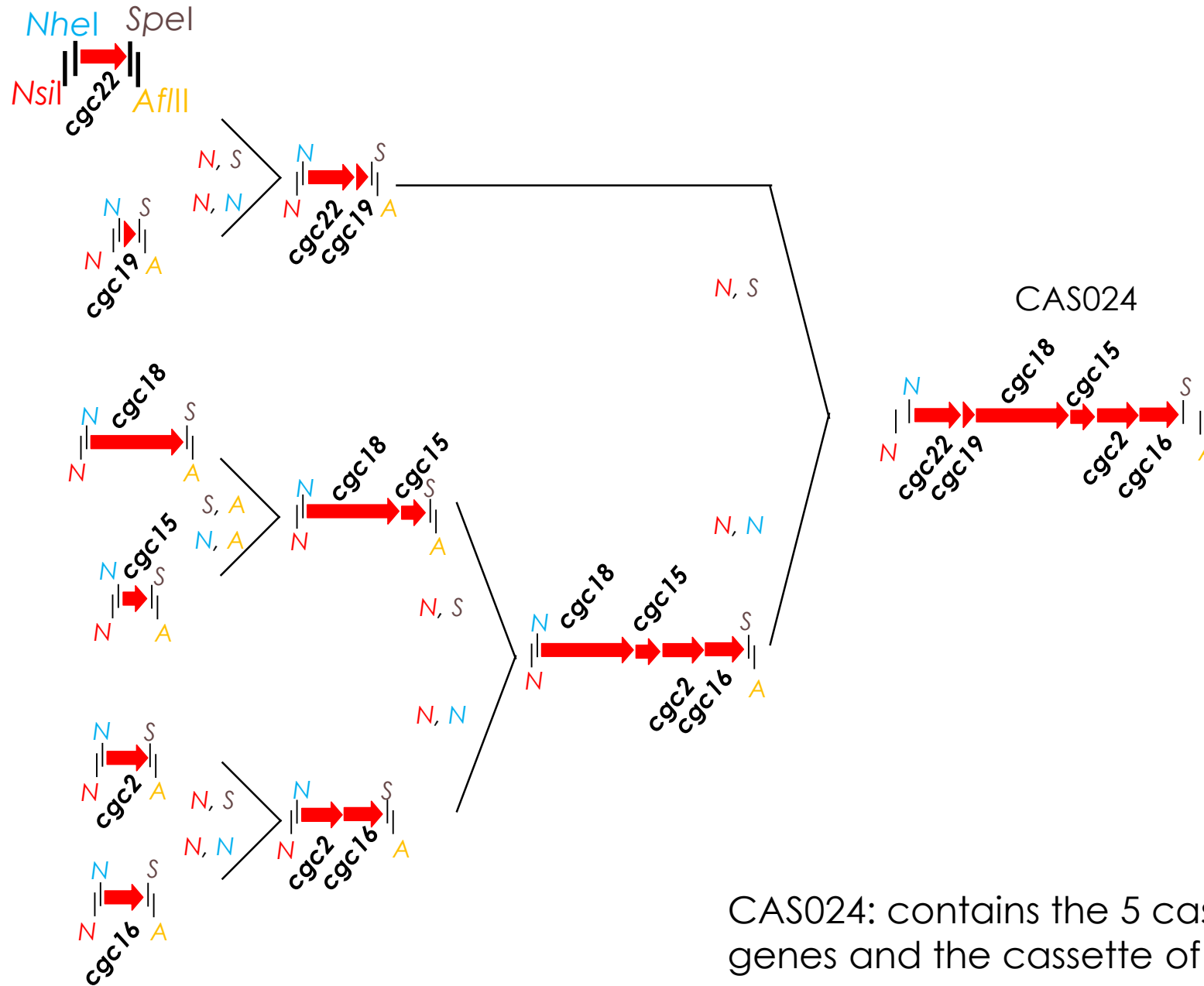


## RESTRICTION ENZYMES

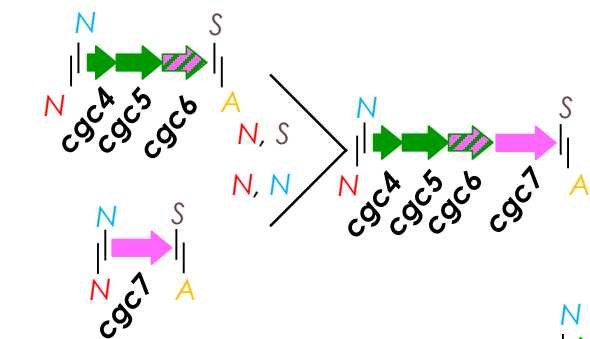
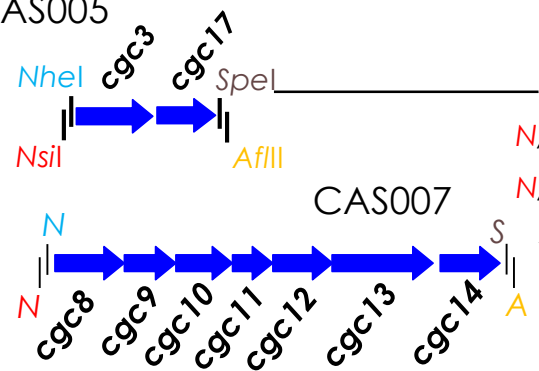


## SIMILAR TO THE BIOBRICK SYSTEM

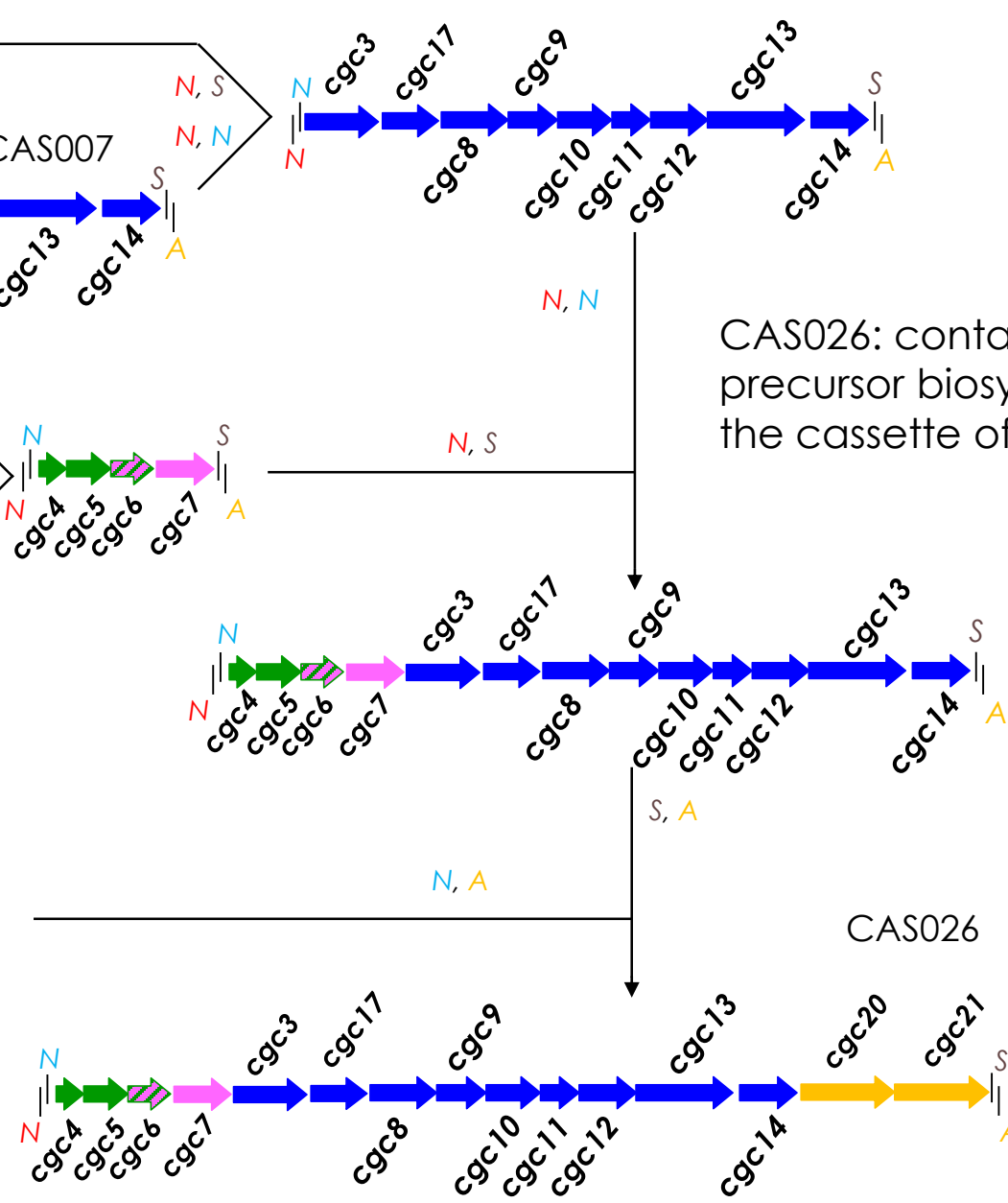
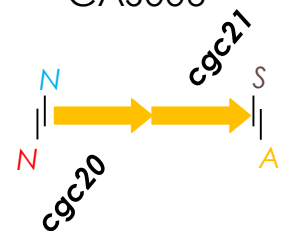




CAS005



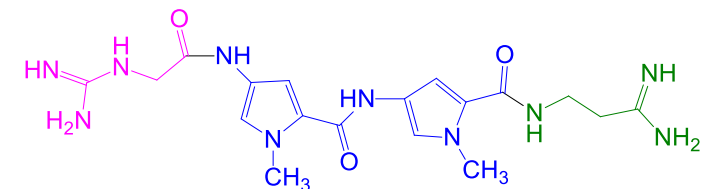
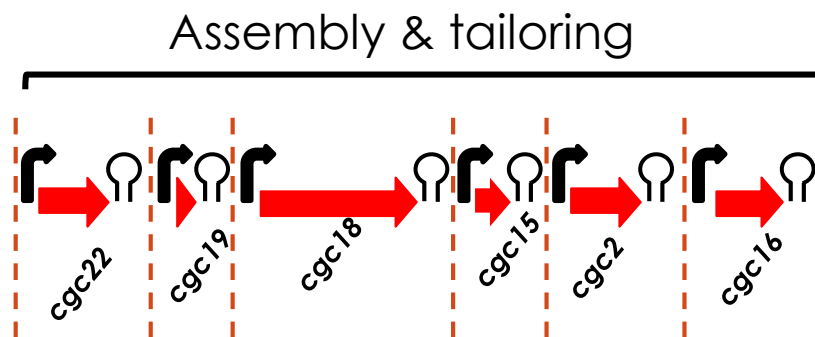
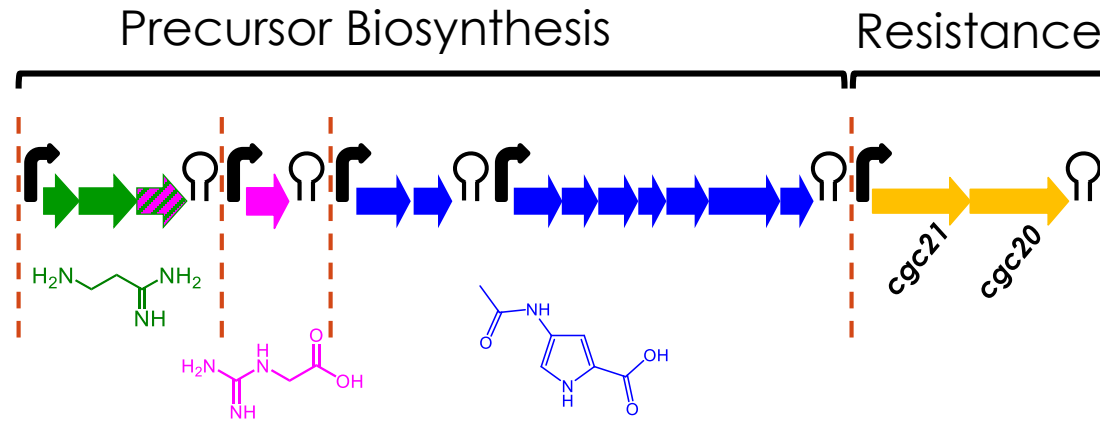
CAS006



CAS026: contains the 4 cassettes of precursor biosynthesis genes and the cassette of resistance genes

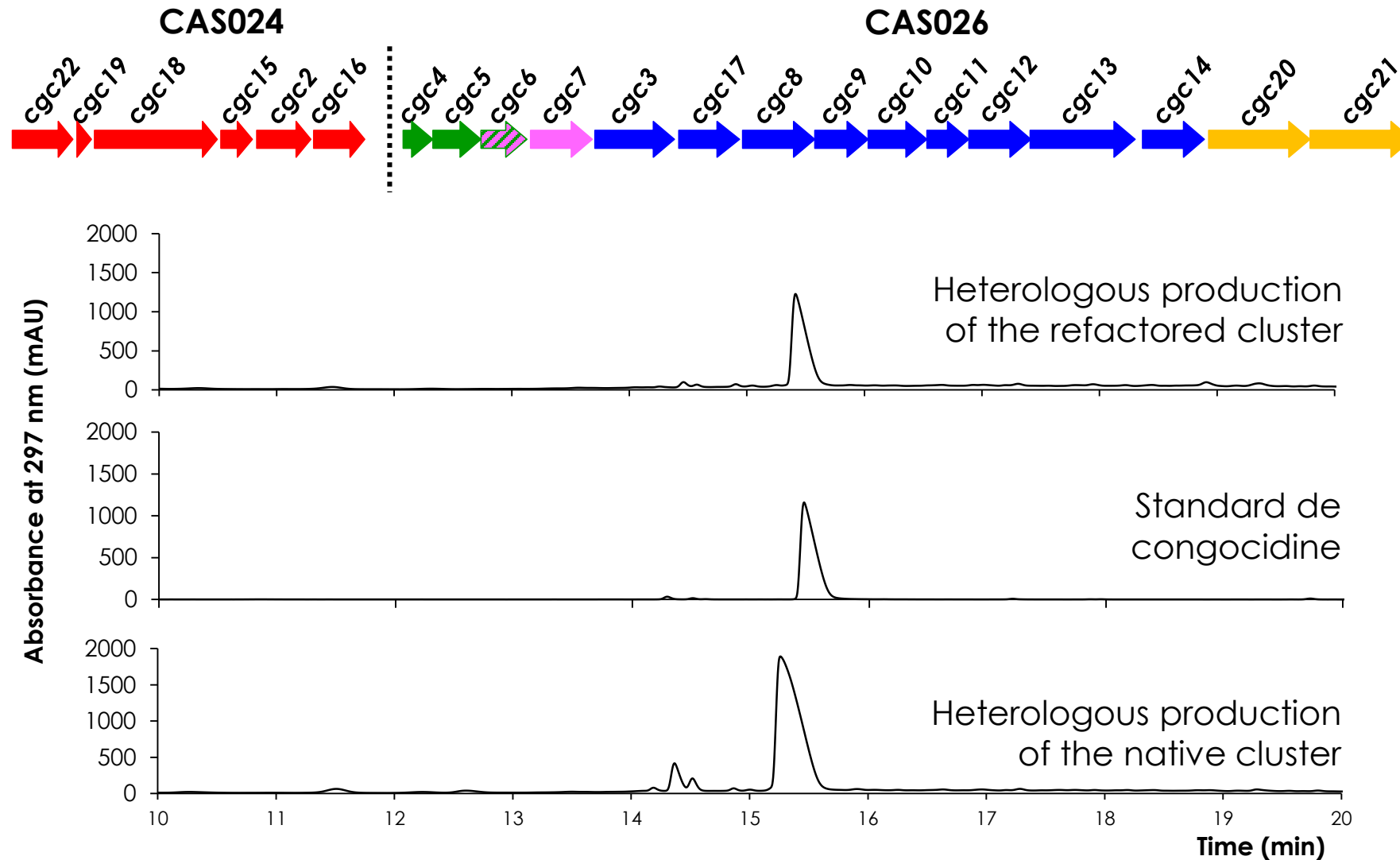
CAS026

## OBTENTION OF TWO FINAL CONSTRUCTIONS

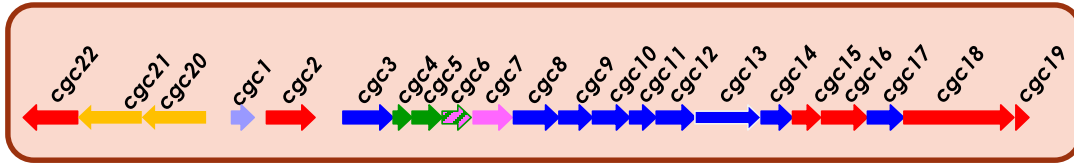


congocidine

## PRODUCTION OF CONGOCIDINE FROM THE REFACTORED GENE CLUSTER

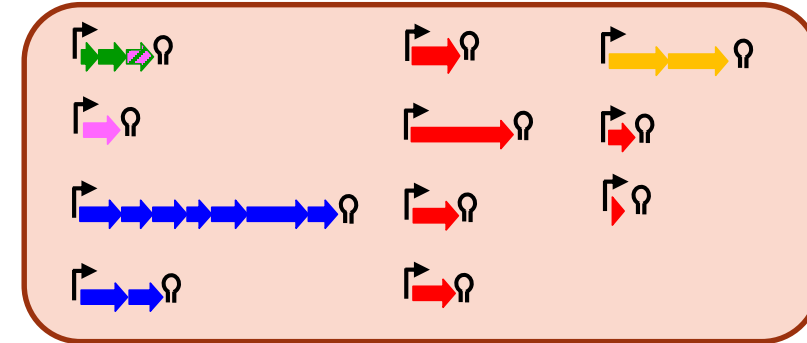


# REFACTORIZING OF CONGOCIDINE BIOSYNTHETIC GENE CLUSTER



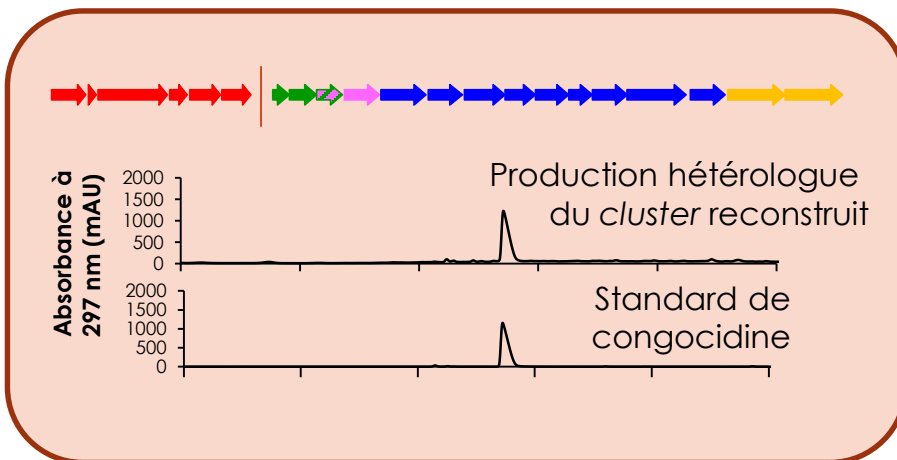
Choice of construction of synthetic operons

