

Synthetic Biology Fits Naturally

A. Malcolm Campbell
Biology Department and **GCAT**

DAVIDSON


University of Puerto Rico - Río Piedras
May 16, 2013

Outline of Presentation

What do we want for our Biology Majors?

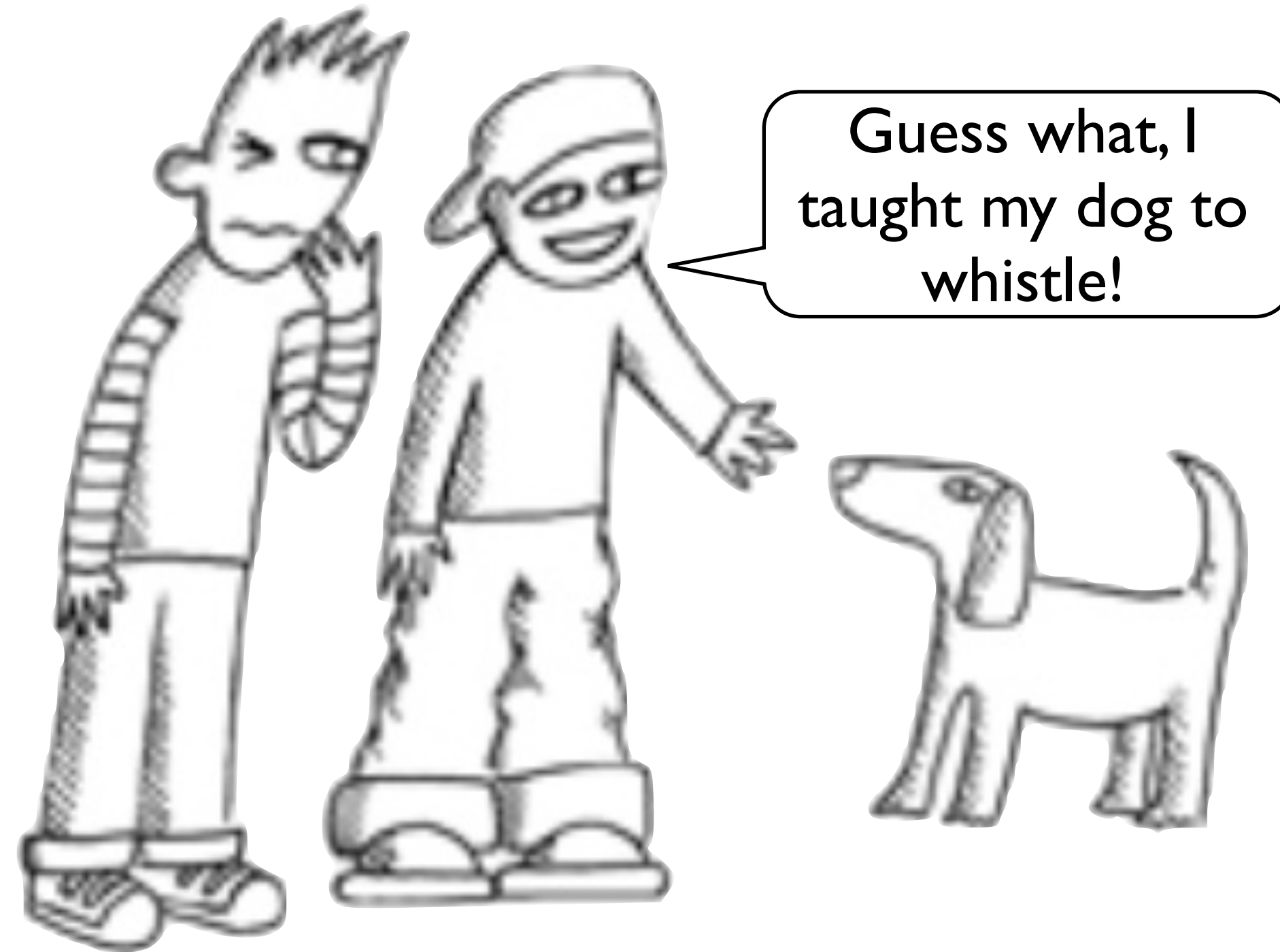
Can students do real research in teaching labs?

Can undergraduates do cutting-edge research?

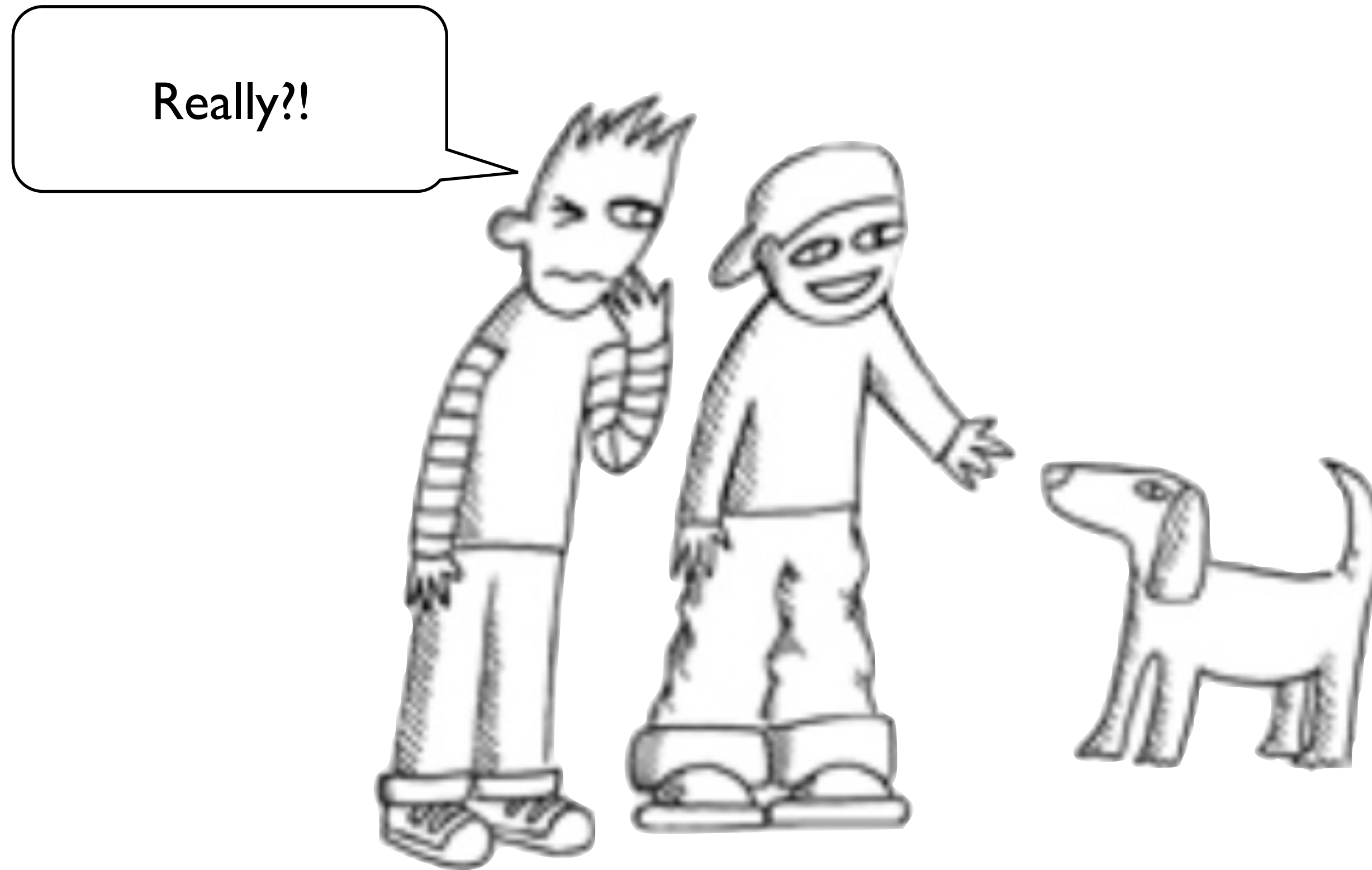
Is there a community of PUI faculty researchers?

What do you want for your Biology Majors?