LCR



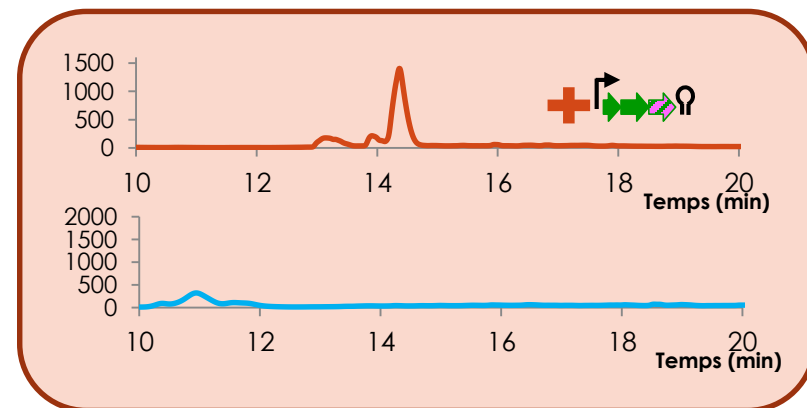
Construction of the cassettes  
Confirmation of the functionality  
of the 11 gene cassettes

Heterologous expression in *S. lividans*

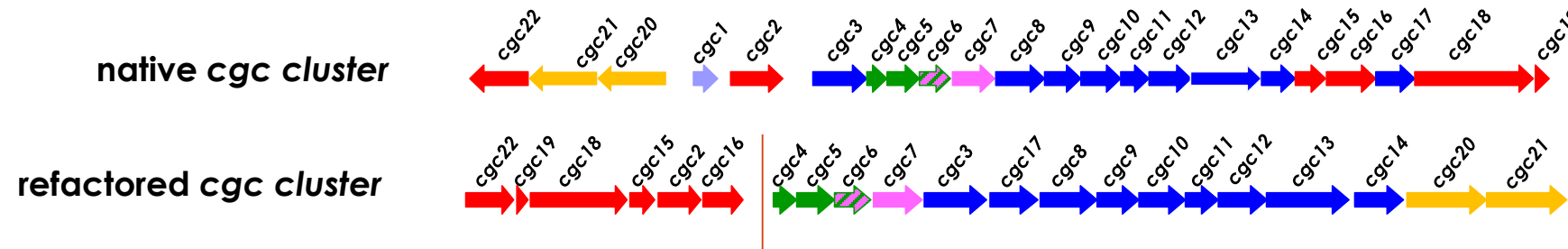


Biobrick assembly

Iterative assembly of the  
cassettes in 2 vectors



# CONCLUSIONS ON THE REFACTORIZING OF THE CONGOCIDINE BIOSYNTHETIC GENE CLUSTER



Each operon now directs:

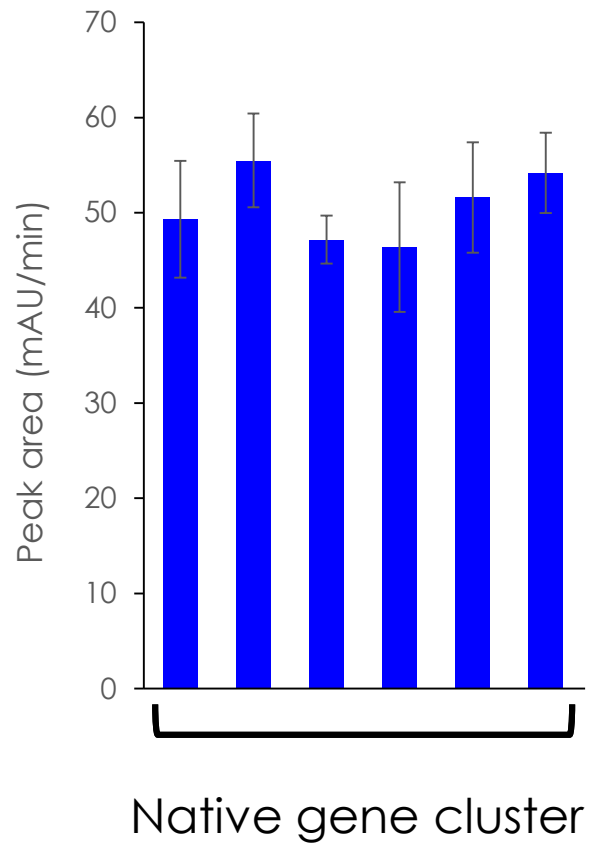
- The biosynthesis of one precursor
- The assembly of two specific precursors
- The export of the final compound

It is then possible to replace one of the operons to produce a hybrid pyrrolamide

But... can we investigate the efficiency of production first?

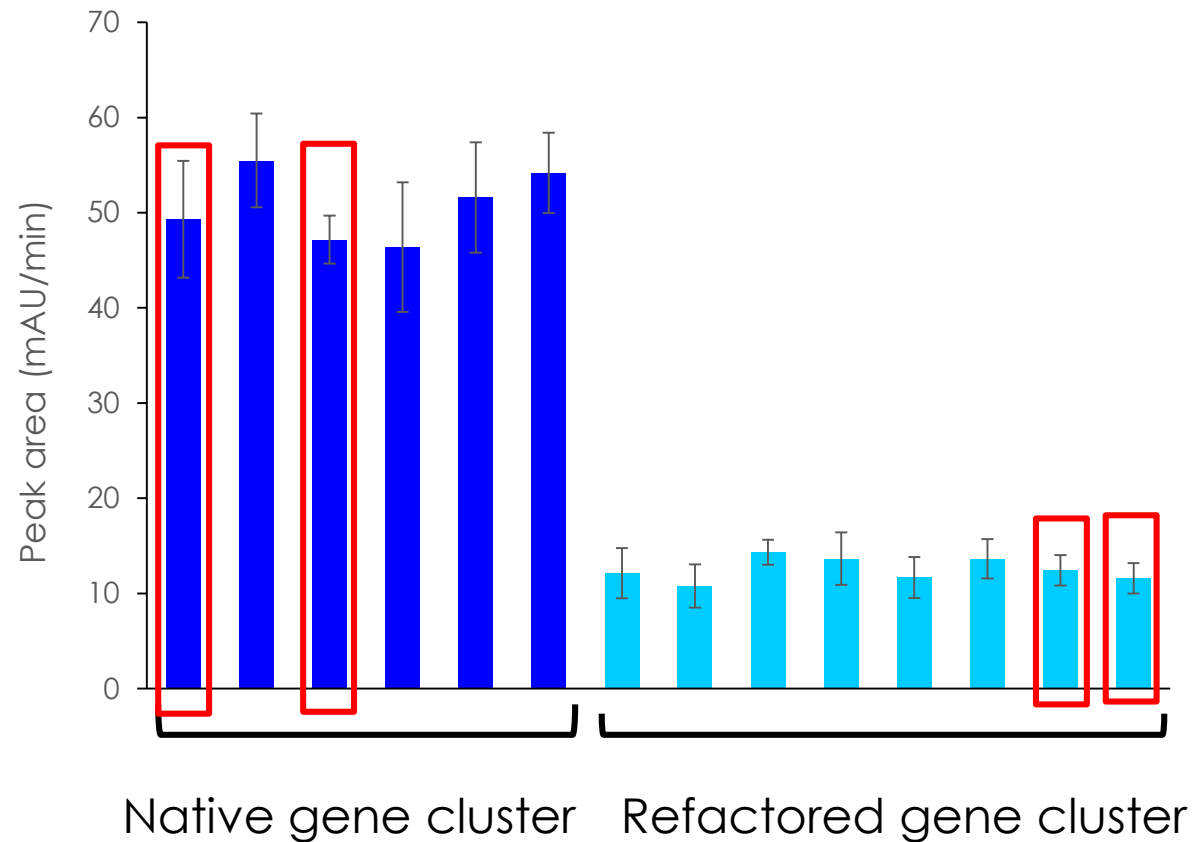


# CONGOCIDINE PRODUCTION: NATIVE VS REFACTORED BGC



- Can we compare the native and the refactored clusters ?

# CONGOCIDINE PRODUCTION: NATIVE VS REFACTORED BGC

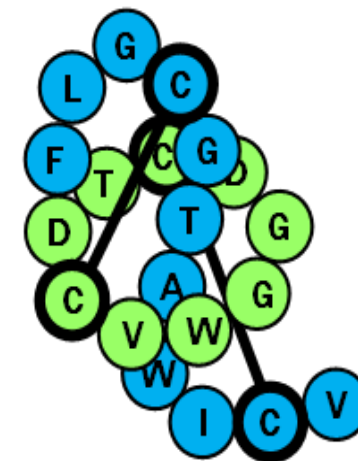


- Congocidine yield for the refactored gene cluster: about 25% of the yield of the native cluster
- Transcription levels?
- Translation levels?

# Summary

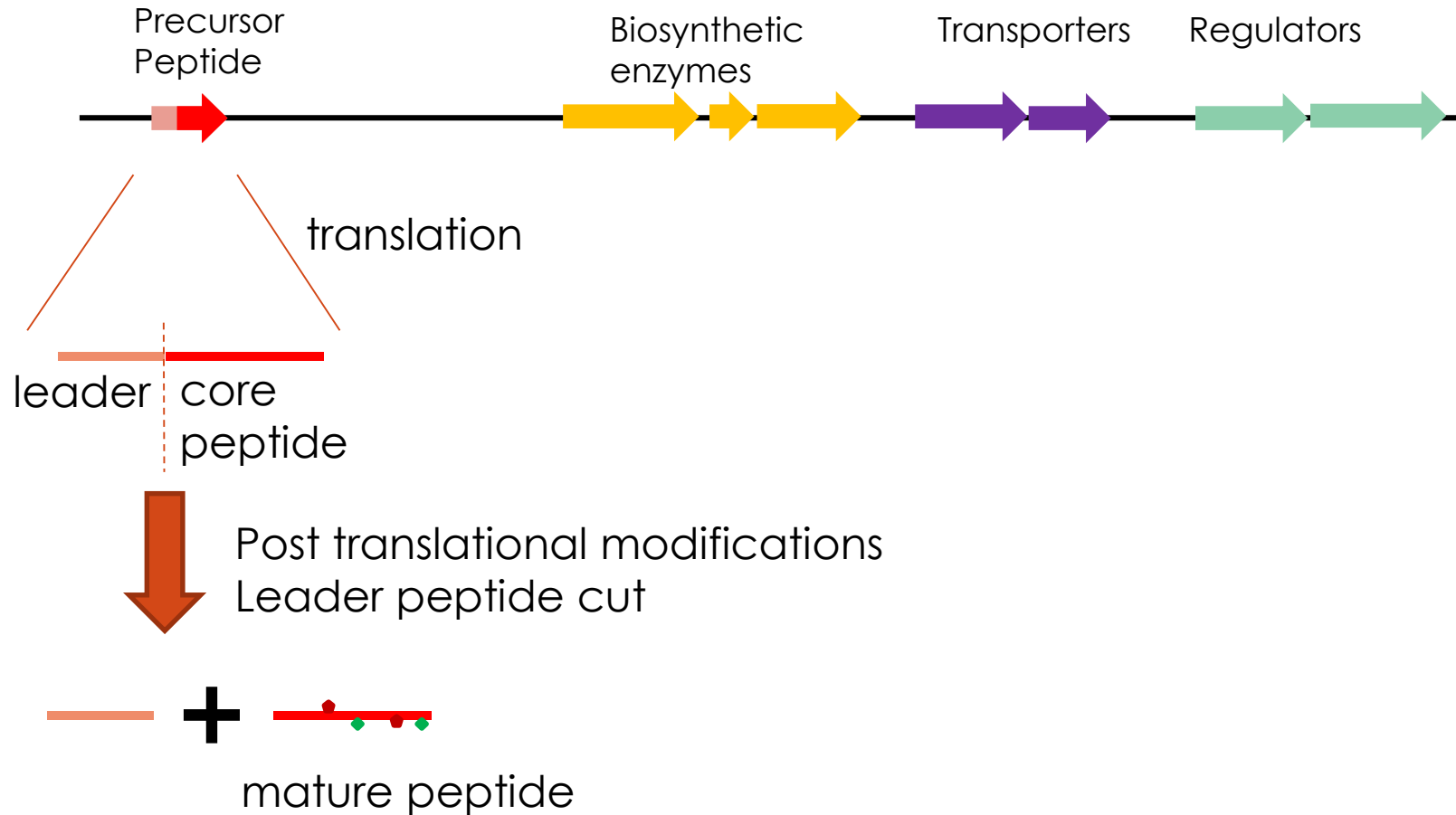
- What we learned here:
  - ❑ We should investigate the four genes that are potentially less expressed
  - ❑ Genes with the same promoter might not have the same expression
  - ❑ Promoter strength evaluated for one gene might not be transferable

All together: synthetic biology is not as well mastered as we would like it to be yet...  
Plenty left to understand!!

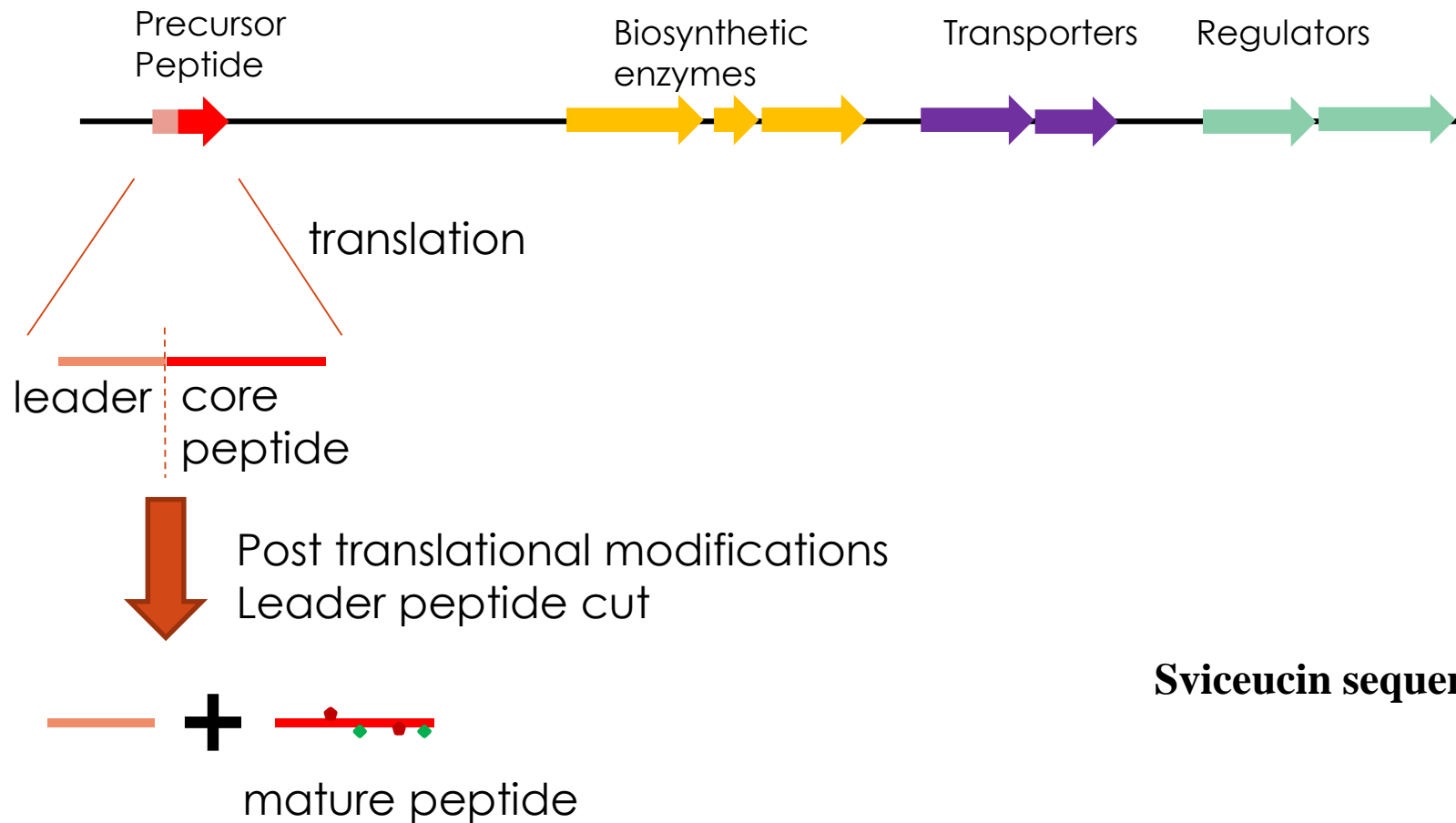


# PRODUCING SVICEUCIN NON NATURAL ANALOGS

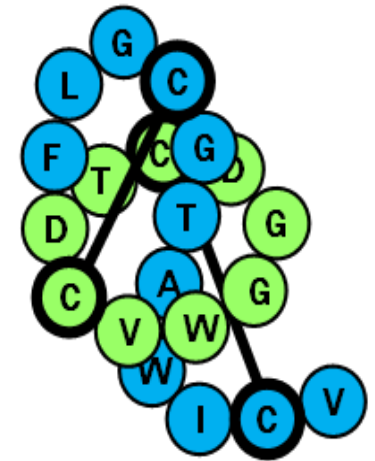
# RIPPs : RIBOSOMALLY SYNTHESIZED AND POST-TRANSLATIONALLY MODIFIED PEPTIDES



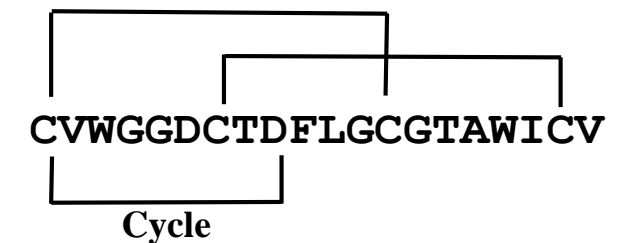
# RIPPs : RIBOSOMALLY SYNTHESIZED AND POST-TRANSLATIONALLY MODIFIED PEPTIDES



**Sviceucin, a lasso peptide**



**Disulfide bonds**

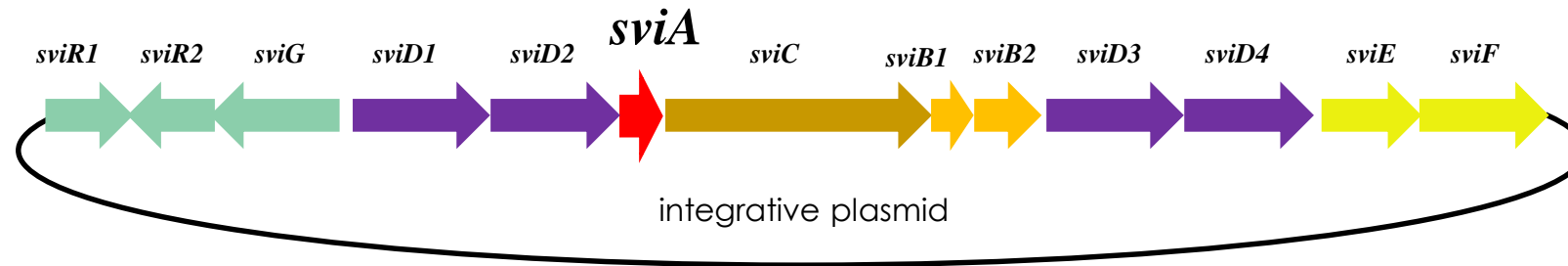


**Sviceucin sequence:**

CVWGGDCTDFLGC GTAWICV

**Cycle**

## SVICEUCIN BIOYNTHETIC GENE CLUSTER



Red box: Precursor

Gold box: Macrolactam synthetase

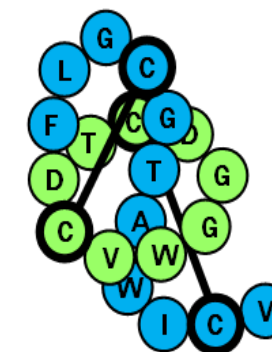
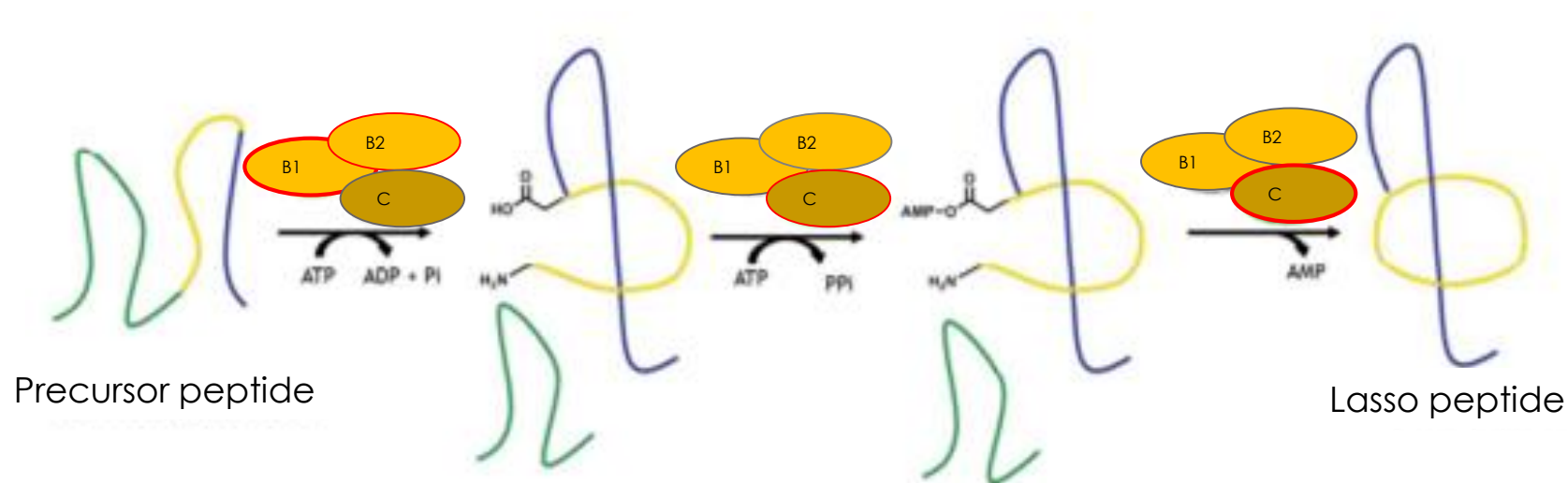
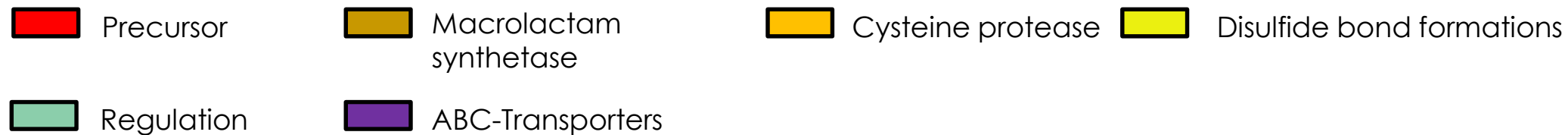
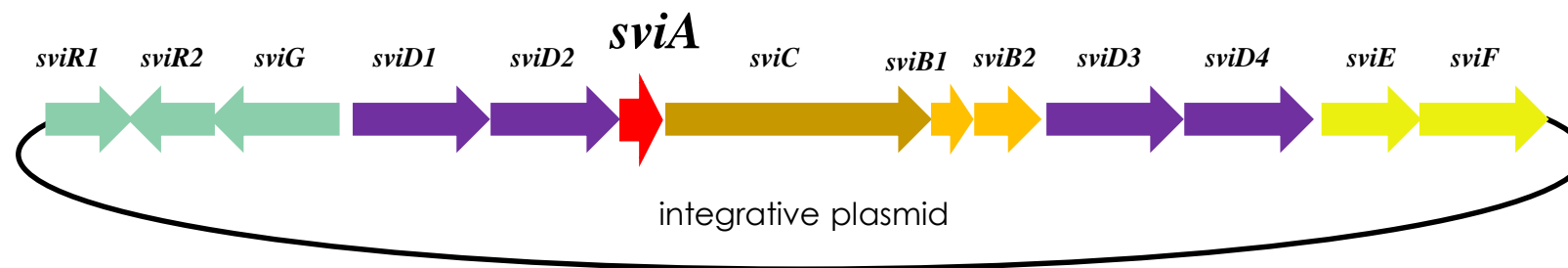
Yellow box: Cysteine protease

Light green box: Disulfide bond formations

Green box: Regulation

Purple box: ABC-Transporters

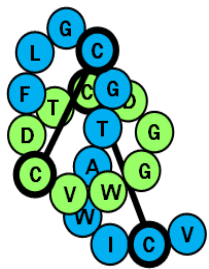
## SVICEUCIN BIOYNTHETIC GENE CLUSTER



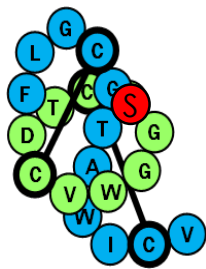


## GENERATING SVICEUCIN ANALOGS

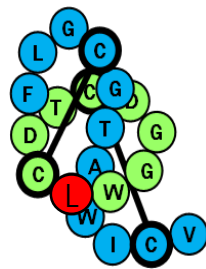
DNA Modification to generate analogs ??



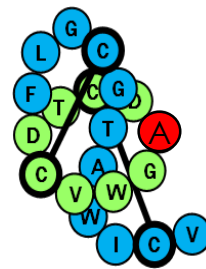
svi



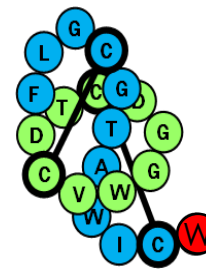
var1



var2



var3



var4

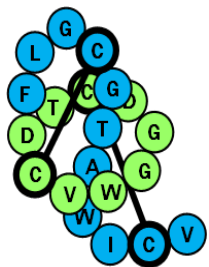


## GENERATING SVICEUCIN ANALOGS

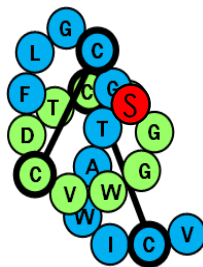
svi	TGTGTGTGGGGCGGAGACTGCACCGACTTCCTCGGCTGCGGCACCGCCTGGATCTGTGTCTGA
var1	TGTGTGTGGGGCGGA <b>AG</b> CTGCACCGACTTCCTCGGCTGCGGCACCGCCTGGATCTGTGTCTGA
var2	TGT <b>CTC</b> TGGGGCGGAGACTGCACCGACTTCCTCGGCTGCGGCACCGCCTGGATCTGTGTCTGA
var3	TGTGTGTGGGGCG <b>CC</b> GACTGCACCGACTTCCTCGGCTGCGGCACCGCCTGGATCTGTGTCTGA
var4	TGTGTGTGGGGCGGAGACTGCACCGACTTCCTCGGCTGCGGCACCGCCTGGATCTGT <b>TGG</b> TGA



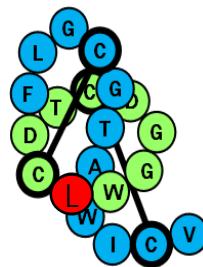
svi	<u>CVWGGDCTDFLGC</u> GTAWICV
var1	<u>CVWGG</u> <b>S</b> <u>CTDFLGC</u> GTAWICV
var2	<b>L</b> <u>WGGDCTDFLGC</u> GTAWICV
var3	<u>CVWG</u> <b>A</b> <u>DCTDFLGC</u> GTAWICV
var4	<u>CVWGGDCTDFLGC</u> GTAWIC <b>W</b>



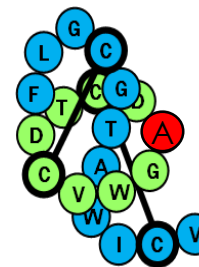
svi



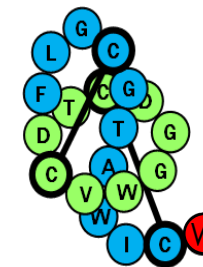
var1



var2



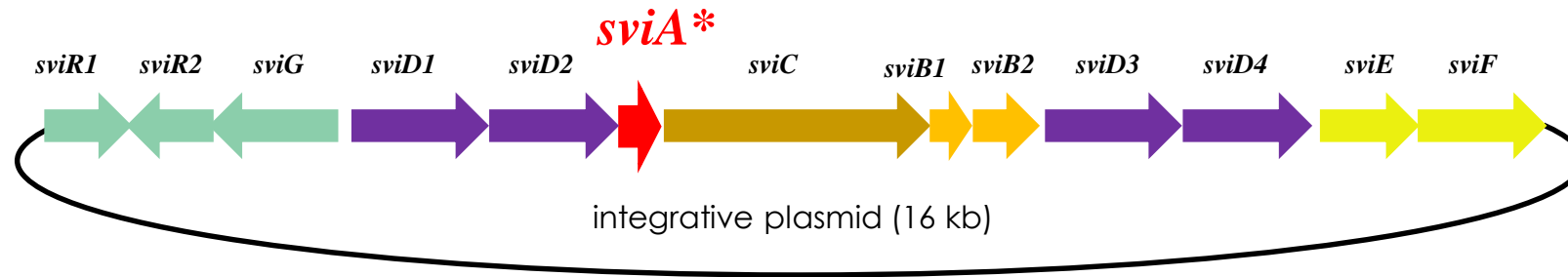
var3



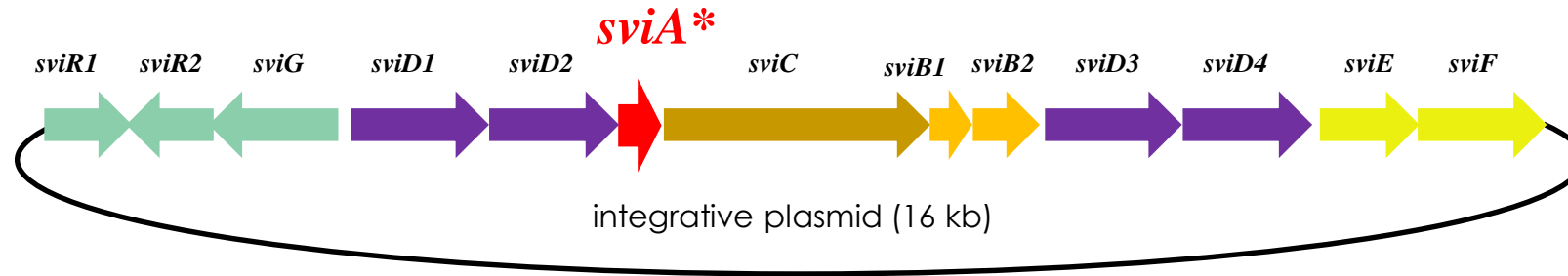
var4



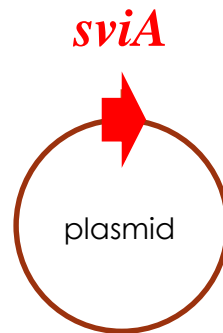
## CHANGING A FEW DNA BASE PAIRS ON A PLASMID



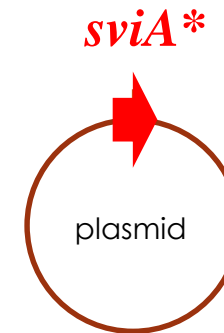
## CHANGING A FEW DNA BASE PAIRS ON A PLASMID



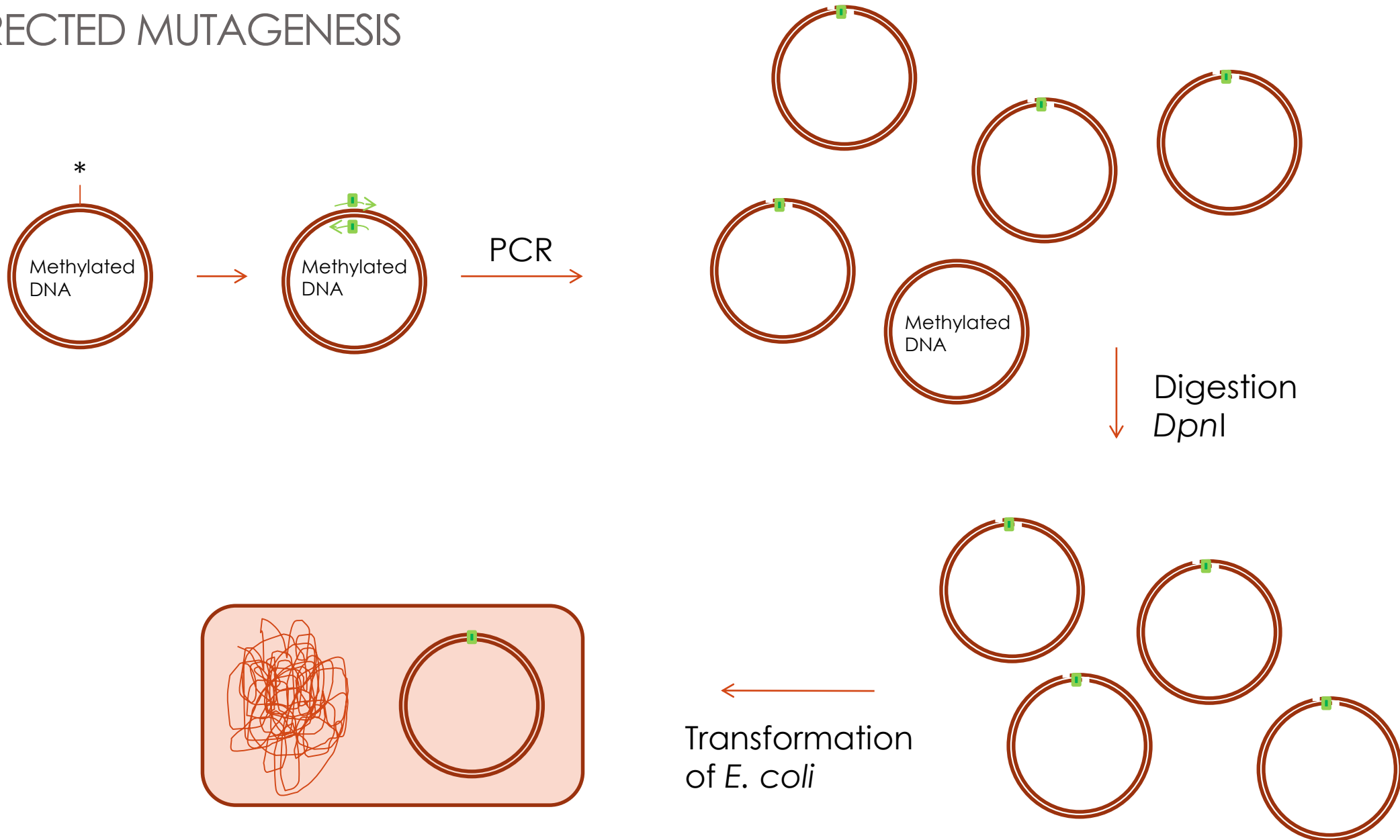
Working on  
a smaller plasmid



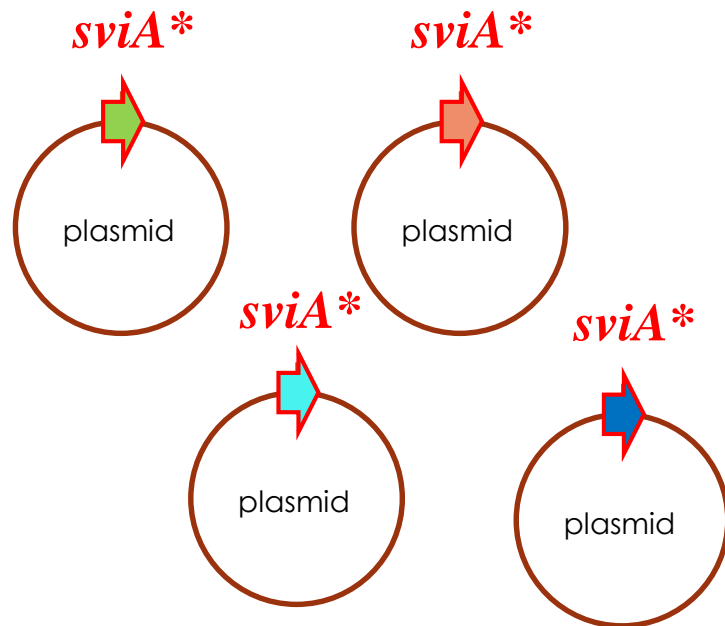
Method to  
modify the DNA ??



## SITE DIRECTED MUTAGENESIS

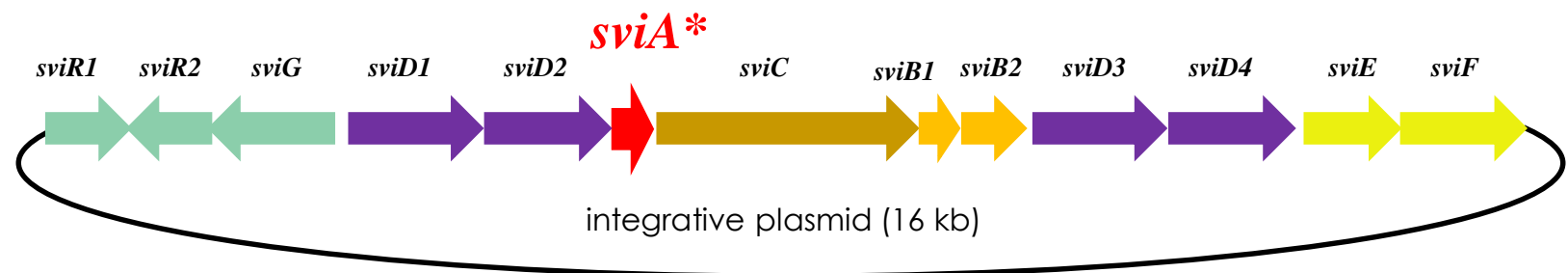
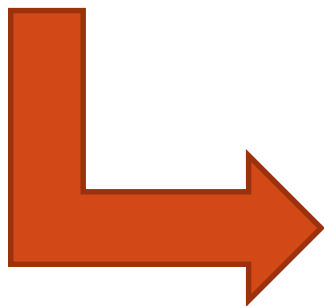


## REPLACING THE MUTATED PRECURSOR GENE IN THE CLUSTER

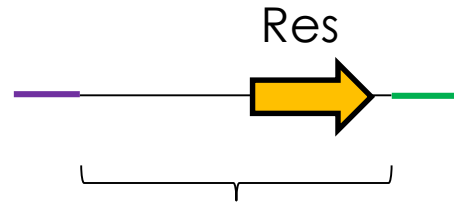


How to replace *sviA\** in the plasmid ??