Teaching vs Learning

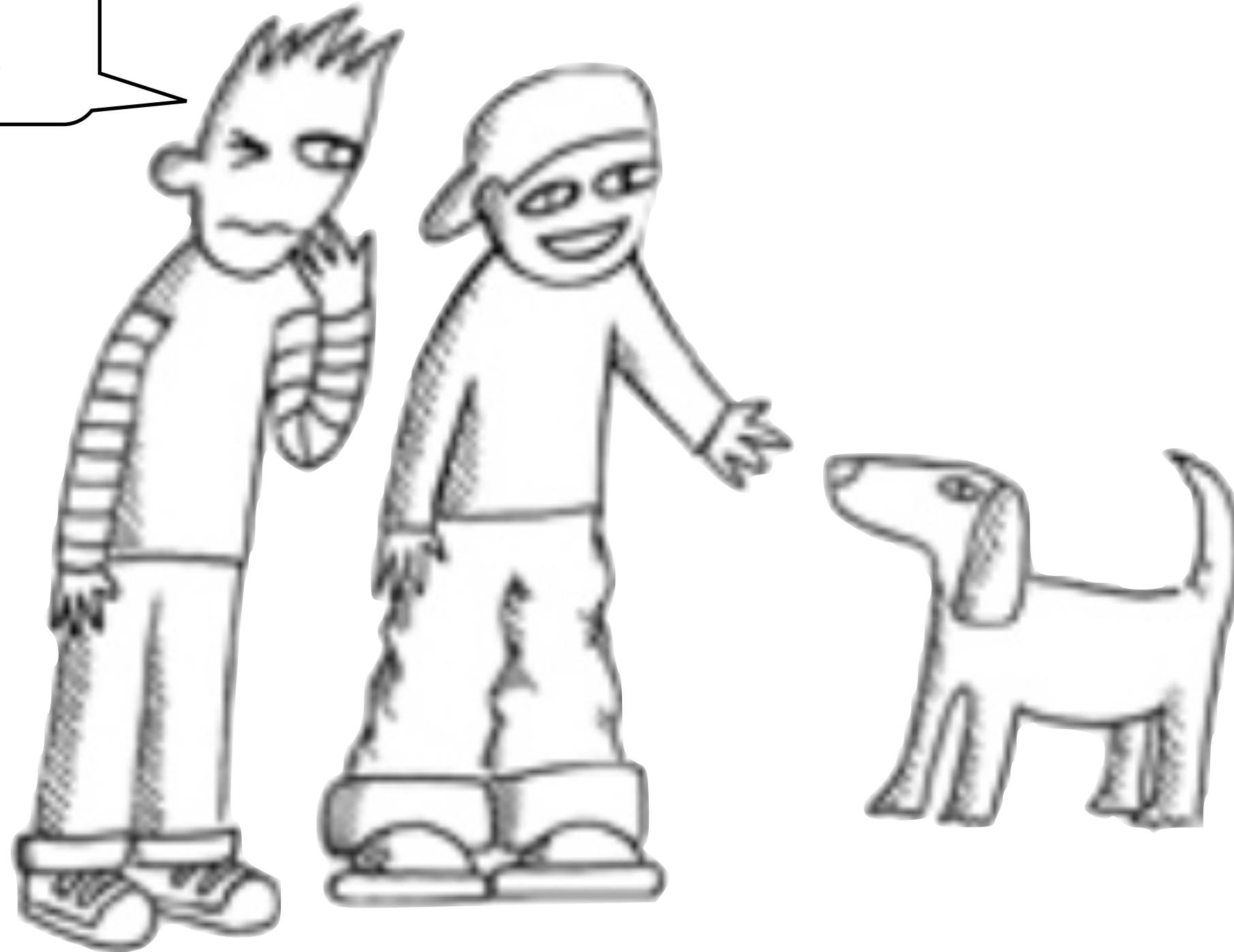


Teaching vs Learning

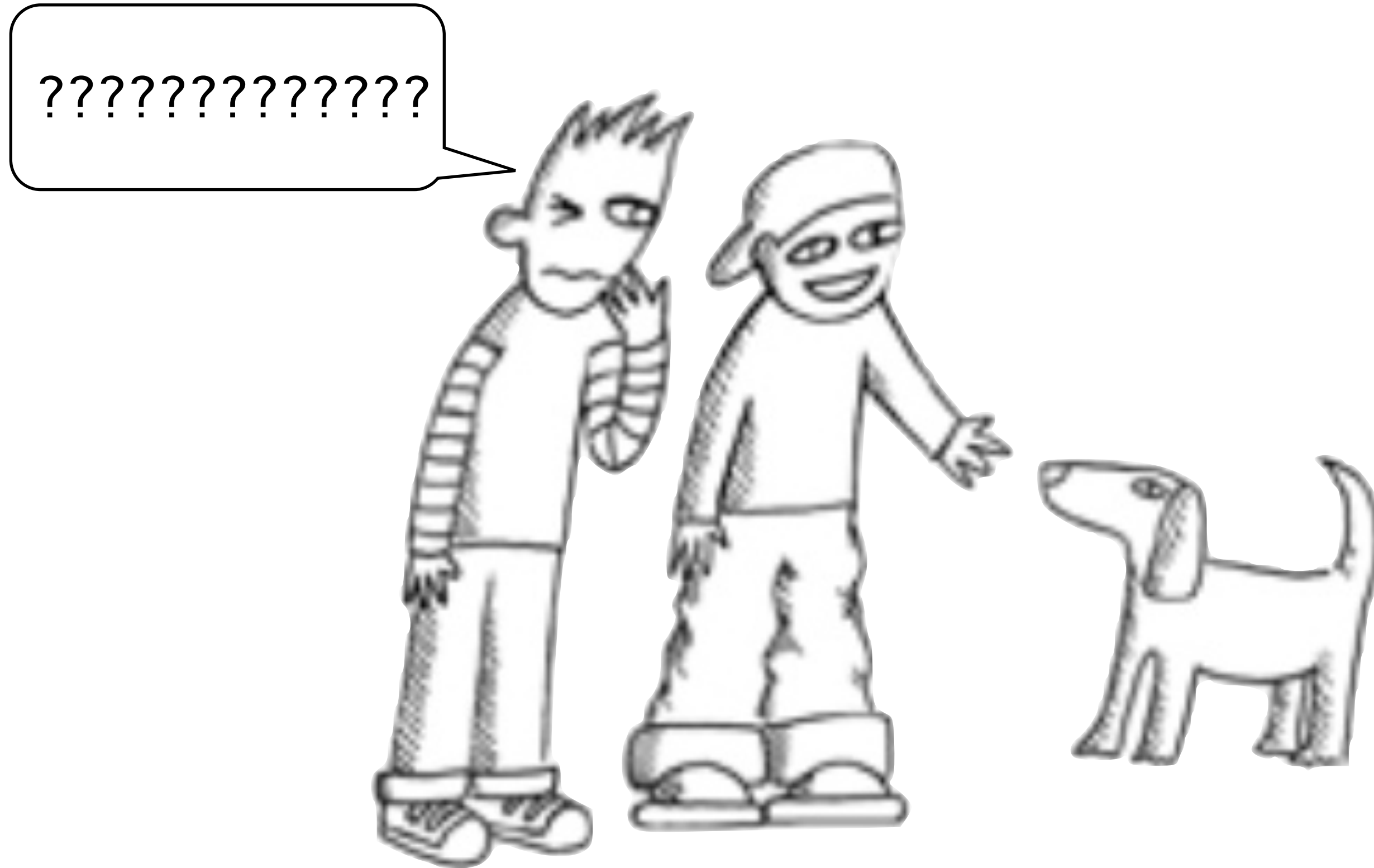


Teaching vs Learning

Whistle! C'mon
boy, whistle!

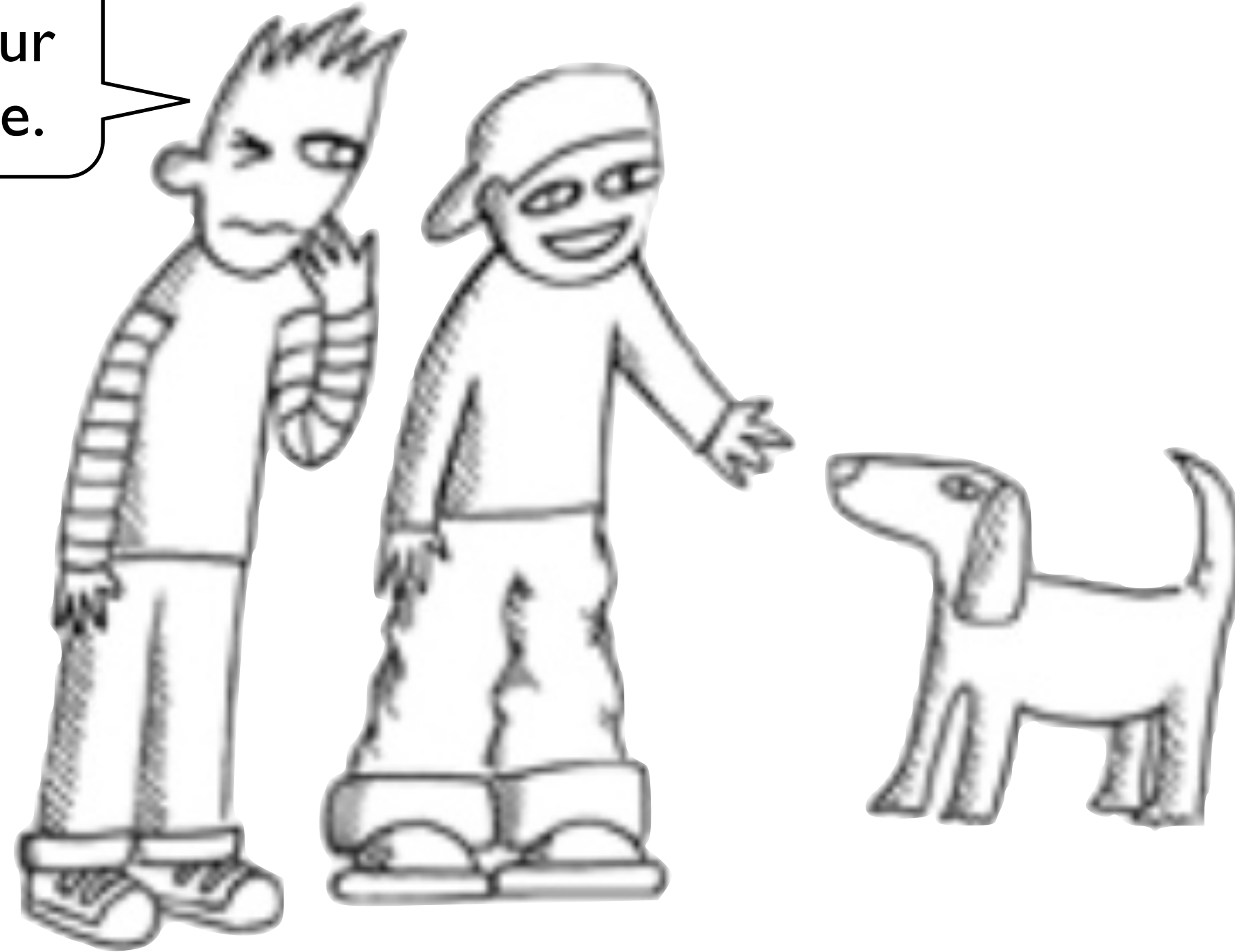


Teaching vs Learning



Teaching vs Learning

I thought you said you taught your dog to whistle.