Necessary to insert restriction sites,  
And to avoid scars



## PCR TARGETING

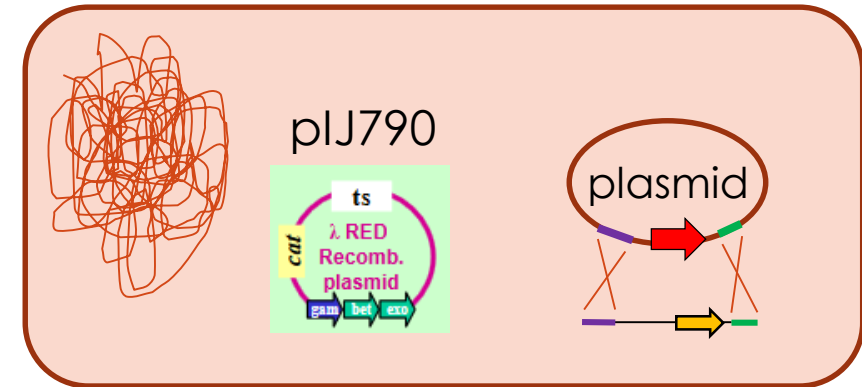


Amplified by PCR, can contain other genes, or restriction sites...

Transformation

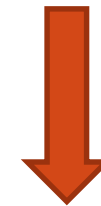


*E. coli* BW25113 pIJ790 / plasmid



Recombination

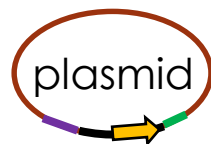
Loss of pIJ790  
(thermosensitive)



*E. coli* BW25113 plasmid

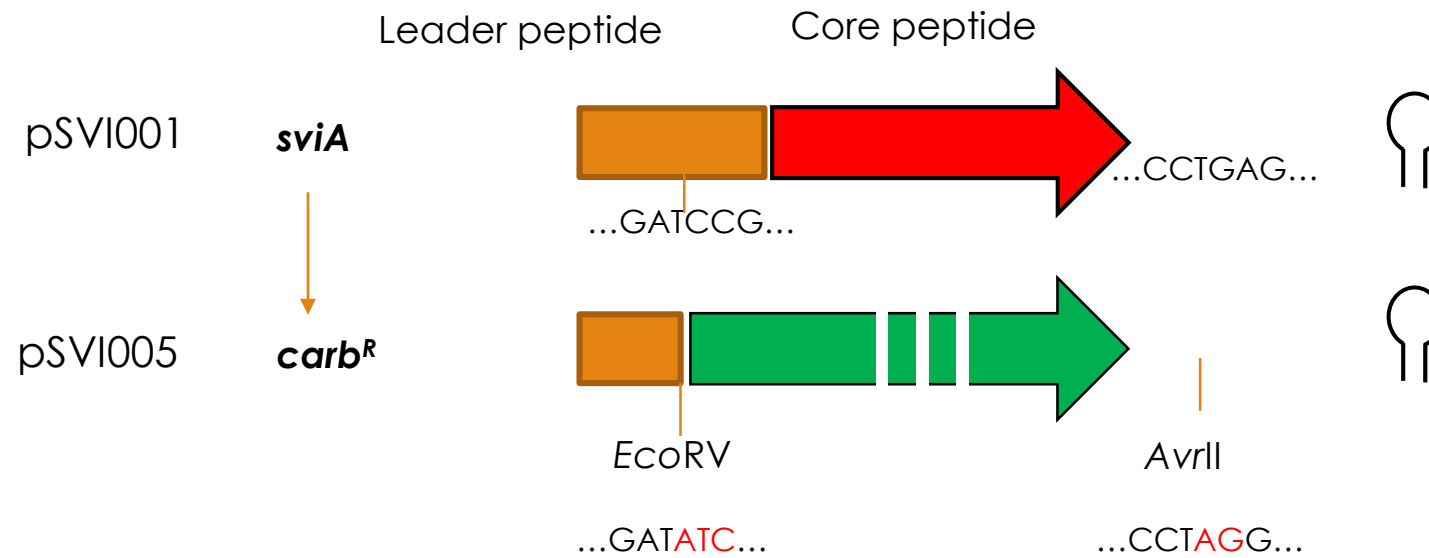


Extraction



## CLOSE UP LOOK ON THE EXPRESSION PLATFORM

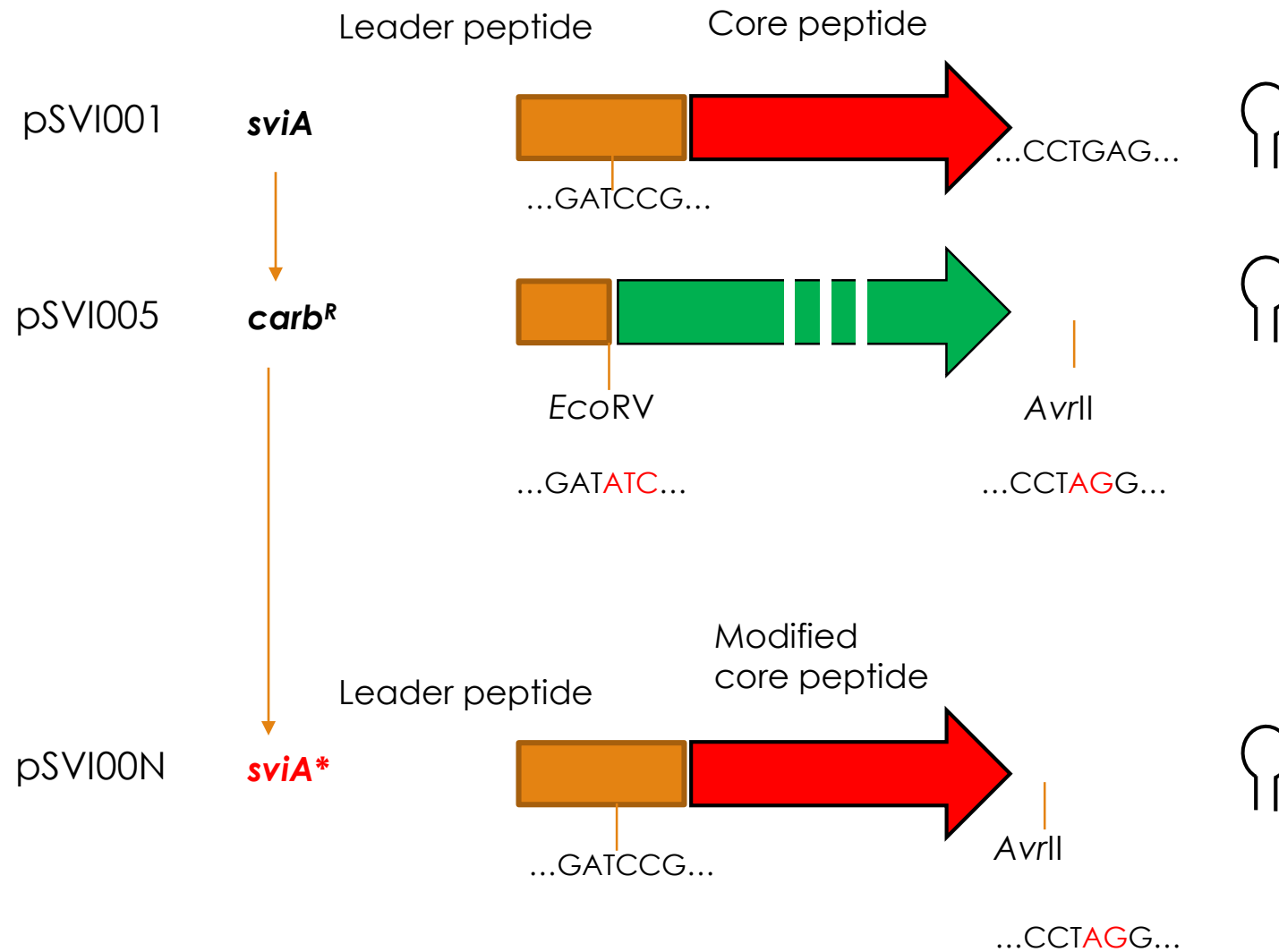
zoom



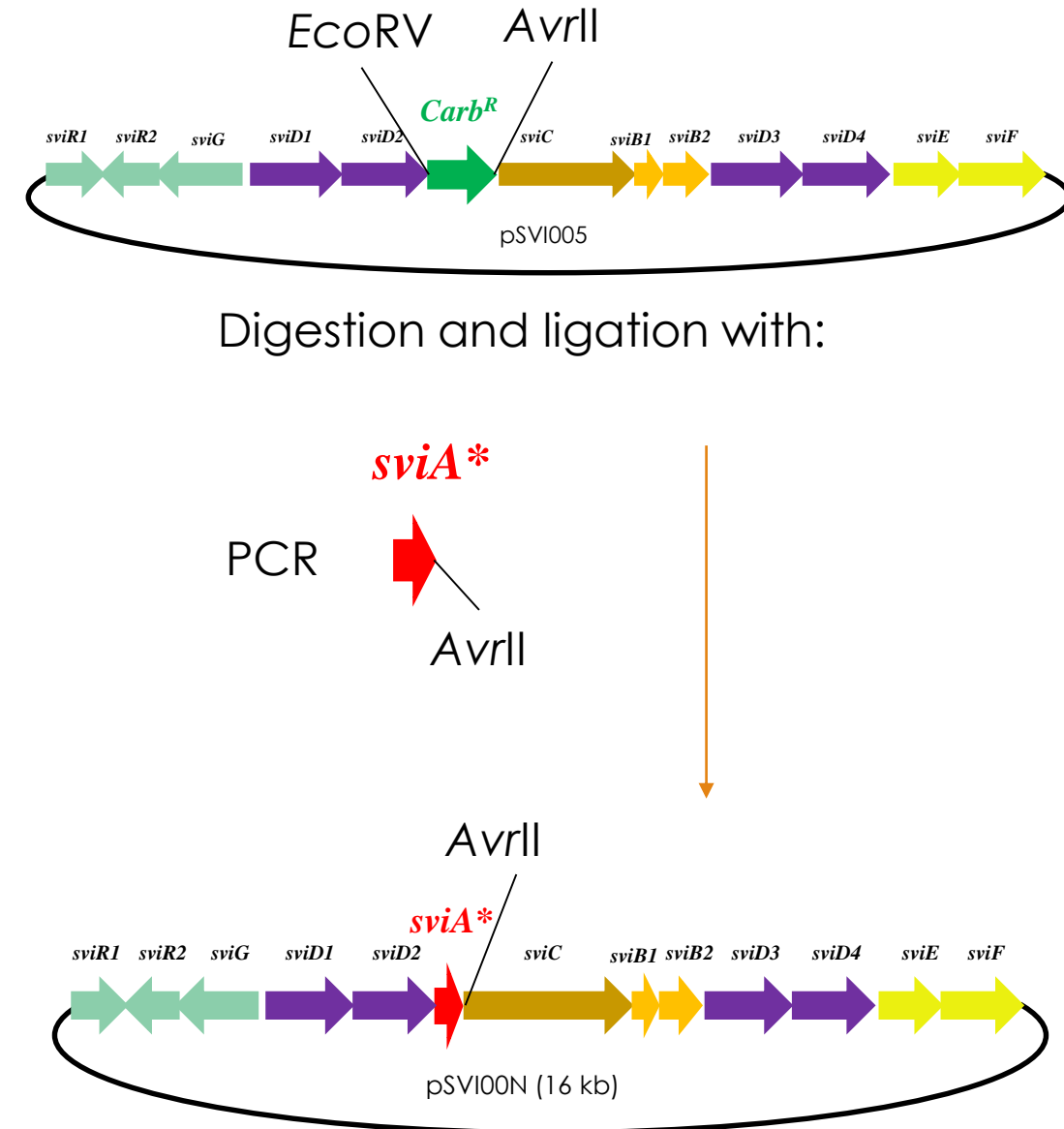
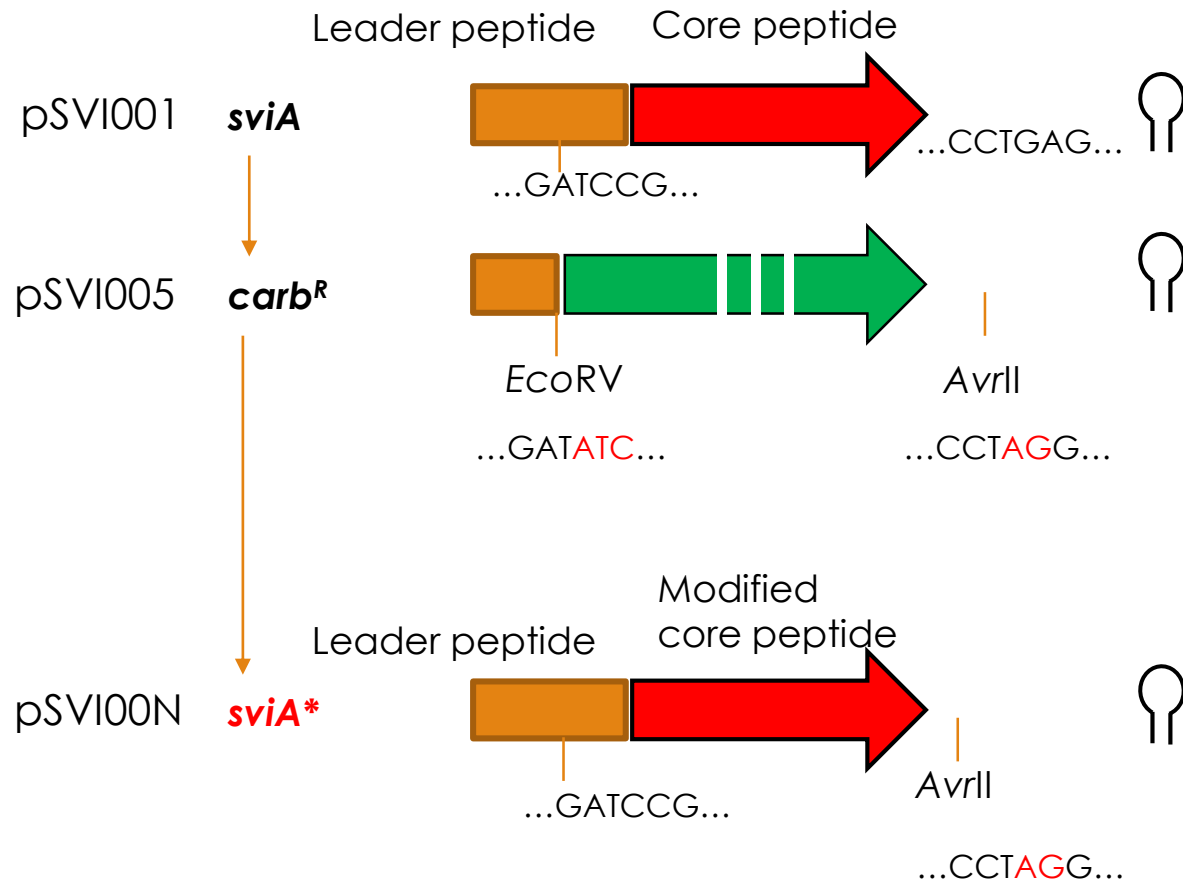


## CLOSE UP LOOK ON THE EXPRESSION PLATFORM

zoom



## SUMMARY OF THE CLONING STRATEGY



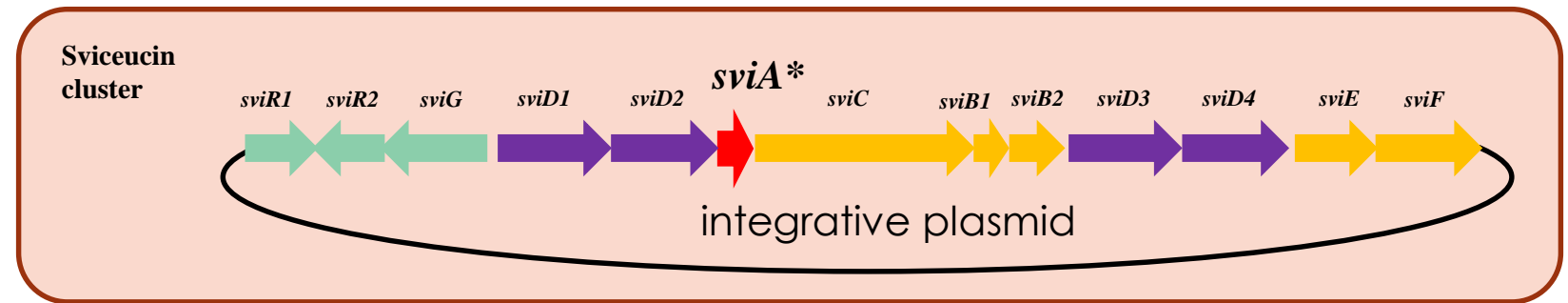
GENERATION SVICEUCIN VARIANTS *IN VIVO*

Site directed mutagenesis of the precursor peptide gene *sviA*

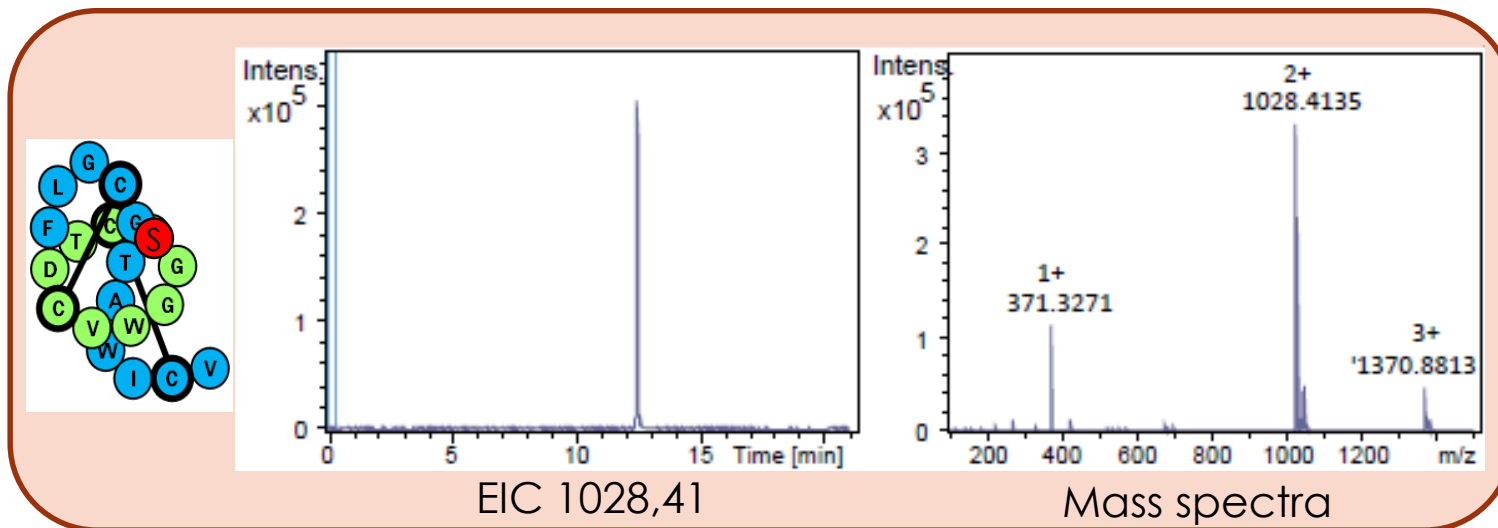


50 *sviA*\* constructed

Ligation in *sviceucin* BGC

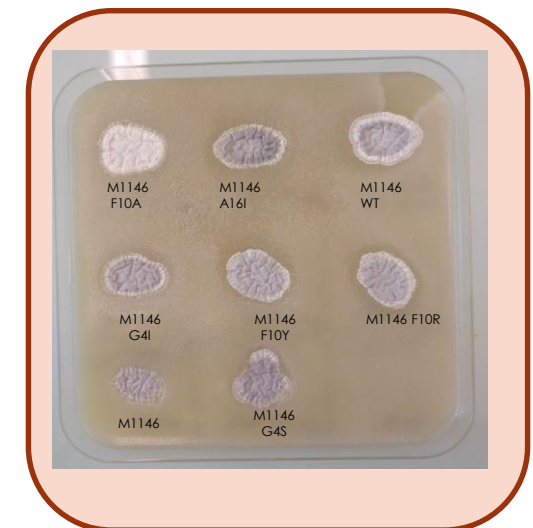


Integration in *S. coelicolor* genome

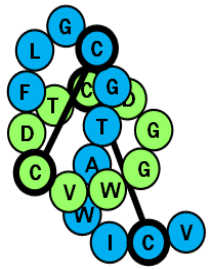


Small scale production

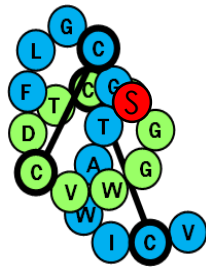
Mass spectrometry analysis (LCMS)



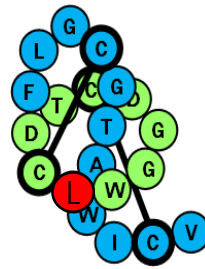
## FURTHER MODIFICATIONS



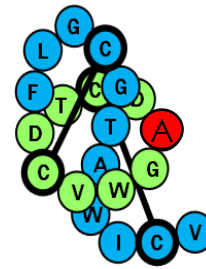
svi



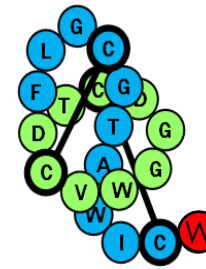
var1



var2



var3



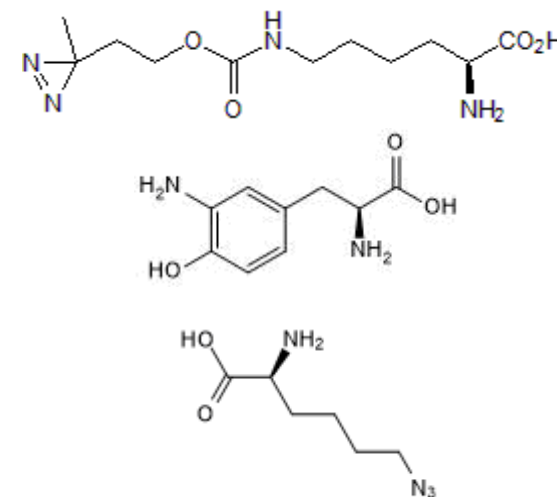
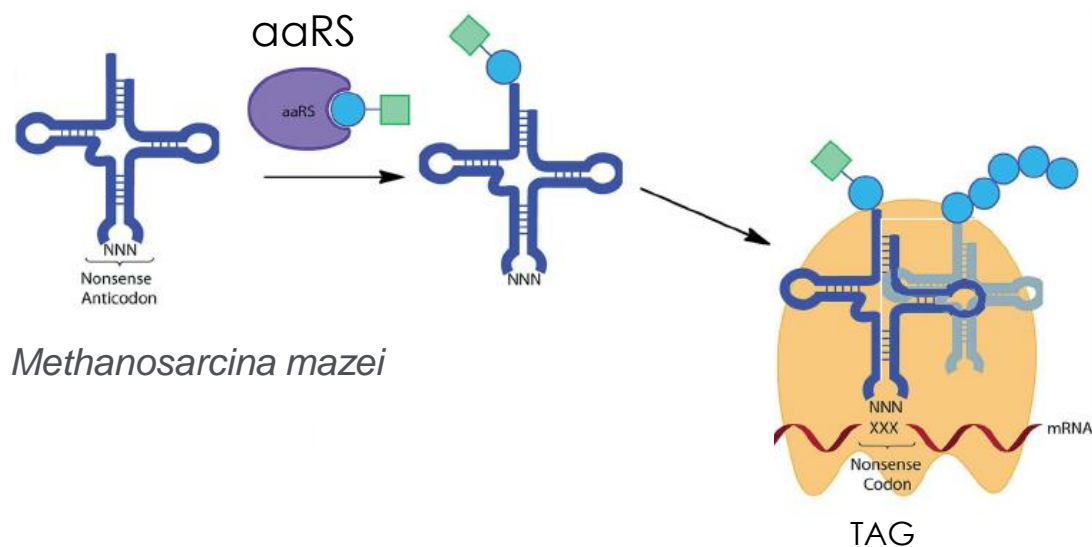
var4



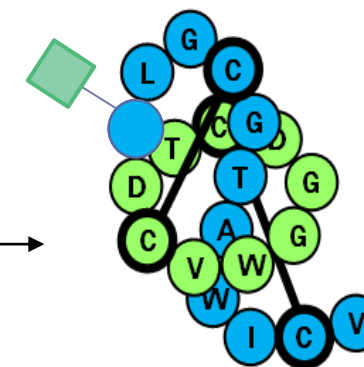
Can we obtain a variant that would contain non natural amino acids ?

# INCORPORATION OF NON NATURAL AMINO ACIDS THROUGH EXTENSION OF THE GENETIC CODE OF *STREPTOMYCES*

Orthogonal tRNA/aa-tRNA synthetase



Peptide with  
non natural  
amino acid



**Reactive group:**

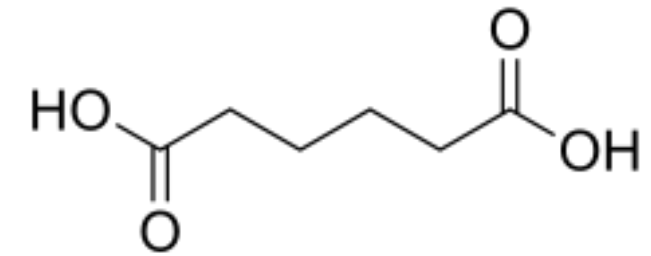
Searching for the target protein,  
Enrichment, Imaging *in situ*

## SUMMARY CONCERNING THE SPECIALIZED METABOLISM

- Presentation of some DNA assembly methods
- Explanation on NRPS and RiPP biosynthesis processes
- Through the two examples on congocidine refactoring, and sviceucin analog production

... but there is much more out there !

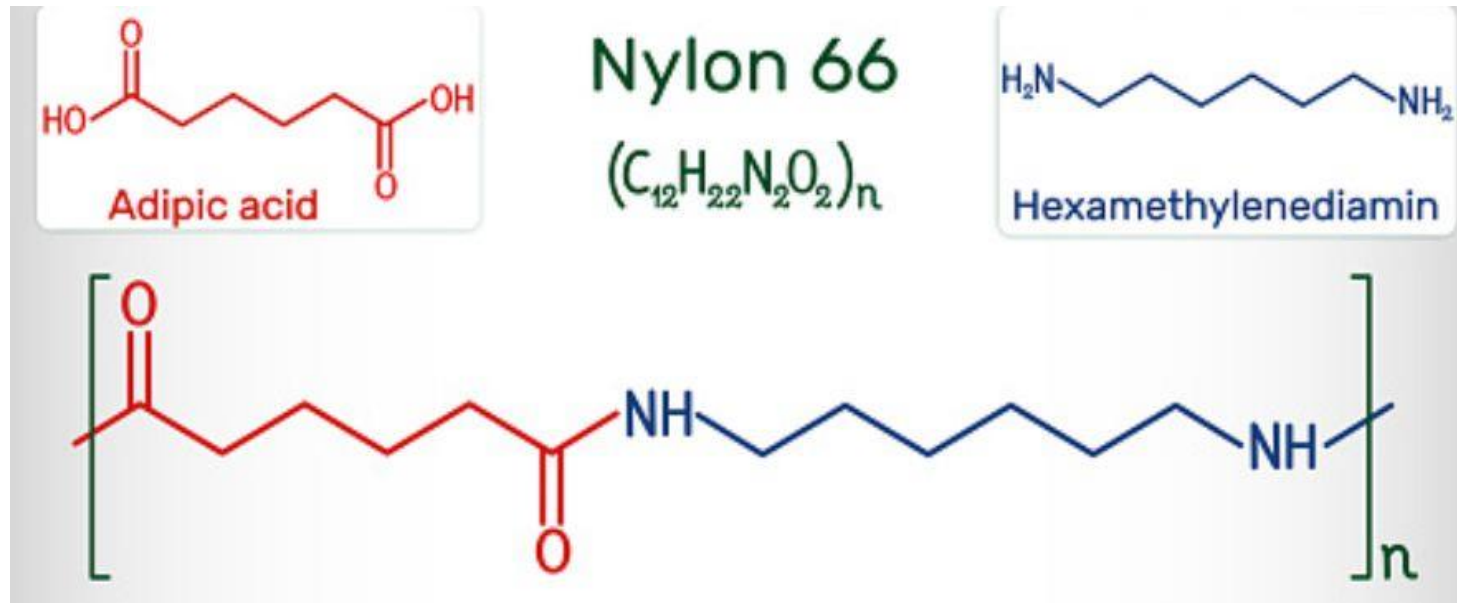
One growing field is to produce interesting molecules from biology, instead of chemistry



---

# PRODUCING ADIPIC ACID

## A COMPONENT OF NYLON (1938)

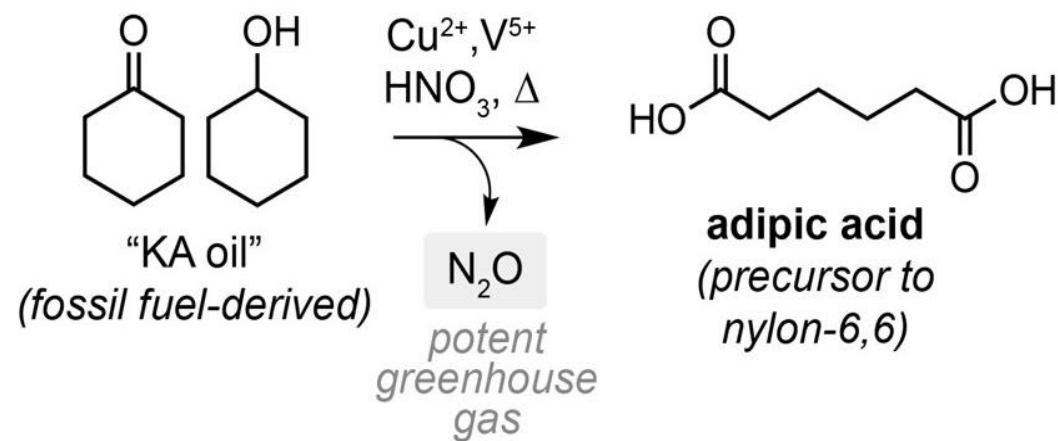


Condensation occurs spontaneously under solvent-free conditions, at elevated temperature and pressure and in high yield



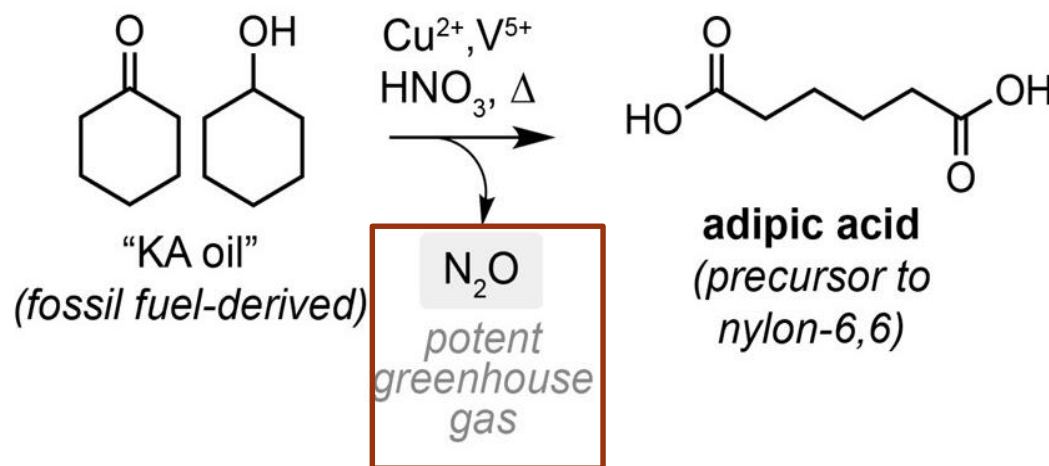
# CHEMICAL SYNTHESIS OF ADIPIC ACID

cyclohexanone and cyclohexanol



# CHEMICAL SYNTHESIS OF ADIPIC ACID

cyclohexanone and cyclohexanol



annual production of  
2.6 million tons

1 kg of N<sub>2</sub>O equates to 298 kg CO<sub>2</sub> equivalents

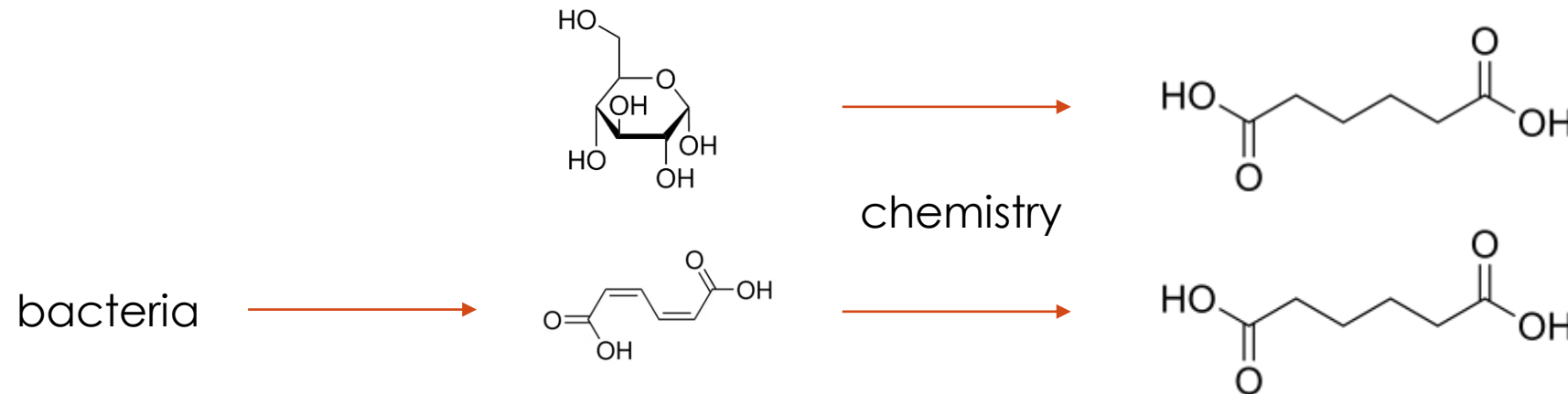
10% of anthropogenic nitrous oxide emissions are emitted from this single industrial reaction to produce nylon

Steele and Wallace *Nature chemistry* vol. 16,5 (2024)

Suitor et al. *ACS synthetic biology* vol. 9,9 (2020): 2472-2476.

## CAN WE PRODUCE ADIPIC ACID DIFFERENTLY?

- Semi synthetic approaches from glucose or cis-cis-muconic acid



Still relies on metal catalysts, petrochemical reagents, elevated reaction temperatures and pressures

## CAN WE PRODUCE ADIPIC ACID DIFFERENTLY?

- Semi synthetic approaches from glucose or cis-cis-muconic acid
- Biological routes: which chassis??

*Escherichia coli*, *Corynebacterium glutamicum*, *Saccharomyces cerevisiae*, *Pseudomonas aeruginosa*...



- Which pathway?? Which carbon source??

Glucose, glycerol, cellulose, lignin, plastics...