Teaching vs Learning



**Can students do real
research in teaching labs?**

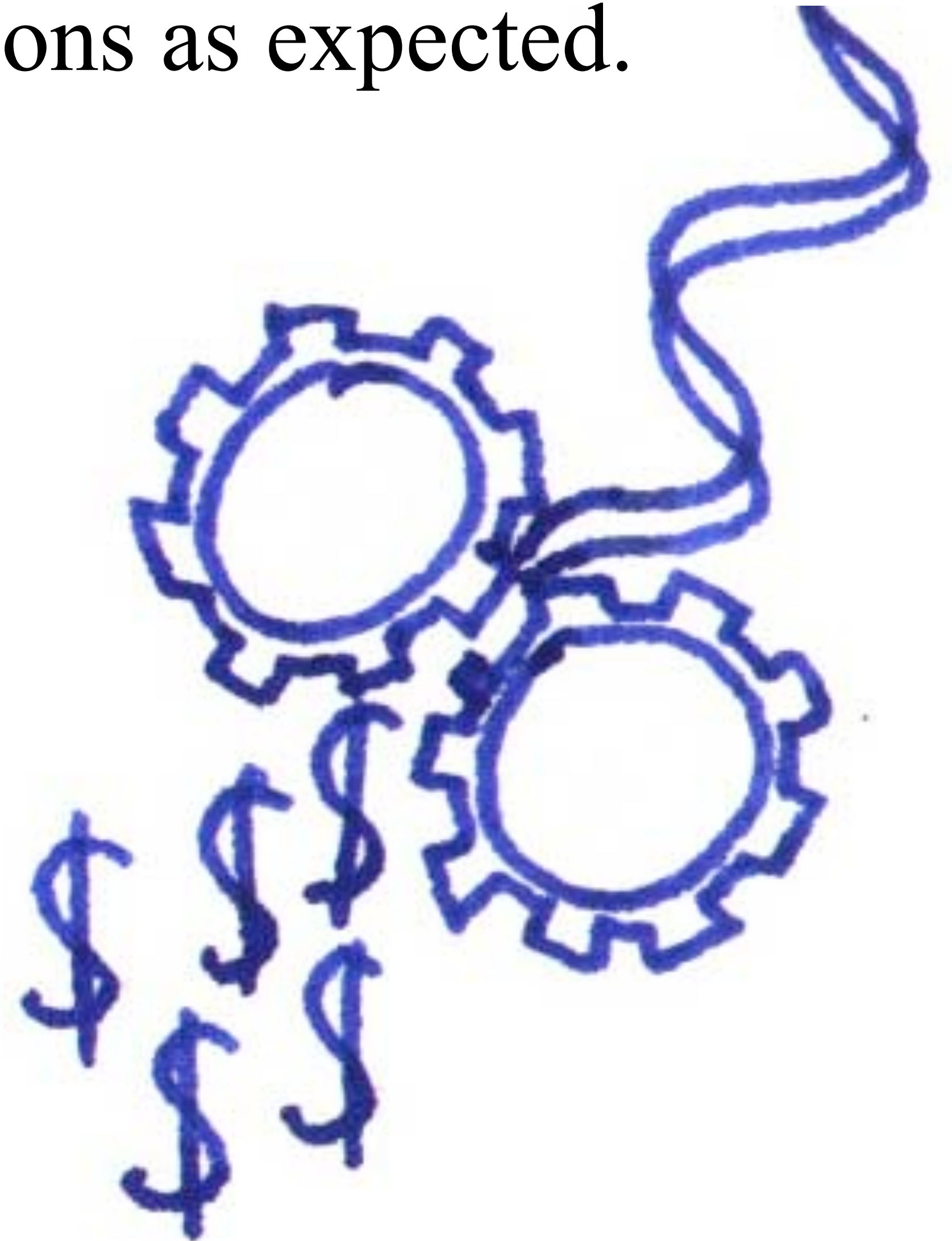
What is Synthetic Biology?

Implementation of engineering principles and mathematical modeling to the design and construction of biological parts, devices, and systems with applications in energy, medicine, and technology.

www.bio.davidson.edu/projects/gcat/Synthetic/What_Is_SynBio.html

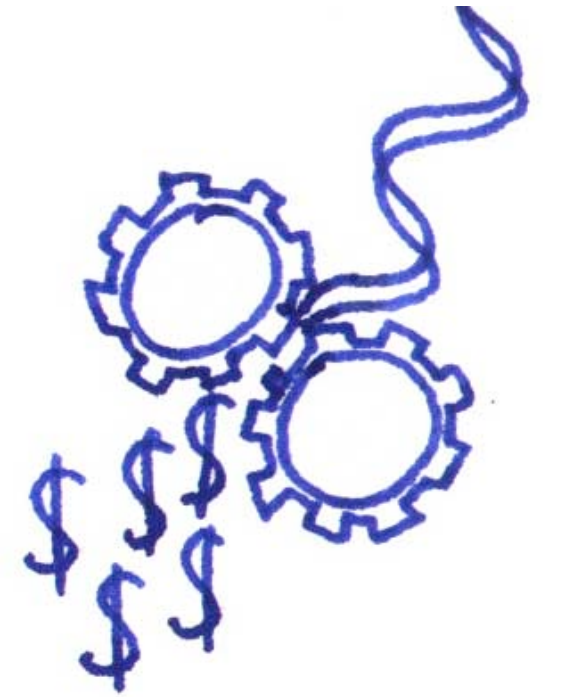
Synthetic Biology: Win-Win

Win #1: your design functions as expected.

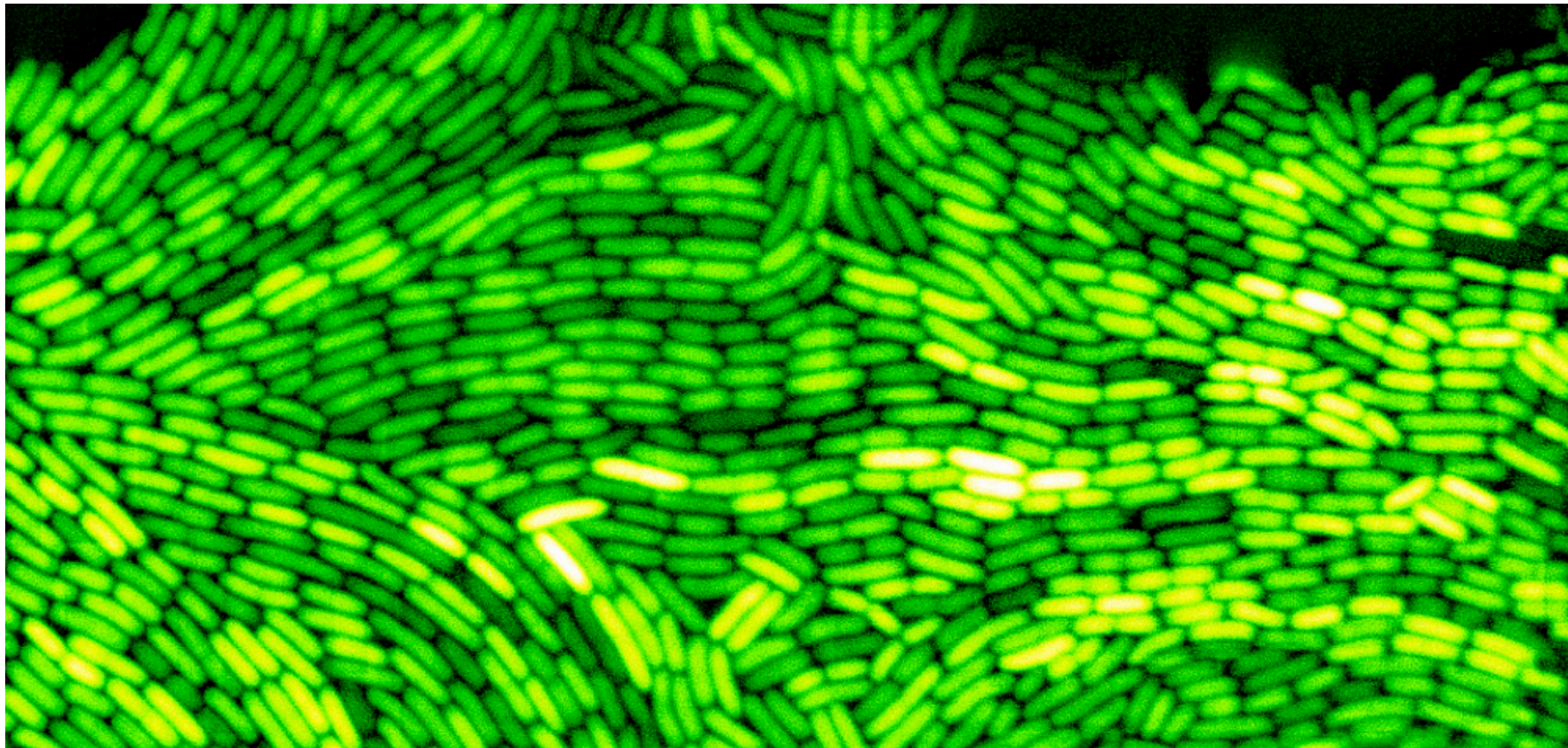


Synthetic Biology: Win-Win

Win #1: your design functions as expected.



Win #2: your design fails but you uncover basic biology



Real World Applications of Synthetic Biology

Land Mine Detection



Land Mine Detection



Synthetic Biology Land Mine Detection



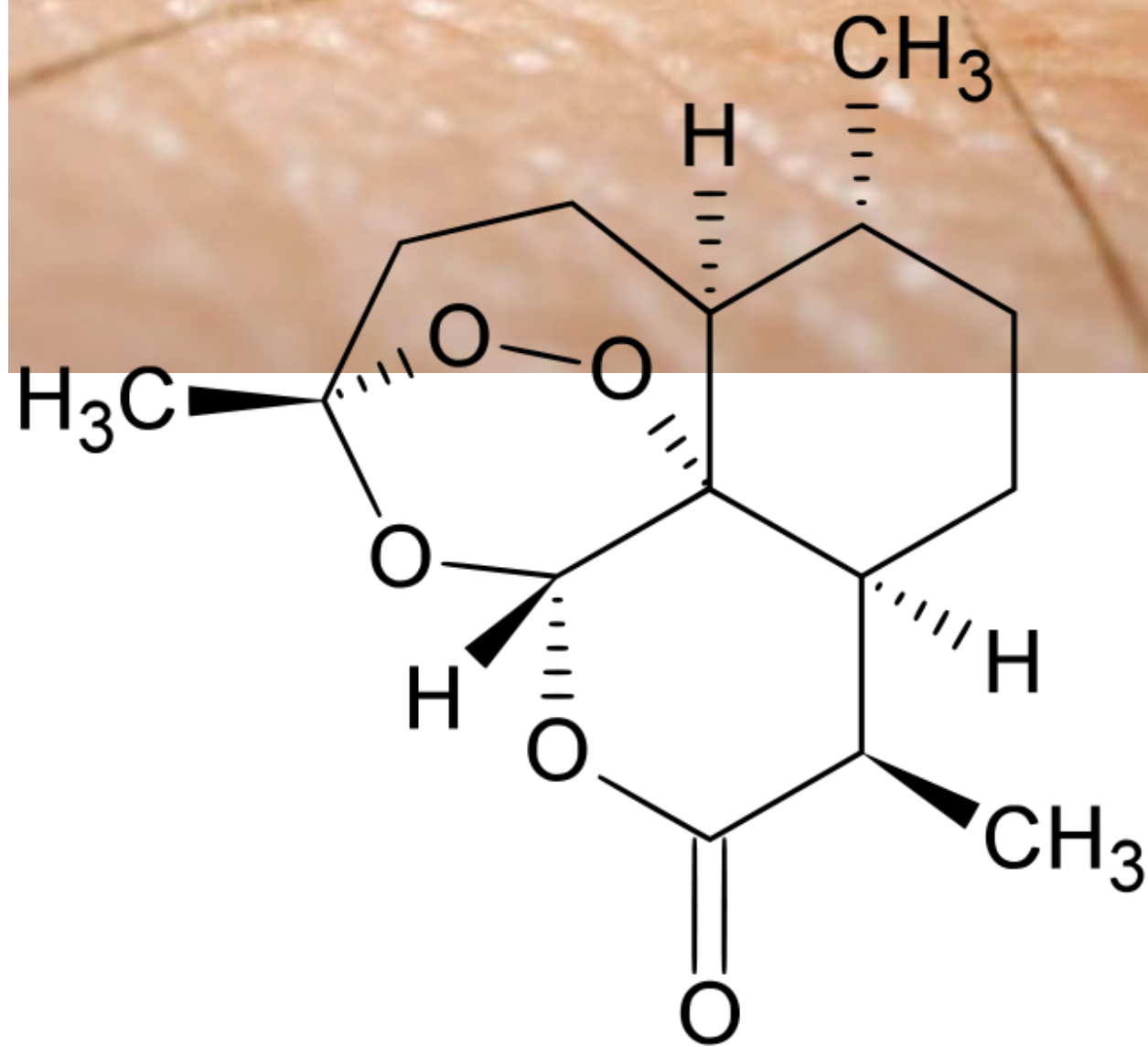
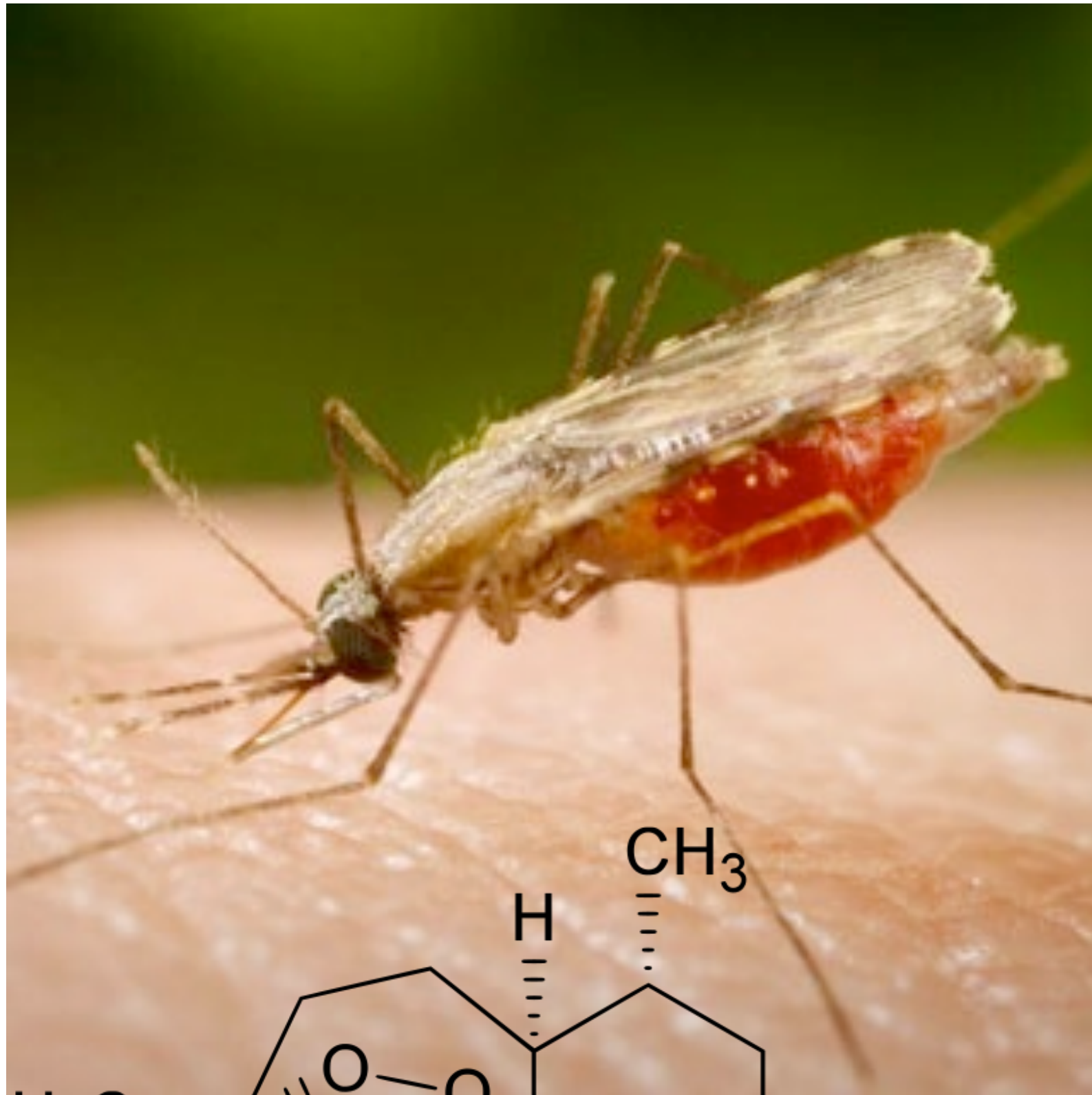
WARNING SIGN: The bioengineered Thales cress turns red when exposed to a mine byproduct.