# CAN WE PRODUCE ADIPIC ACID DIFFERENTLY?

ACS  
central  
science

Open Access

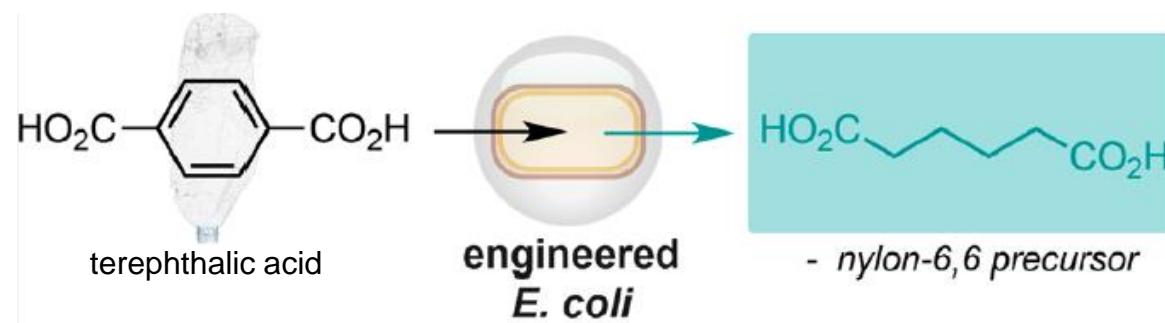
This article is licensed under [CC-BY 4.0](https://creativecommons.org/licenses/by/4.0/)  

<http://pubs.acs.org/journal/acscii>

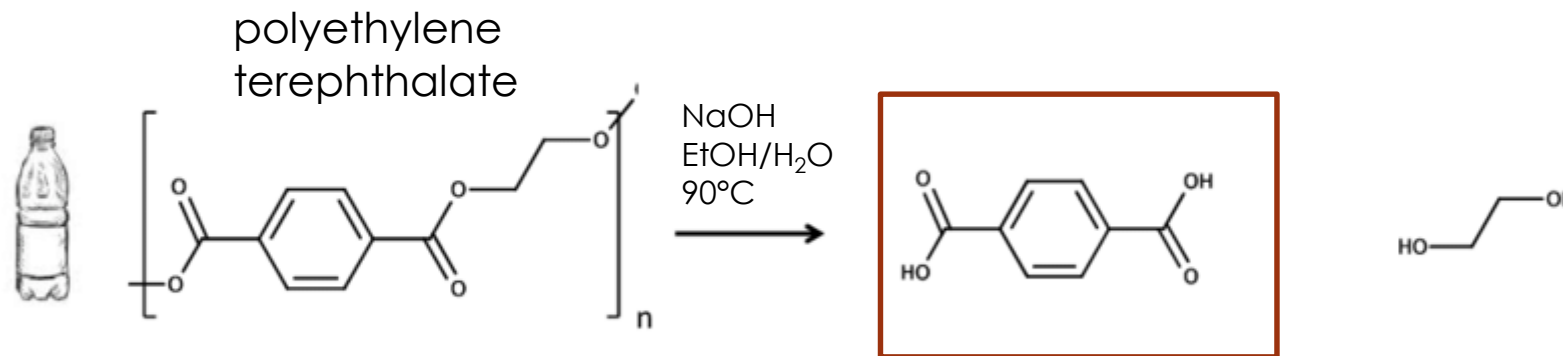
Article

## Microbial Upcycling of Waste PET to Adipic Acid

Marcos Valenzuela-Ortega,<sup>§</sup> Jack T. Suitor,<sup>§</sup> Mirren F. M. White, Trevor Hinchcliffe, and Stephen Wallace\*



## PET WASTE

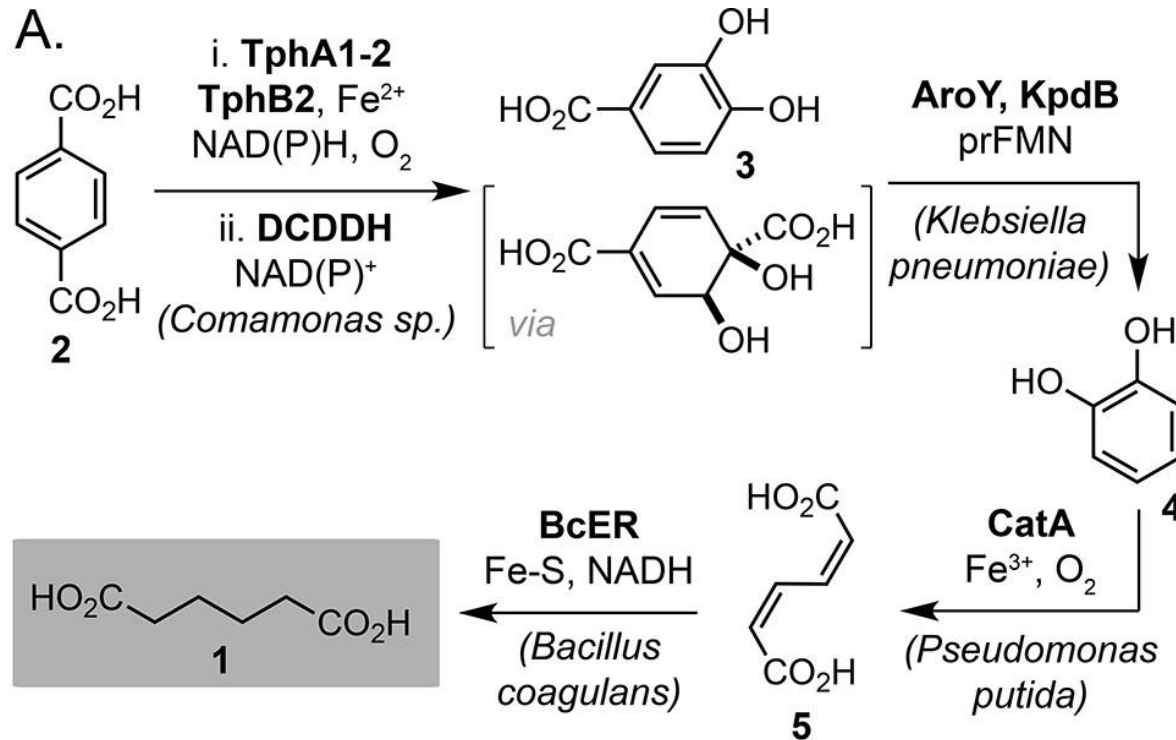


terephthalic acid (TA) and ethylene glycol

About 25 M  
ton/year  
of post-consumer  
PET waste

# THE PROPOSED PATHWAY FROM TA TO ADIPIC ACID (AA)

terephthalic acid (TA)



Adipic acid (AA)

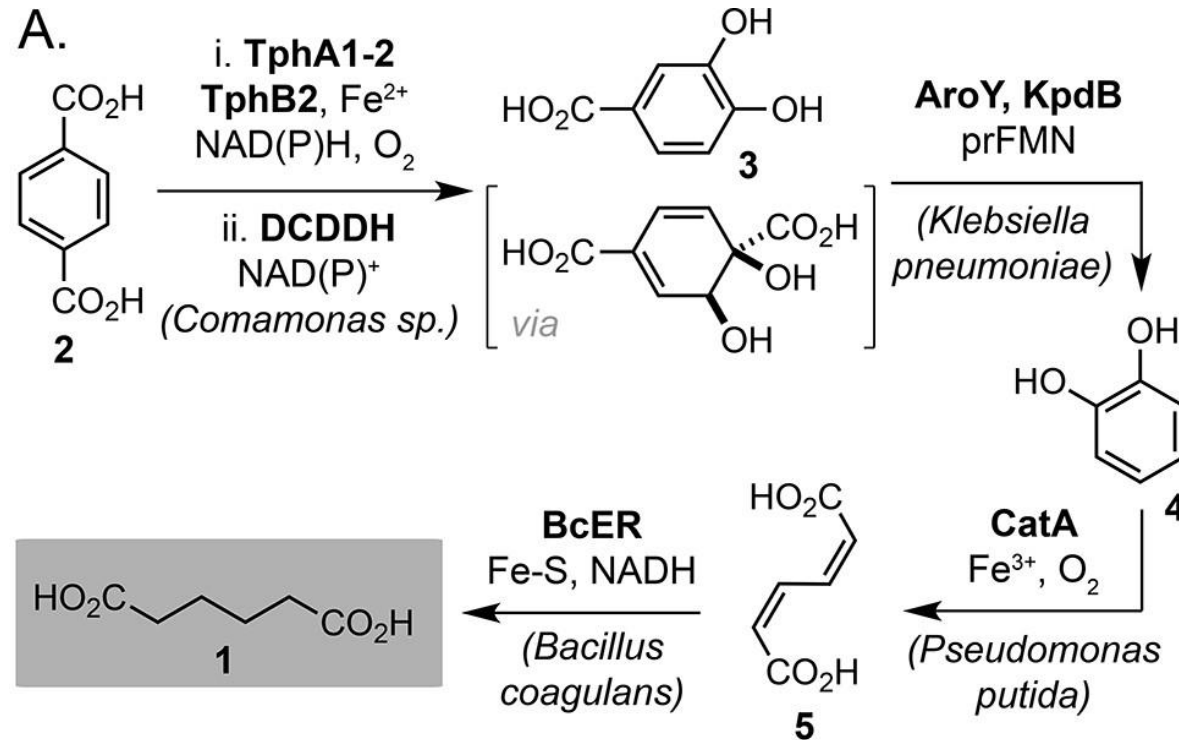
**TPADO**, a heterotrimeric  $\text{O}_2$ -dependent dioxygenase  
**DCDDH**, a  $\text{NAD}^+$ -dependent dehydrogenase

**AroY**, a protocatechuate decarboxylase, **KpdB** is the Bsubunit of 4-hydroxybenzoate decarboxylase

**CatA** is a non-heme  $\text{Fe(III)}$ -dependent dioxygenase  
**BcER** is a  $[4\text{Fe-4S}]$ -dependent oxidoreductase

# THE PROPOSED PATHWAY FROM TA TO ADIPIC ACID (AA)

terephthalic acid (TA)



Adipic acid (AA)

**TPADO**, a heterotrimeric O<sub>2</sub>-dependent dioxygenase  
**DCDDH**, a NAD<sup>+</sup>-dependent dehydrogenase

**AroY**, a protocatechuate decarboxylase, **KpdB** is the Bsubunit of 4-hydroxybenzoate decarboxylase

**CatA** is a non-heme Fe(III)-dependent dioxygenase  
**BcER** is a [4Fe-4S]-dependent oxidoreductase

Construction of one vector with *aroY*, *kpdB*, *catA* and *bcER*

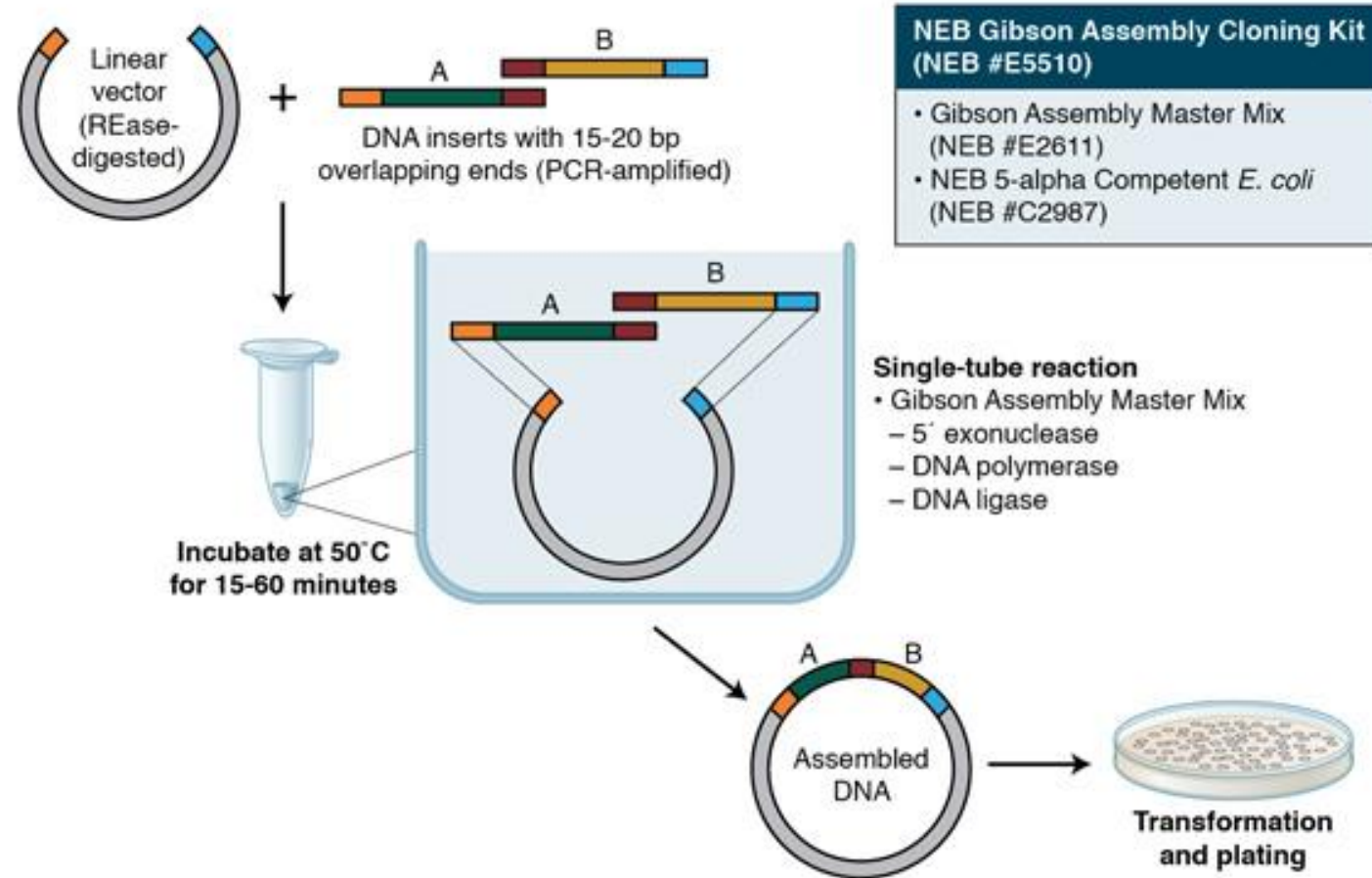
How do they proceed??



## METHODOLOGY TO CONSTRUCT THE VECTORS

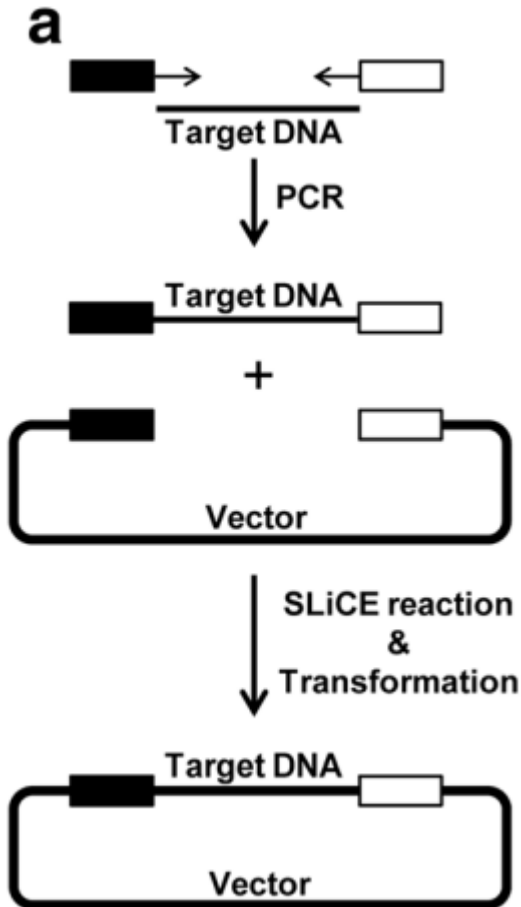
- All genes are codon-optimized and synthesized
- Genes are introduced in vectors using **restriction enzymes**
- Genes are combined using **SLiCE cloning: SEAMLESS LIGATION CLONING EXTRACT**

## GIBSON ASSEMBLY



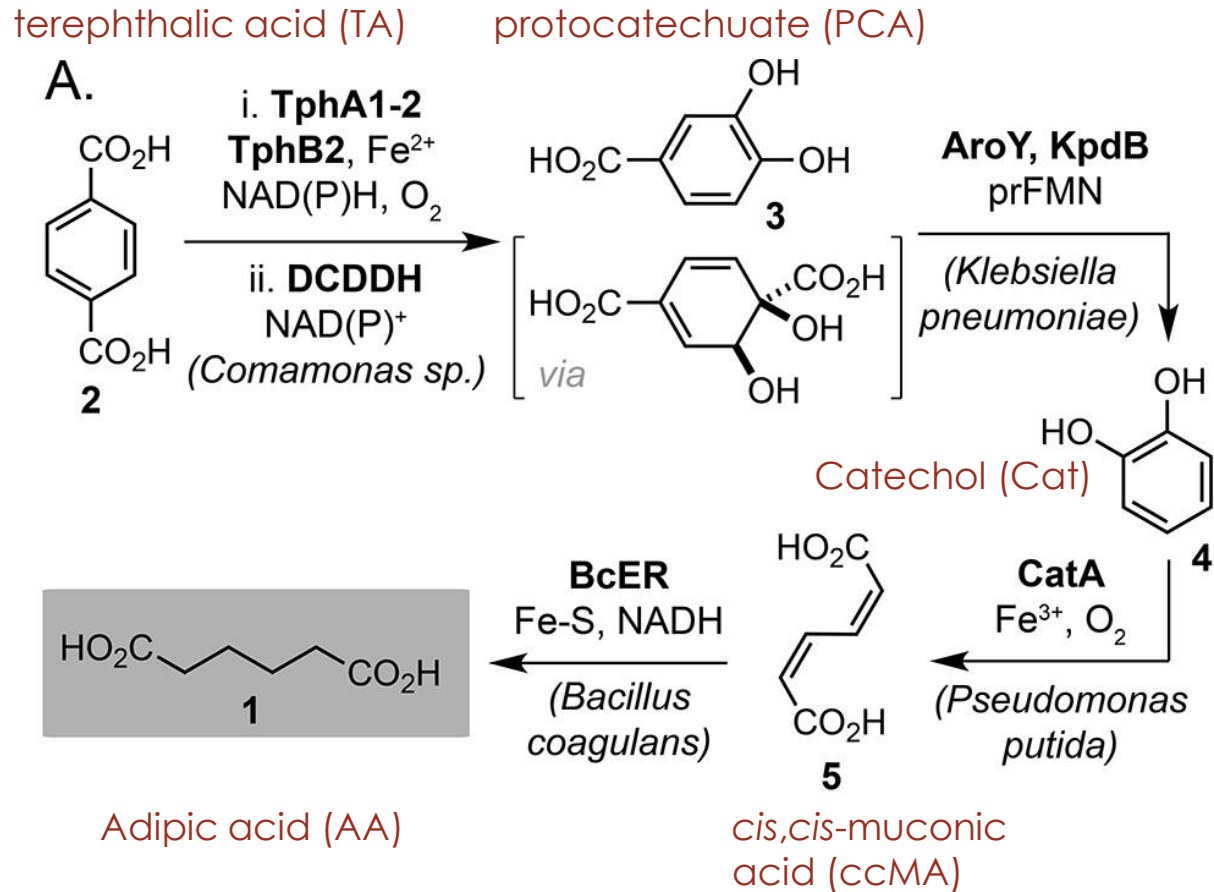
- <https://www.neb.com/en/applications/cloning-and-synthetic-biology/dna-assembly-and-cloning/gibson-assembly>

## SEAMLESS LIGATION CLONING EXTRACT (SLICE) CLONING METHOD



- in vitro recombination (1h, 37°C) between short regions of homologies (15–52 bp) in bacterial cell extracts
- does not require the use of enzymes for the modification of vector and insert end sequences

## THE PROPOSED PATHWAY FROM TA TO ADIPIC ACID (AA)

**B.**

**St1:** *\_pQLinkN-aroY/kpdB*



**St2b:** *\_pAA2*



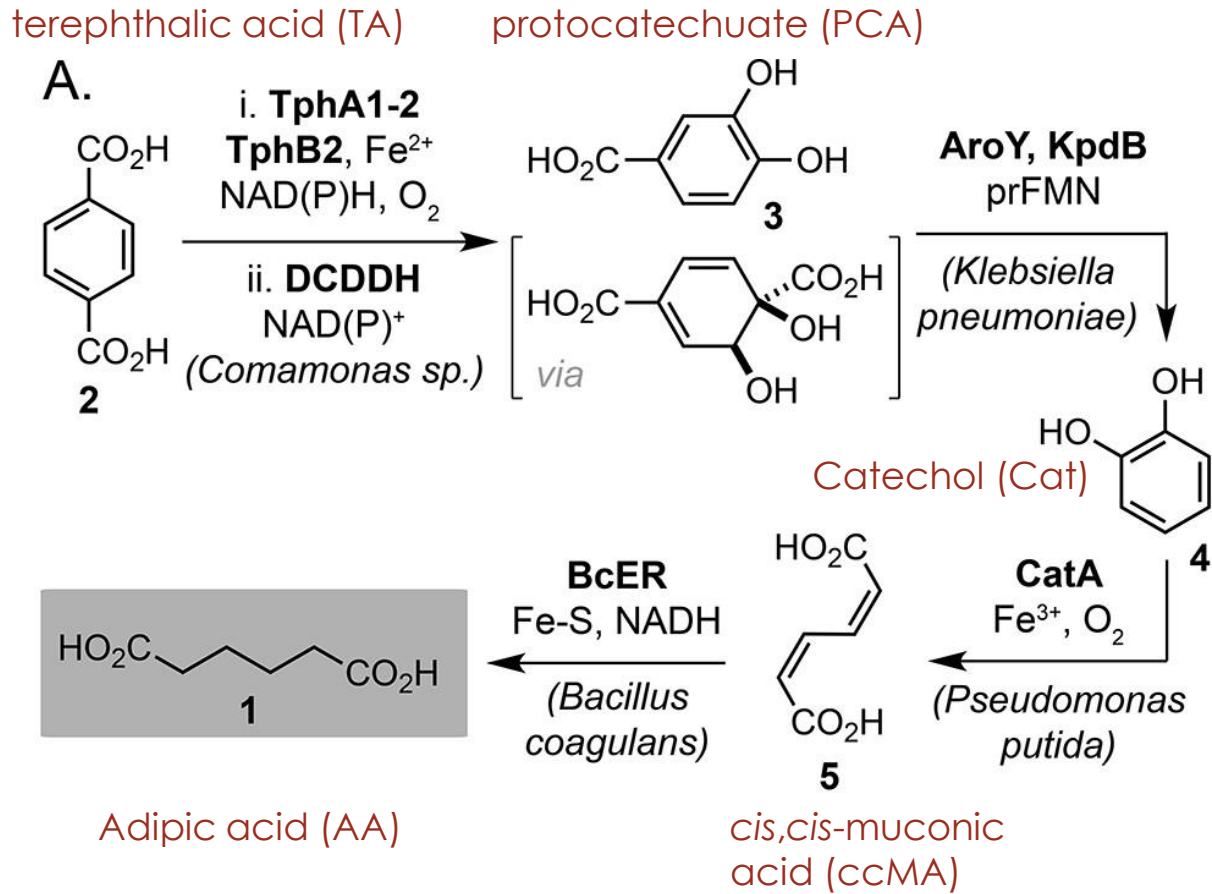
**St3:** *\_pVan1*



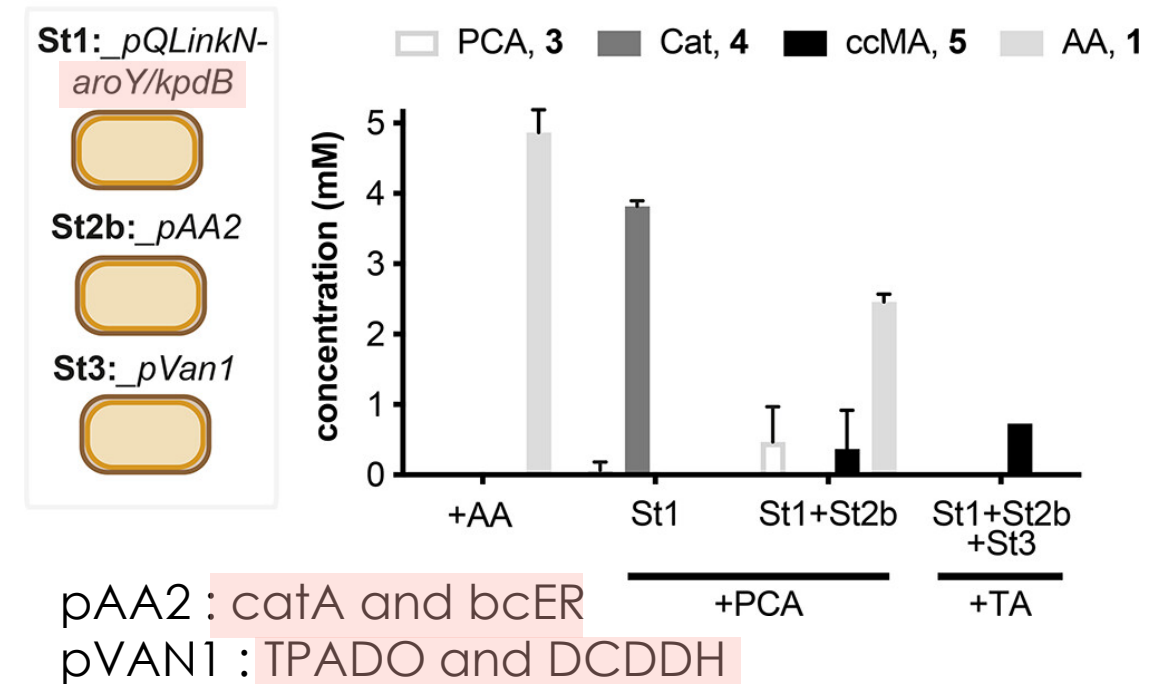
*pAA2* : *catA* and *bcER*

*pVAN1* : *TPADO* and *DCDDH*

# THE PROPOSED PATHWAY FROM TA TO ADIPIC ACID (AA)



**B.**

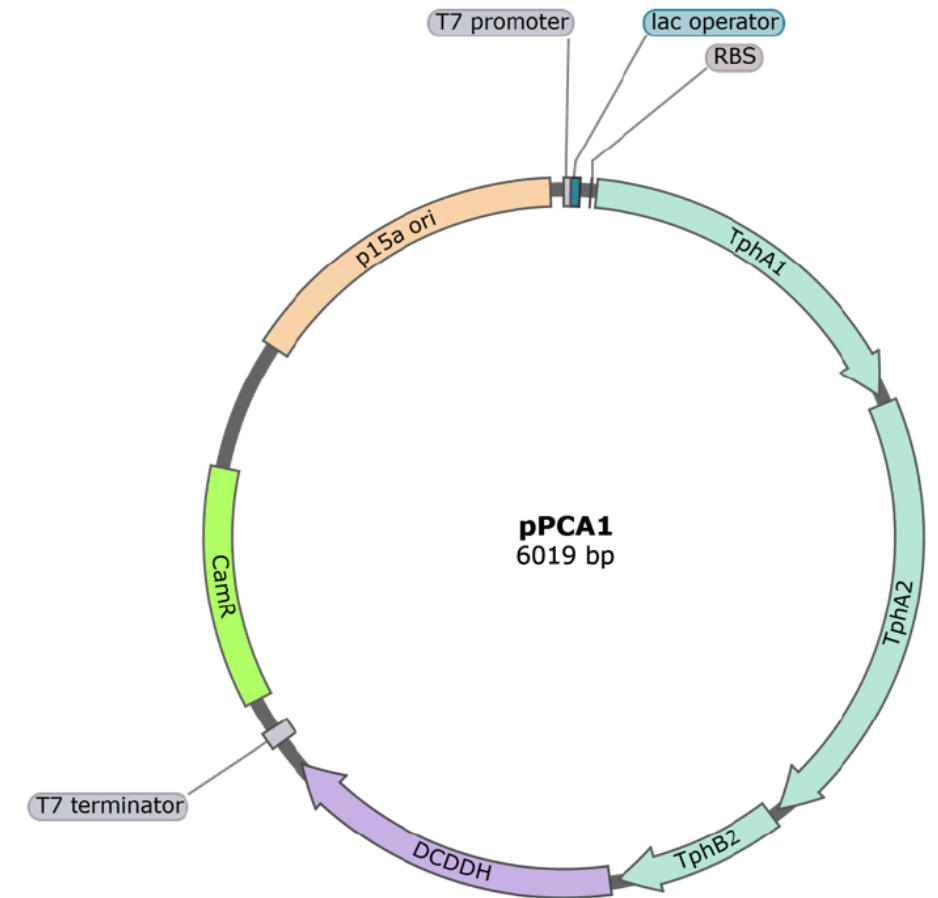
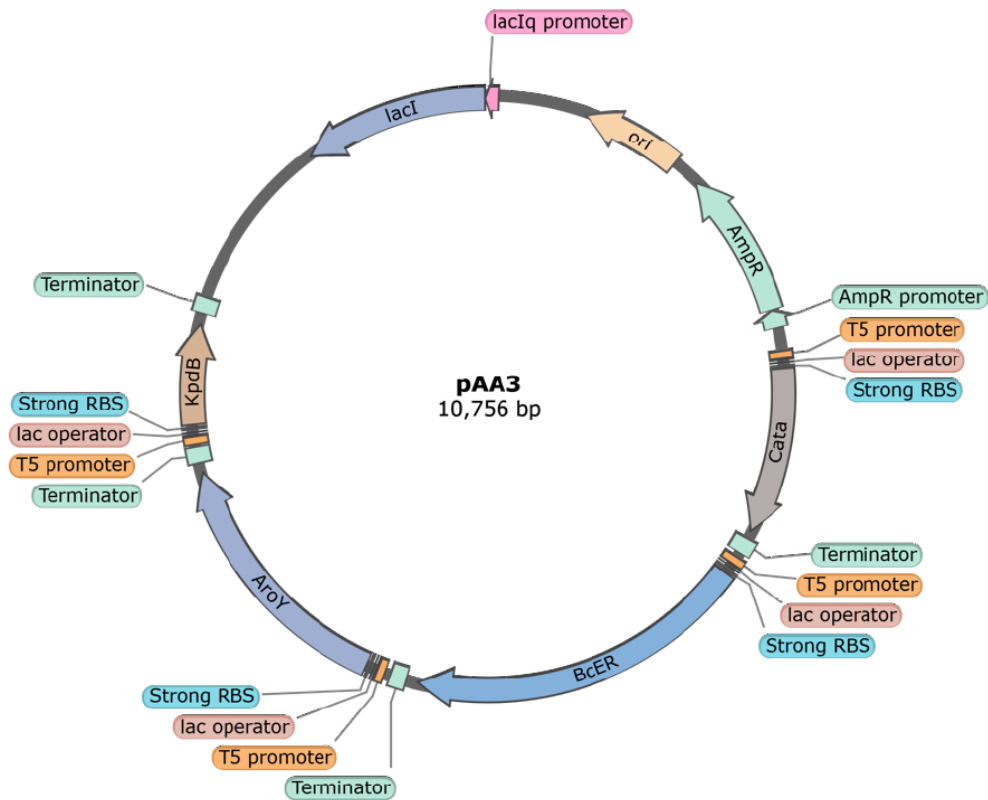


From PCA, they manage to produce AA, but not from TA  
TPADO and bcER are evaluated as bottlenecks

## HOW TO IMPROVE A YIELD?

- Localize all the pathway enzymes in a single cell, on two plasmids

Technique : **SLiCE cloning: seamless ligation cloning extract**

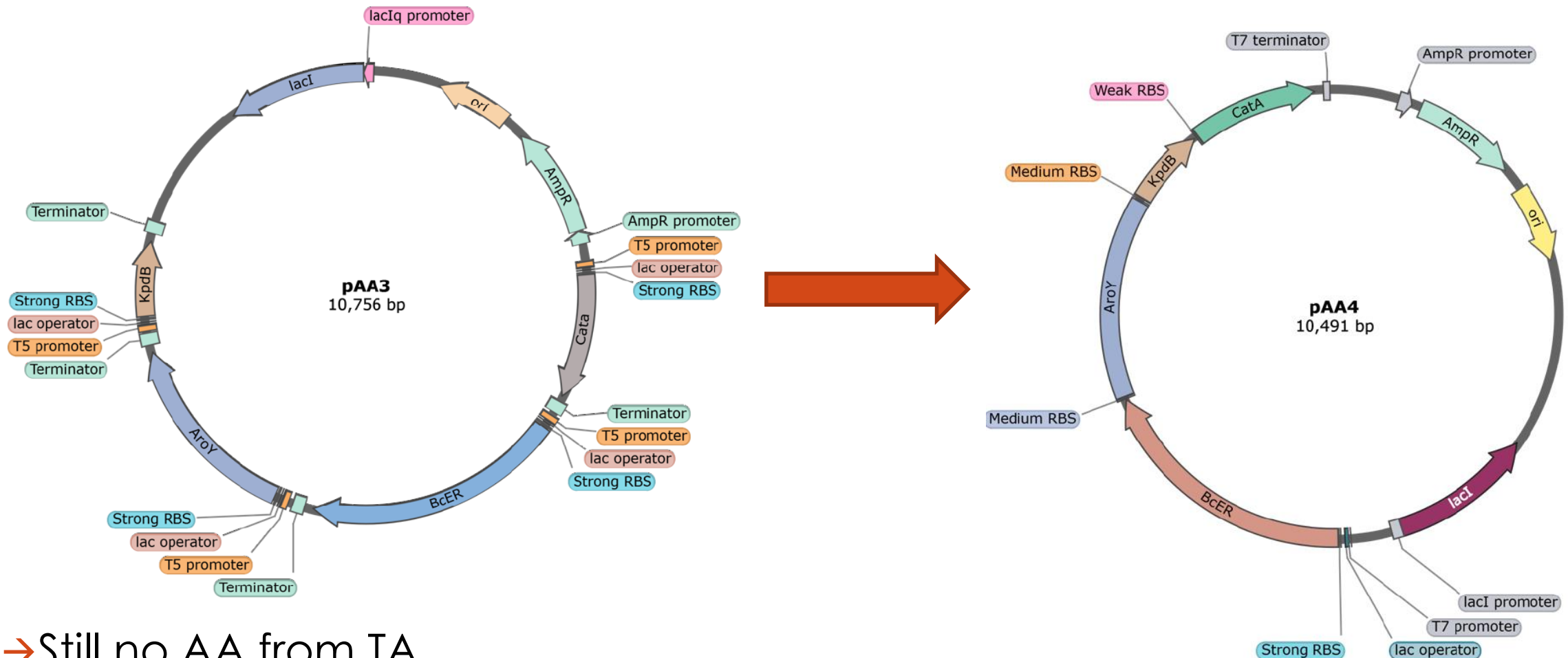


→ Plenty of ccMA (better product flux), but no AA

→ BcER is a limiting step

## HOW TO IMPROVE A YIELD?

- Modify the plasmid to make a polycistronic mRNA



→ Still no AA from TA

→ 19% yield AA from ccMA

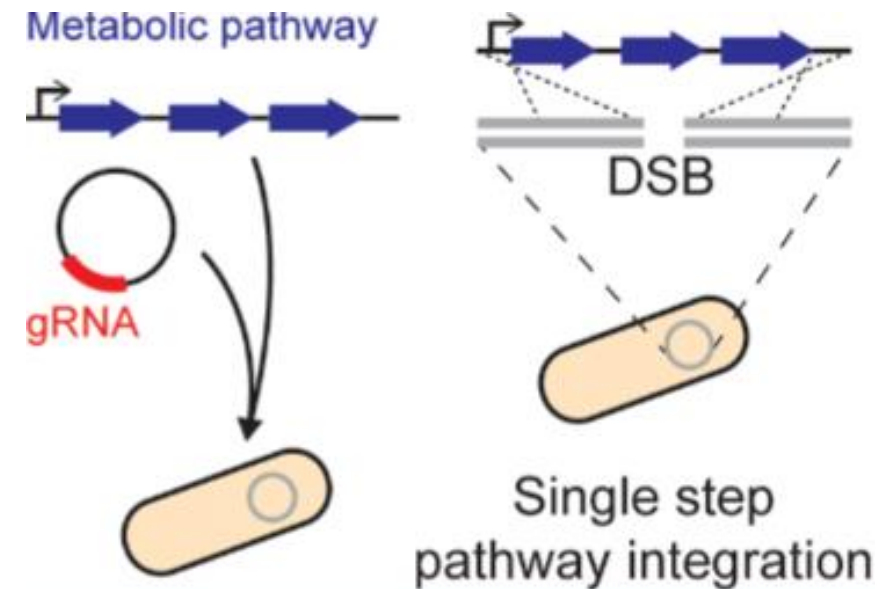
## HOW TO IMPROVE A YIELD?

- Modify the plasmid to make a polycistronic mRNA  
→ Still no AA from TA
- Genome integration of genes TPADO and DCDDH  
CRISPR-Cas9/ $\lambda$ -red method



## CRISPR-Cas9/ $\lambda$ -red method

- Integration of the cassette from pPCA1 coding for *tphA1*, *tphA2*, *tphB2*, *dcddh*
- Donor plasmid with locus-specific 600-bp homology arms amplified from *E. coli* BL21 (DE3) genomic DNA and the cassette amplified from pPCA1
- gRNA plasmid was generated by PCR and SLiCE assembly
- co-transforming the locus-specific gRNA, donor plasmid and pX2-Cas9
- Integration was confirmed by colony PCR
- CRISPR plasmids were cured by growing cells at 42 °C overnight without antibiotic selection



## HOW TO IMPROVE A YIELD?

- Modify the plasmid to make a polycistronic mRNA
  - Still no AA
- Genome integration of genes TPADO and DCDDH
  - No AA, even less ccMA

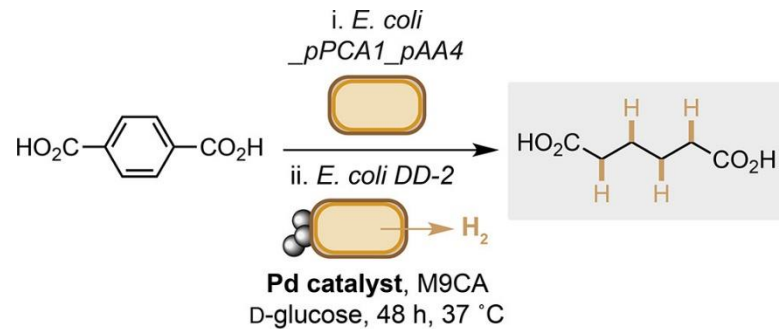
## HOW TO IMPROVE A YIELD?

- Modify the plasmid to make a polycistronic mRNA
  - Still no AA
- Genome integration of genes TPADO and DCDDH
  - No AA, even less ccMA
- Chaperone co-expression
  - also makes it worse (no AA, less ccMA)
- Swapping the genes from the two plasmids
  - Faster production of PCA, but less yield

Back to pPCA1 and pAA4, the two plasmid system, focus on optimization of the whole-cell biotransformation

## CHEMICAL APPROACH TO OVERCOME BcER LIMITATIONS

Biocompatible chemistry to replace the activity of BcER by converting ccMA to AA using a H<sub>2</sub>-generating strain of *E. coli* (DD-2) and a membrane-bound Pd catalyst.