COURTESY OF ARESA BIODETECTION

New weed may flag land mines

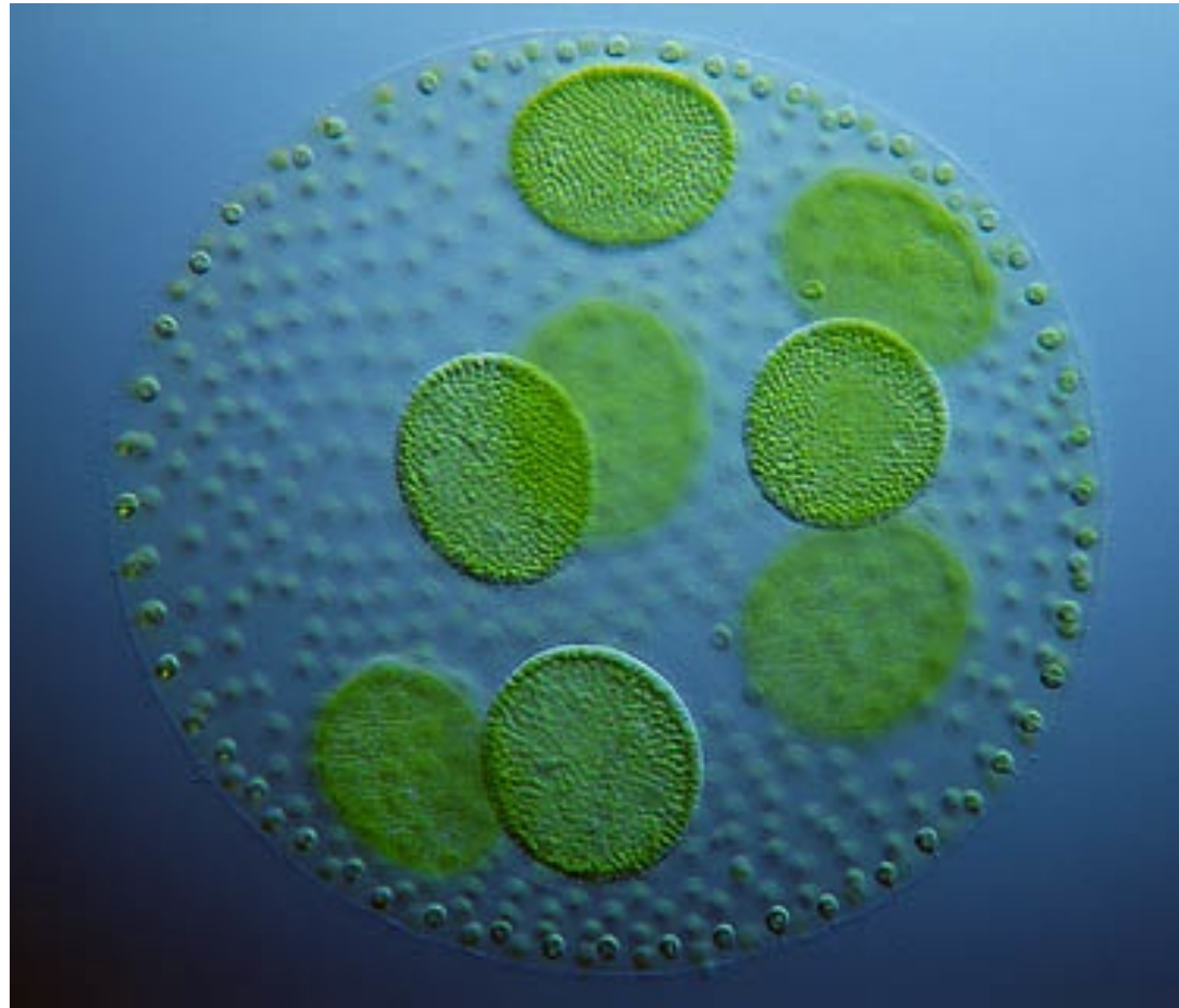
By John K. Borchardt | *Contributor to The Christian Science Monitor*

Production of Medicines



\$1 per pill

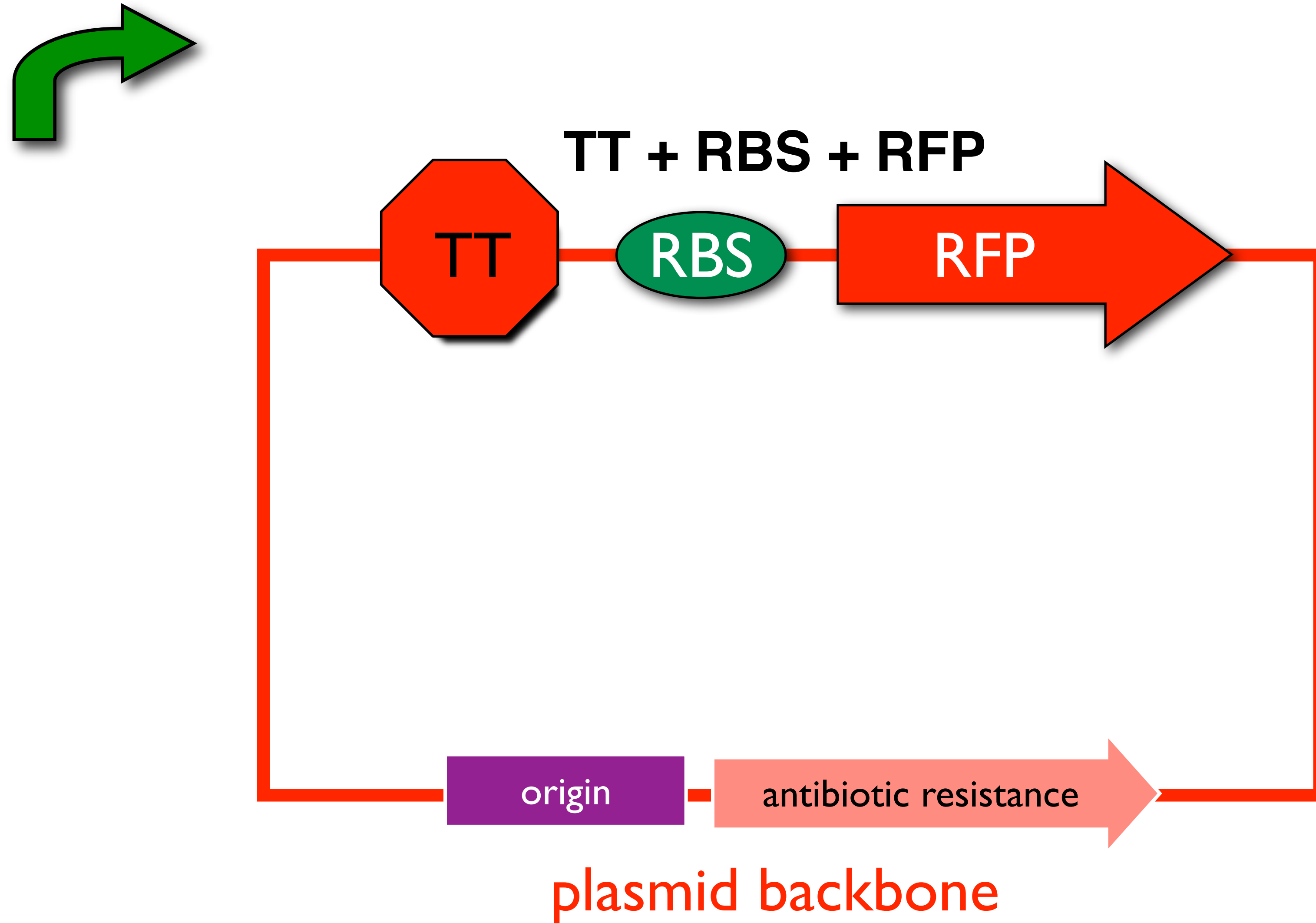
Biofuels from Algae



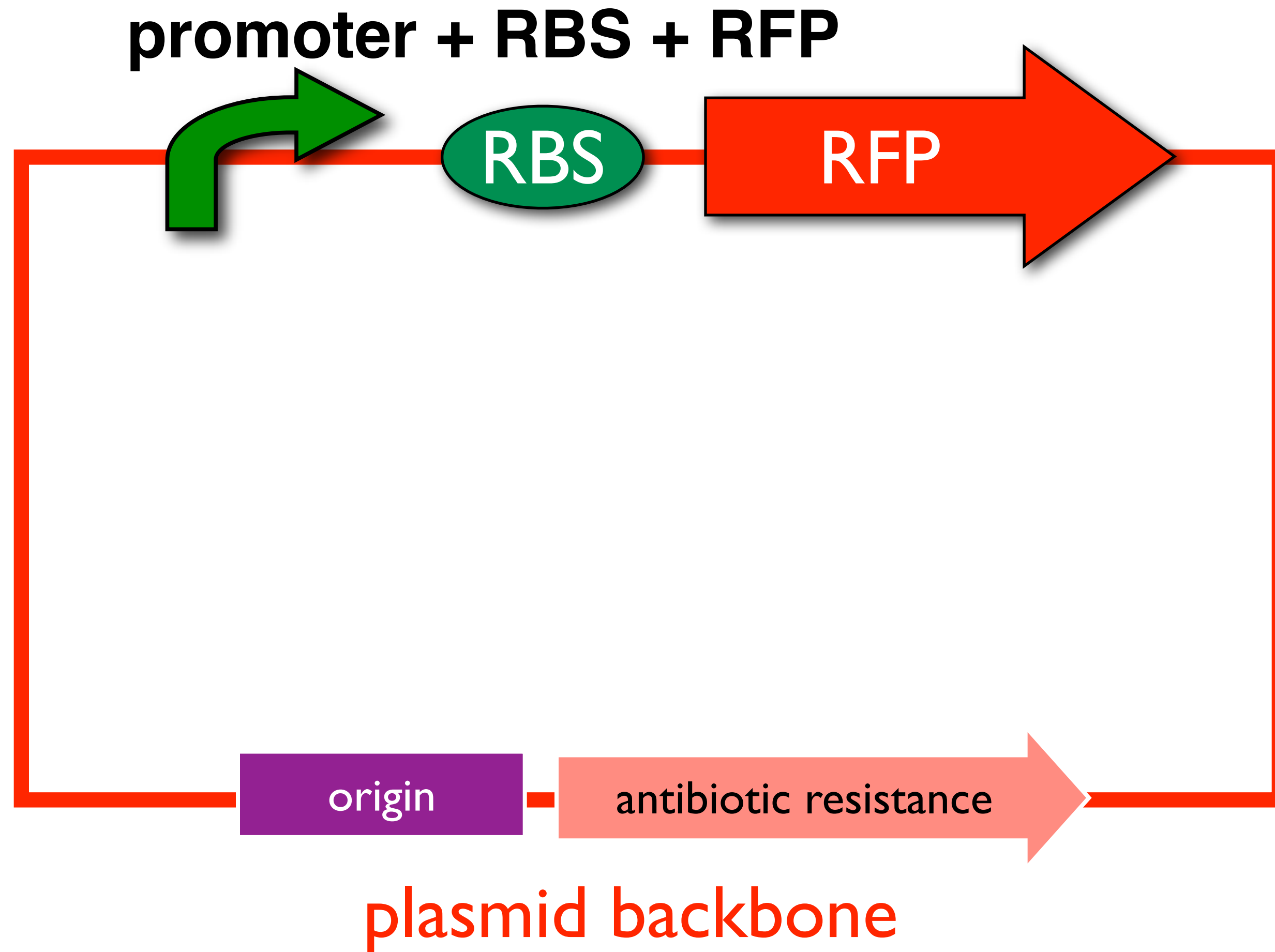
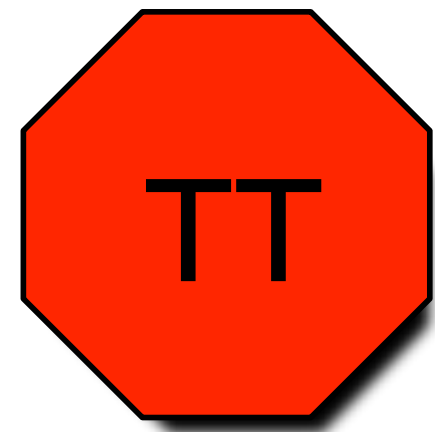
CO₂-neutral
1,000,000 gallons in 2008

Promoter Research Using Synthetic Biology

Golden Gate Assembly Method



Golden Gate Assembly Method



Eco RI

GAATTC

CTTAAG

palindrome

type II

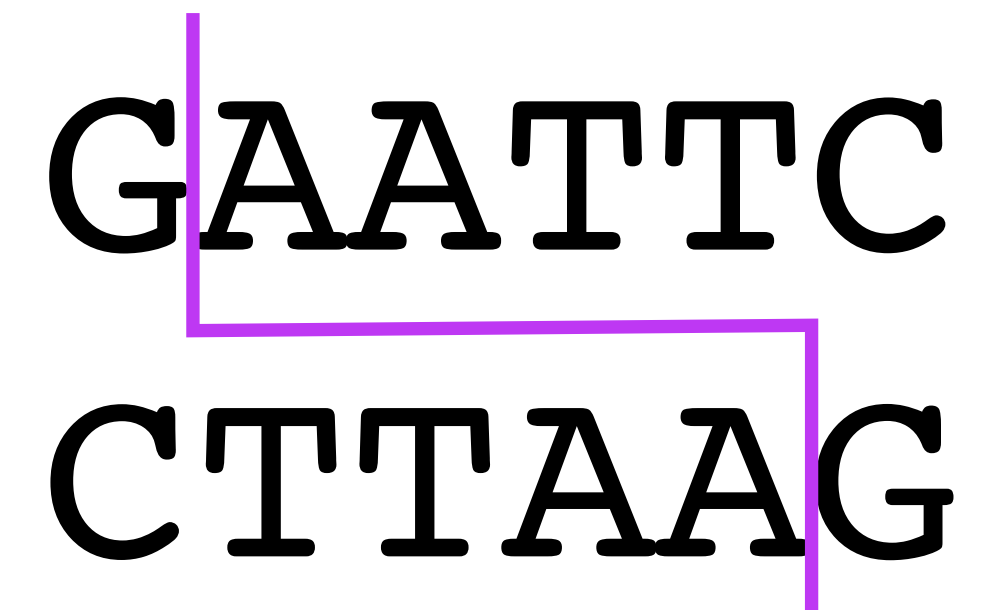
Eco RI

GAATTC
CTTAAG

palindrome

type II

Eco RI



type II

Eco RI

G

CTTAA

AATTC

G

type II

Bsa I

GAGACC

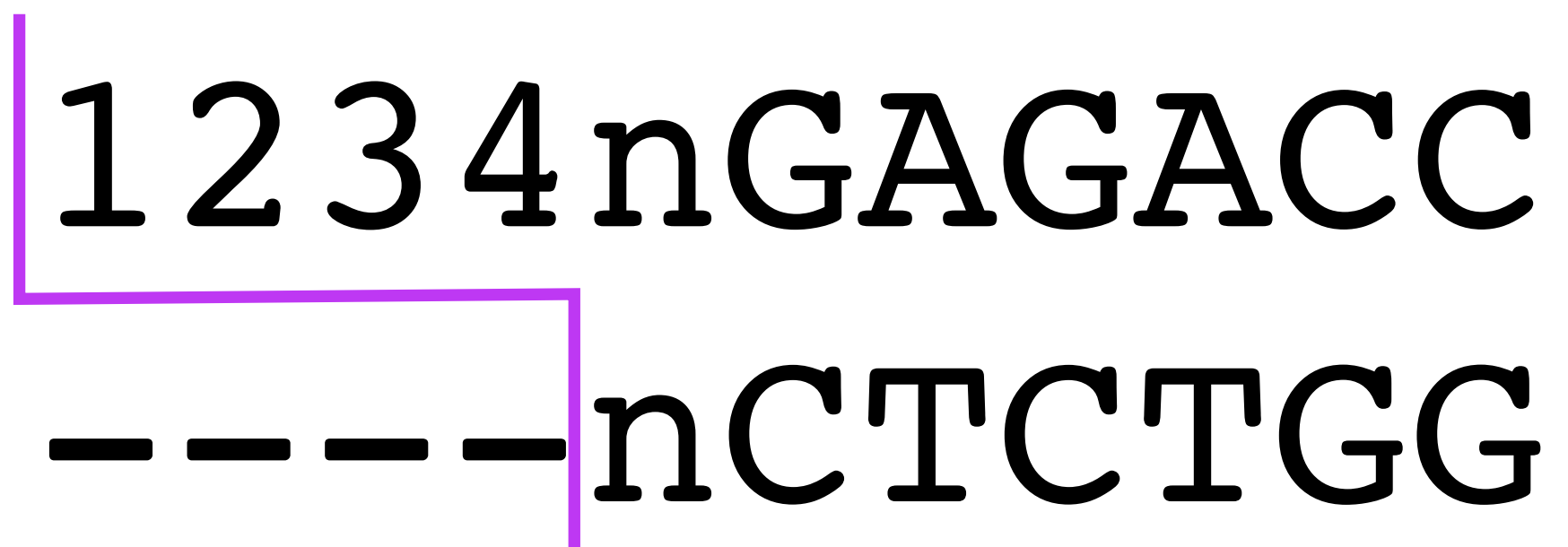
CTCTGG

not a
palindrome

type II

Bsa I

1 2 3 4 n G A G A C C
- - - - n C T C T G G



type II

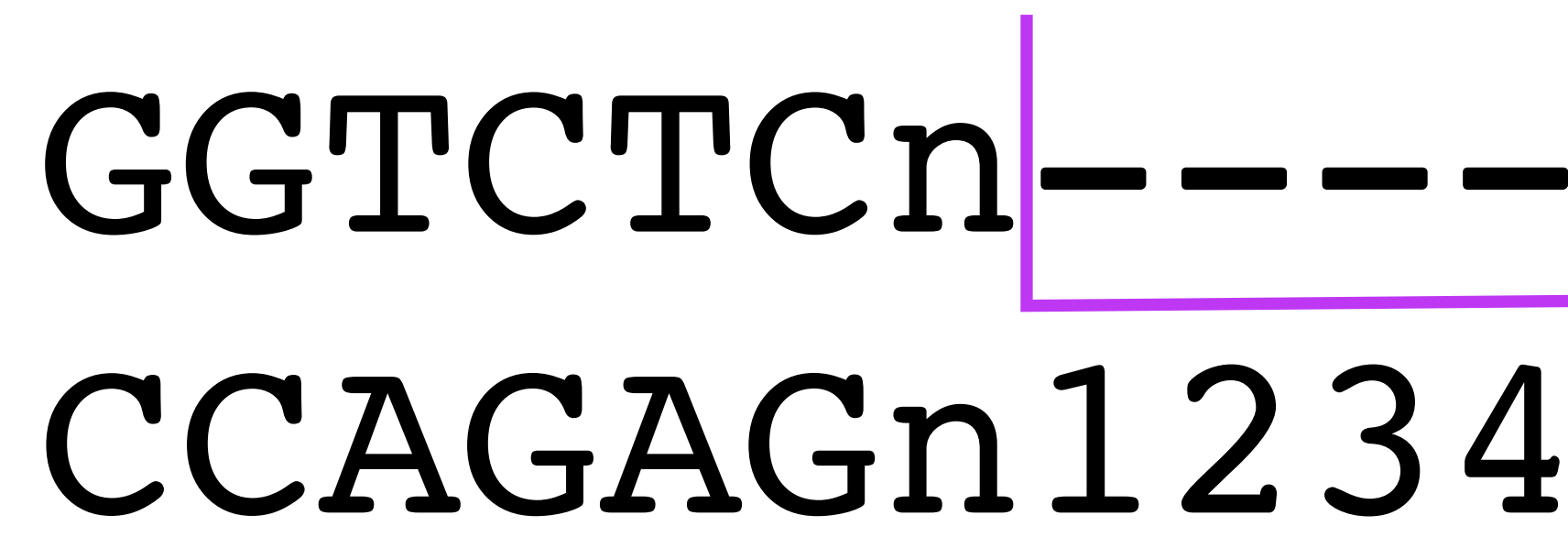
Bsa I

1 2 3 4 n G A G A C C
n C T C T G G

— — — —

type II

Bsa I



type II

Bsa I

GGTCTCn

CCAGAGn 1 2 3 4

type II

Bsa I

cuts
left