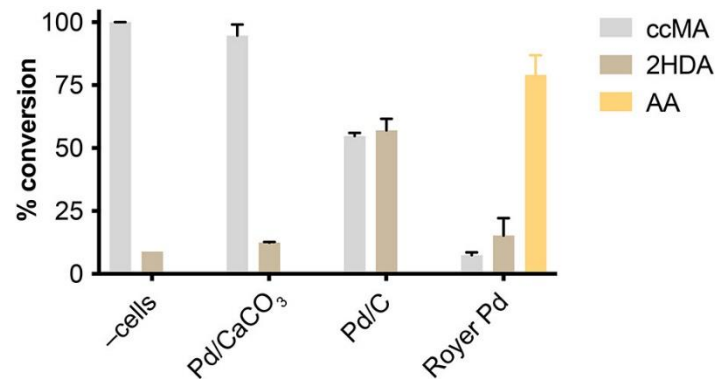
ccMA produced by the *E. coli* pPCA1\_pAA4



Removal of cells by centrifugation



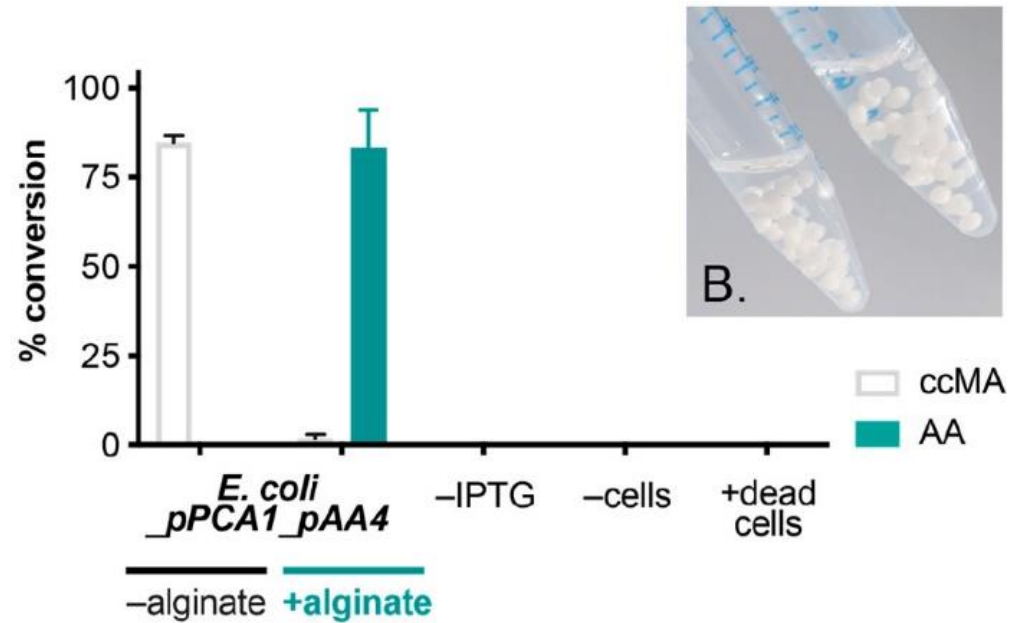
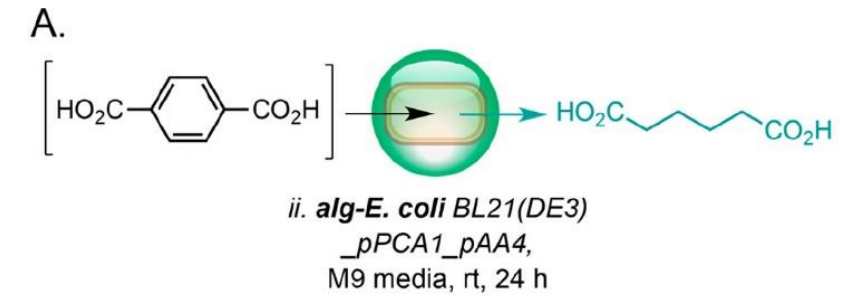
Supernatant introduced to a culture of *E. coli* DD-2



*E. coli* DD2 has a pathway consisting of a **pyruvate ferredoxin oxidoreductase** (PFOR) from *Desulfovibrio africanus*, **hydrogenase maturation factors** from *Chlamydomonas reinhardtii*, and a **ferredoxin and [Fe-Fe] hydrogenase** from *Clostridium acetobutylicum*, which together enable the anaerobic production of H<sub>2</sub>(g) from D-glucose

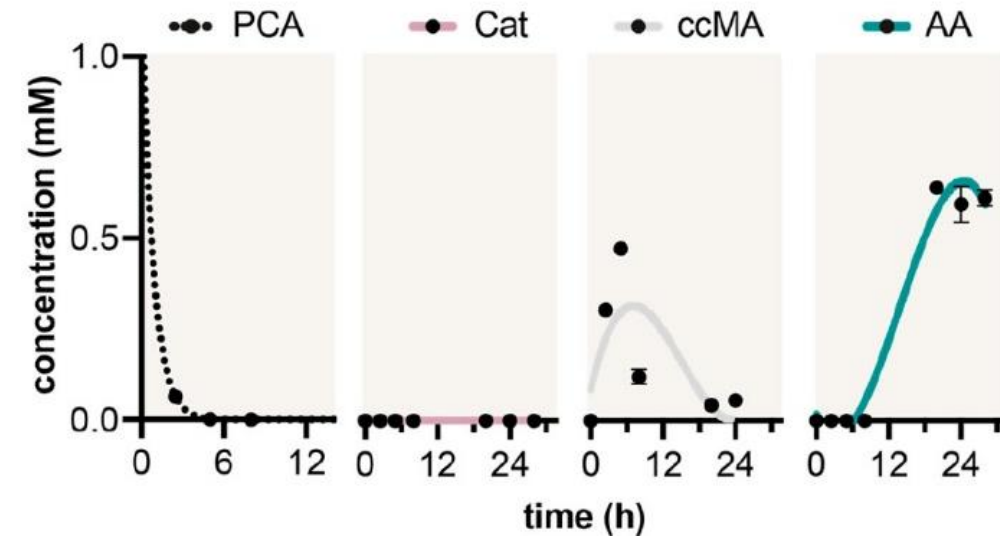
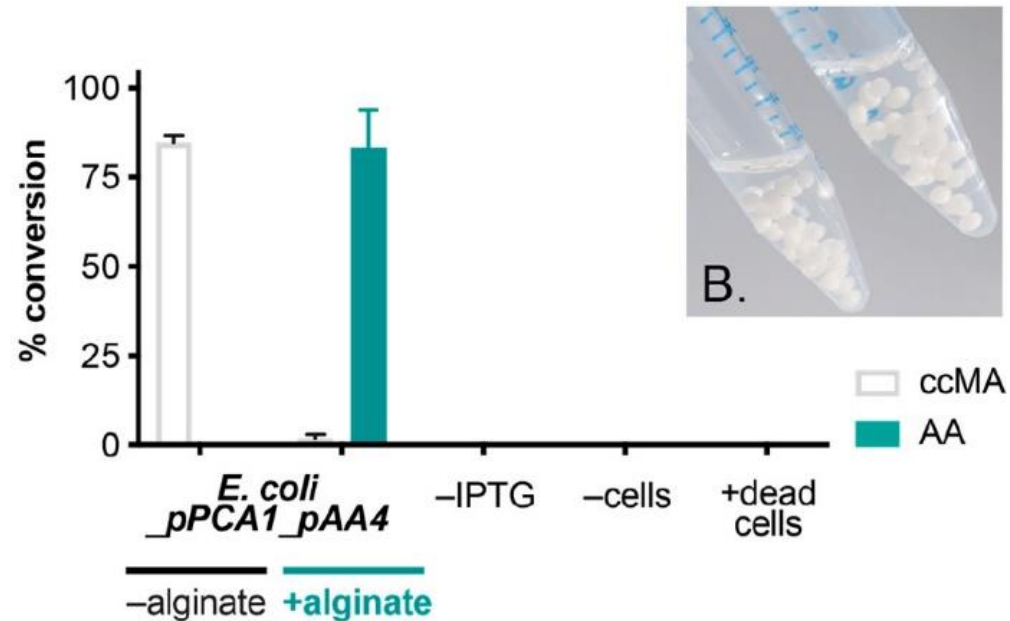
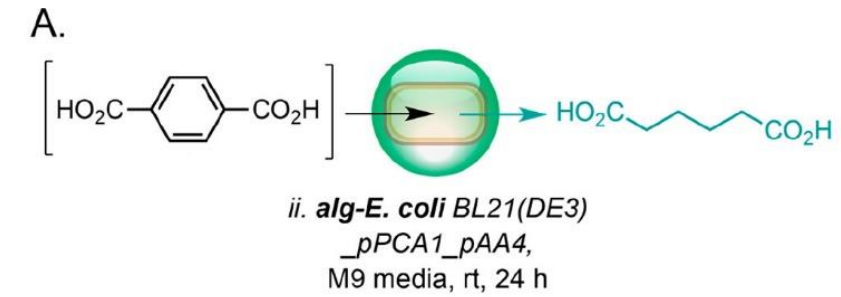
# USE OF CELLS SUPPORTED IN ALGINATE HYDROGEL

Alginate hydrogel is known to increase the stability of enzymes *in vitro*



# USE OF CELLS SUPPORTED IN ALGINATE HYDROGEL

Alginate hydrogel is known to increase the stability of enzymes *in vitro*



Alginate support likely improves the oxygen tolerance and/or stability of the [4Fe-4S]-containing BcER enzyme.

## MORE THINGS THEY TRIED

- Increase NADH availability

Coexpression of NAD<sup>+</sup>-dependent formate dehydrogenase

Switching the carbon source from D-glucose to D-mannitol or D-sorbitol

Co-addition of glucose and sorbitol at 1:1 mol equivalent or increasing the concentration of glucose 2-fold

Things they say they will study in more details:

- Examine the inhibition of BcER by TA
- Study pH-dependent TA diffusion and flux at physiological pH

## THEIR PROOF OF CONCEPT IN “REAL CONDITIONS”

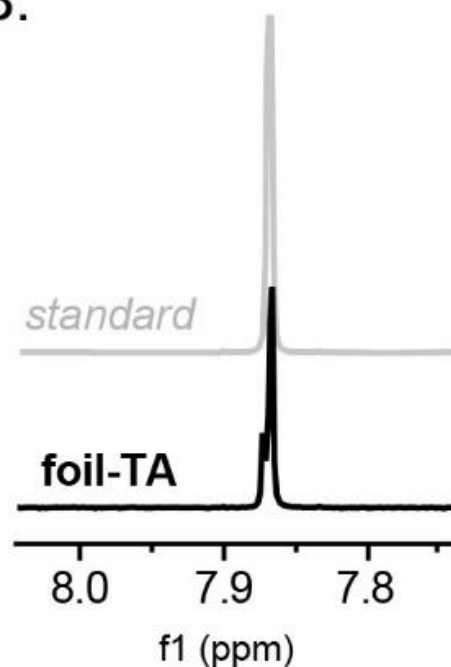
A.



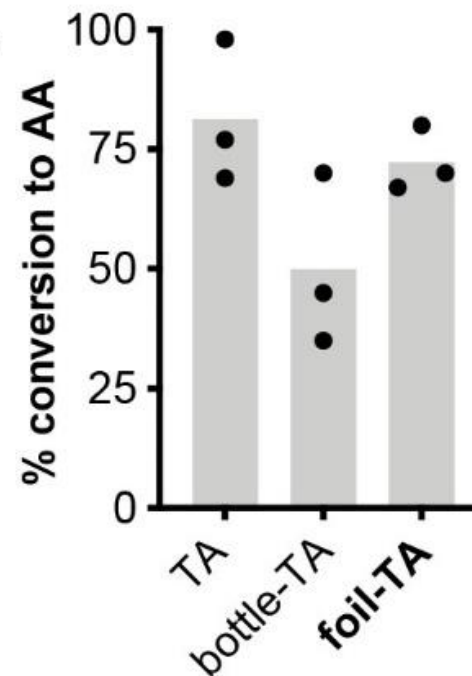
stamping foil

alkaline hydrolysis conditions  
(aq. NaOH, EtOH, 90°C, 1 h)

B.



C.



Their conclusion:

Product conversion is high (79%, 115 mg/L) and occurs in aqueous media under ambient conditions (room temperature, pH 7.4) in 24 h.



# Conclusions to keep in mind

- Do not underestimate the versatility of microorganisms!
- Keep an open mind: what is specific to your project?  
There is no perfect host, no perfect assembly method, but to take into account their specificities is an opportunity
- Do not limit yourself to one field, combining methods/tools from different fields is also an advantage
- And of course... reality remains challenging, so be prepared for failure...

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Jennifer Perrin  
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Arul Marie  
Soumaya Najah  
All BIM and CPNFB teams

## Collaborators

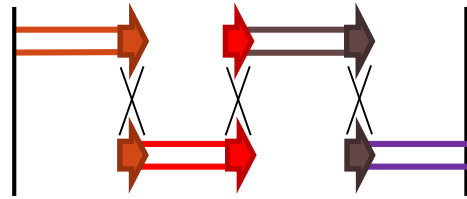
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Pascal Belin  
Carine Tellier-Lebègue  
Matthieu Fonvielle  
All the team



## DNA ASSEMBLY METHODS

Site-specific recombination

**ΦBT1 Site-specific integrase**

In vitro

**ΦC31 Site-specific integrase**

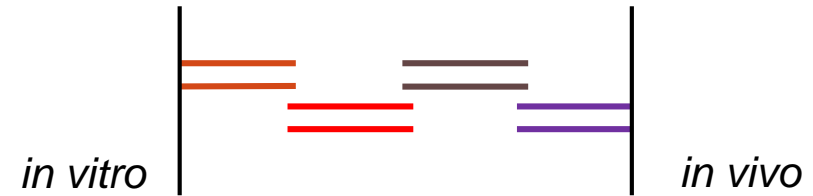
In vitro

Bridging oligos

**LCR**

Ligase cycling reaction

One step, scarless

Homologous recombination

**Gibson assembly**

One step

3' overhang, T5 exonuclease

**DNA assembler**

*Saccharomyces cerevisiae*

**SLIC**

Sequence and ligation-independent cloning

5' overhang, T4, RecA

**LLHR**

Linear to linear homologous recombination

RedET-mediated in *E. coli*

*In vivo* assembly

Restriction digestion/ligation

**Biobrick**

*EcoRI, XbaI, SpeI, PstI*

**Golden Gate**

*BsaI*, one step

## DIVERSITY OF DNA ASSEMBLY METHODS:

In vivo Assembly

linear-linear homologous recombination

modular cloning (MoClo)

LCR

Phage  $\phi$ BT1 integrase-mediated site-specific recombination

GoldenBraid

PIPE cloning

SLIC, SLiCE, USER

TAR cloning

Gibson assembly

Direct Pathway cloning

iBrick

Biobrick, BglBrick

Modular Overlap-Directed Assembly with Linkers (MODAL)

BASIC

Restriction enzymes

Golden Gate

DNA assembler

MASTER

Site-specific recombination-based tandem assembly (SSRTA)

CPEC

PaperClip

AQUA Cloning

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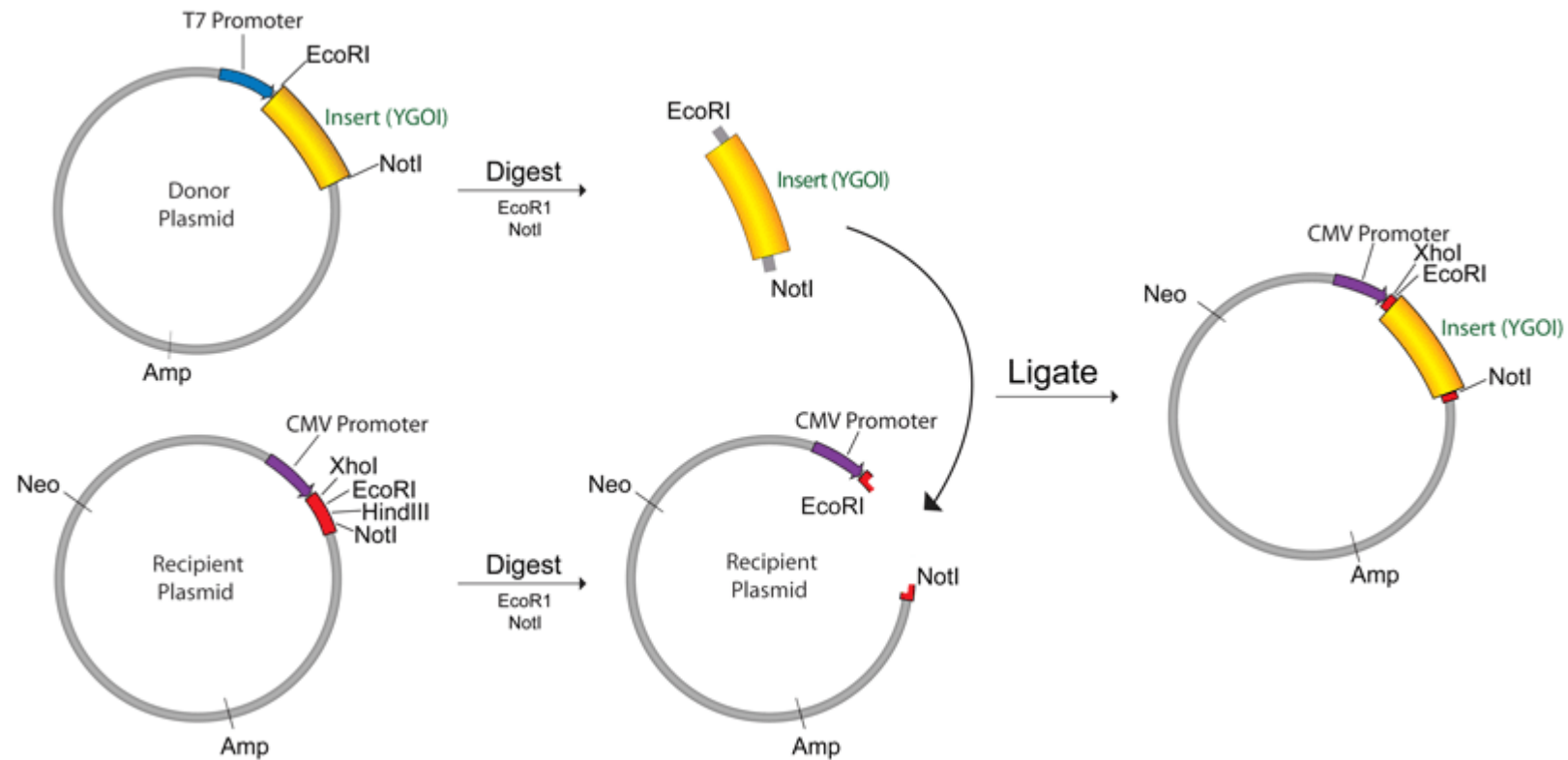
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# Cloning by restriction - ligation



# The biobricks system