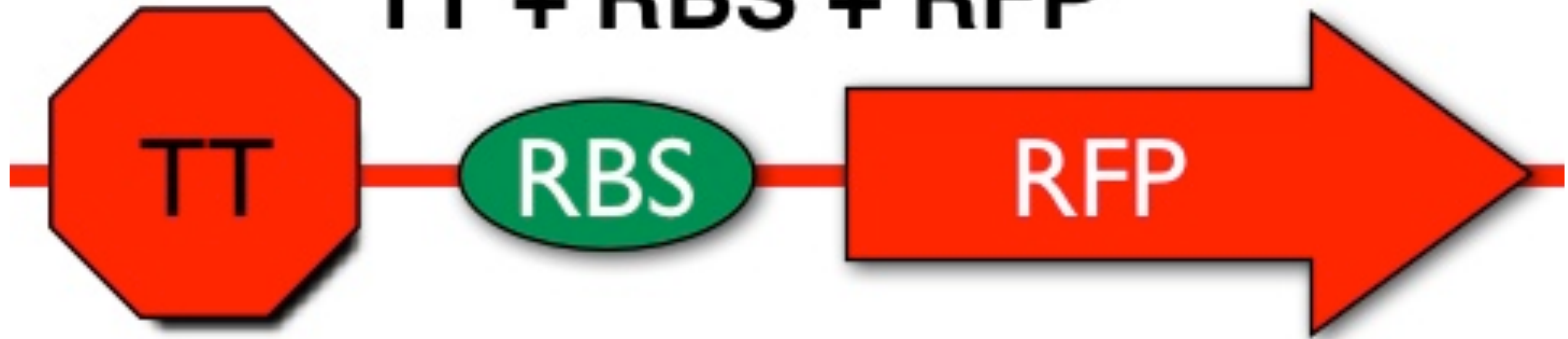
1 2 3 4 n GAGACC
- - - - n C T C T G G

GGTCTCn - - - -

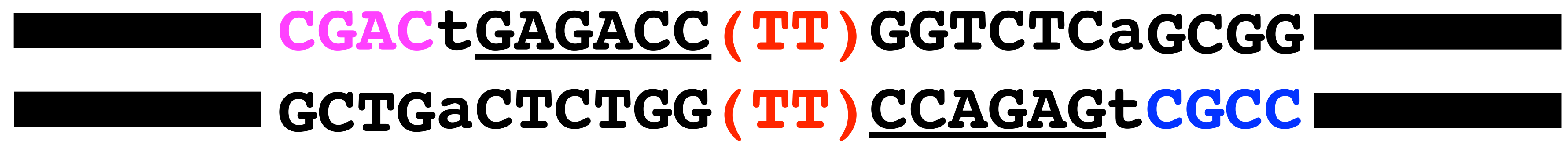
CCAGAGn 1 2 3 4

cuts
right

TT + RBS + RFP



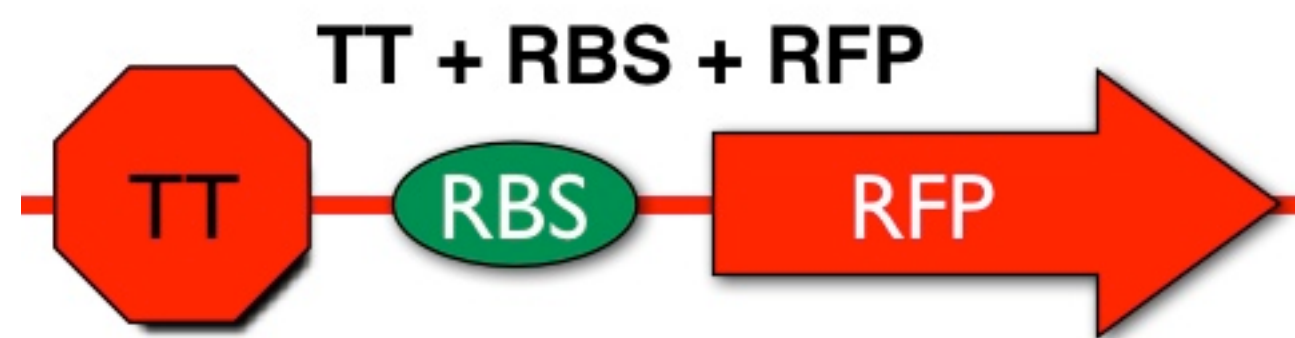
Bsa I



ligase

Bsa I

ligase



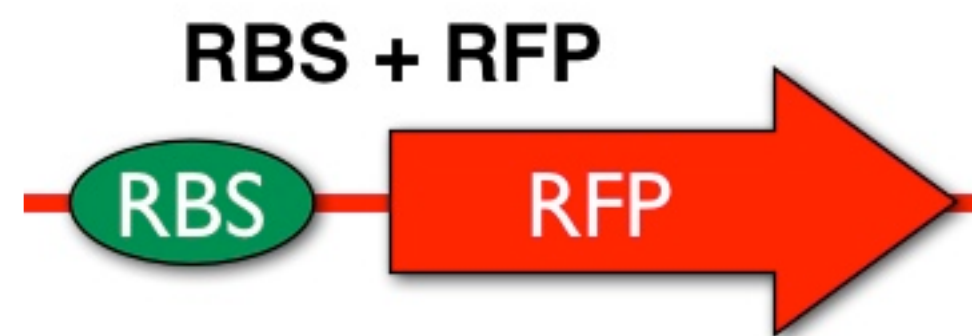
CGACtGAGACC (**TT**) GGTCTCa
aCTCTGG (**TT**) CCAGAGt**CGCC**

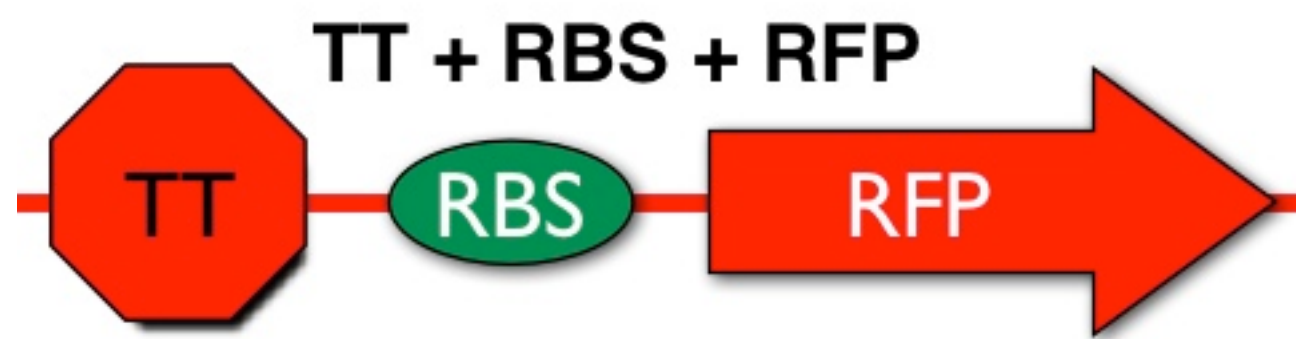
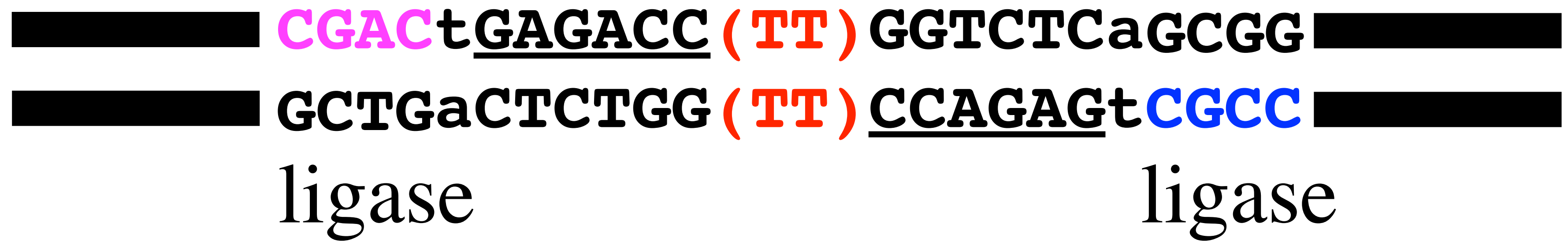
██████████
██████████ **GCTG**

ligase

GCGG ██████████
██████████

ligase





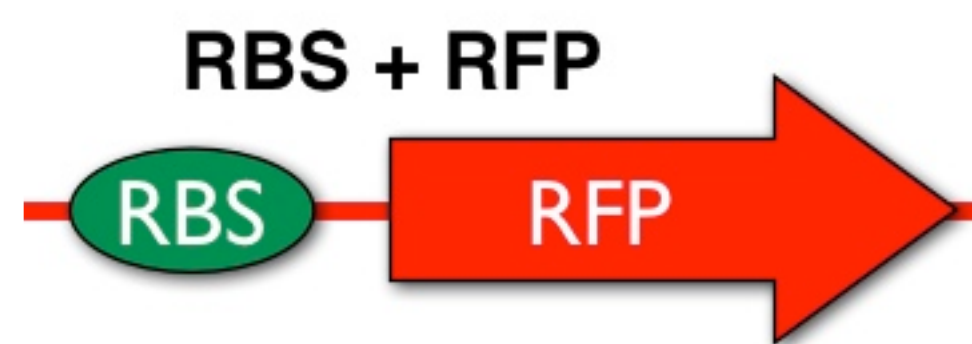
CGACt**GAGACC** (**TT**) **GGTCTCa**
aCTCTGG (**TT**) **CCAGAGt****CGCC**

██████████
██████████ **GCTG**

ligase

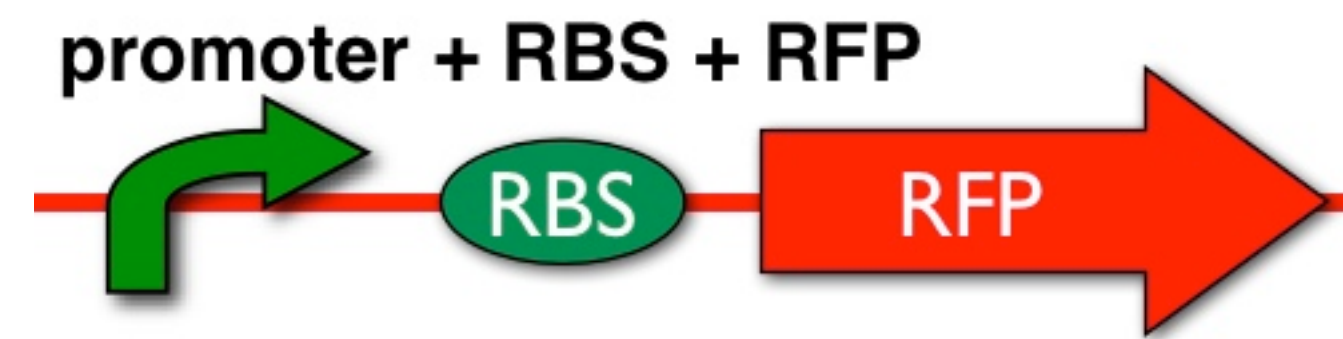
GCGG ██████████
██████████

ligase

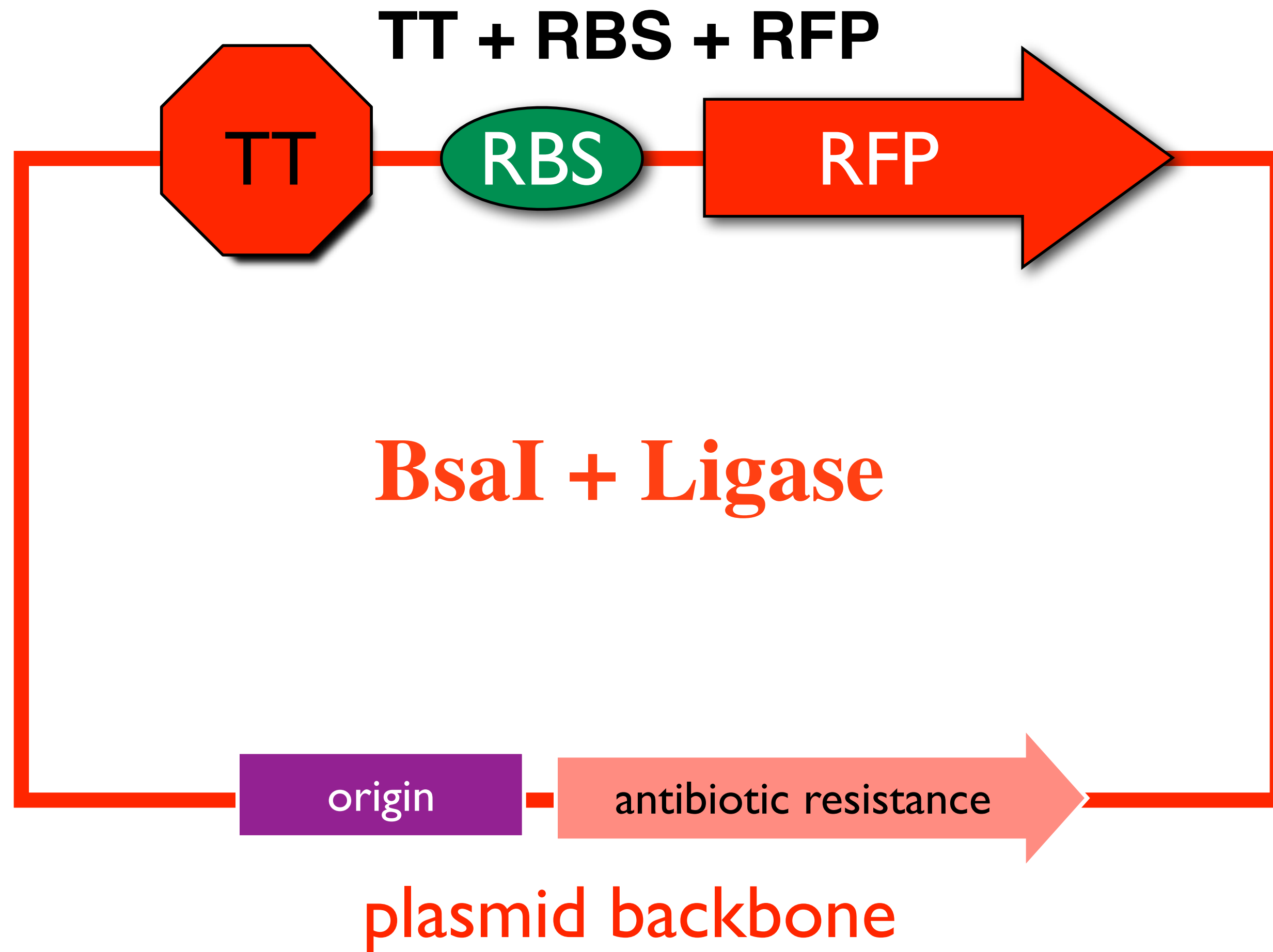
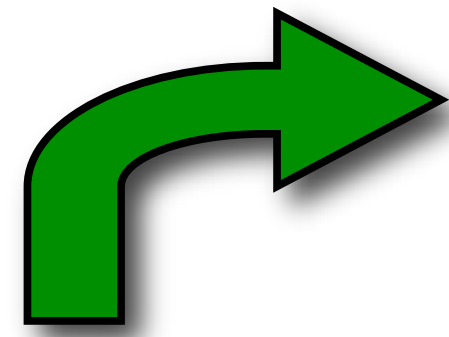


CGAC (promoter)
(promoter) **CGCC**

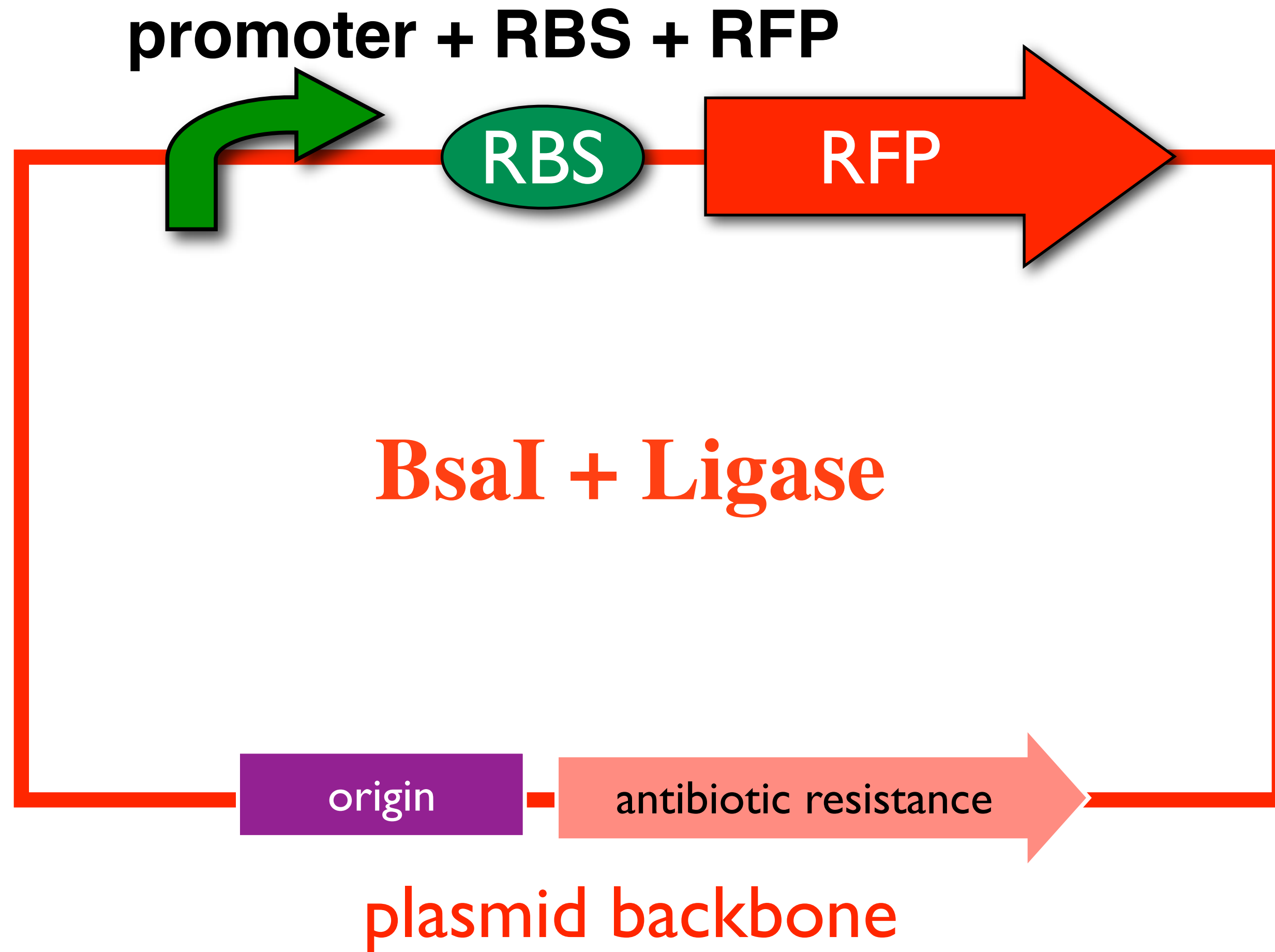
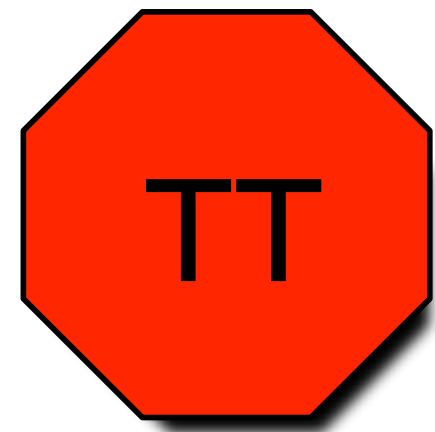
CGACtGAGACC (TT) GGTCTCa
aCTCTGG (TT) CCAGAGtCGCC



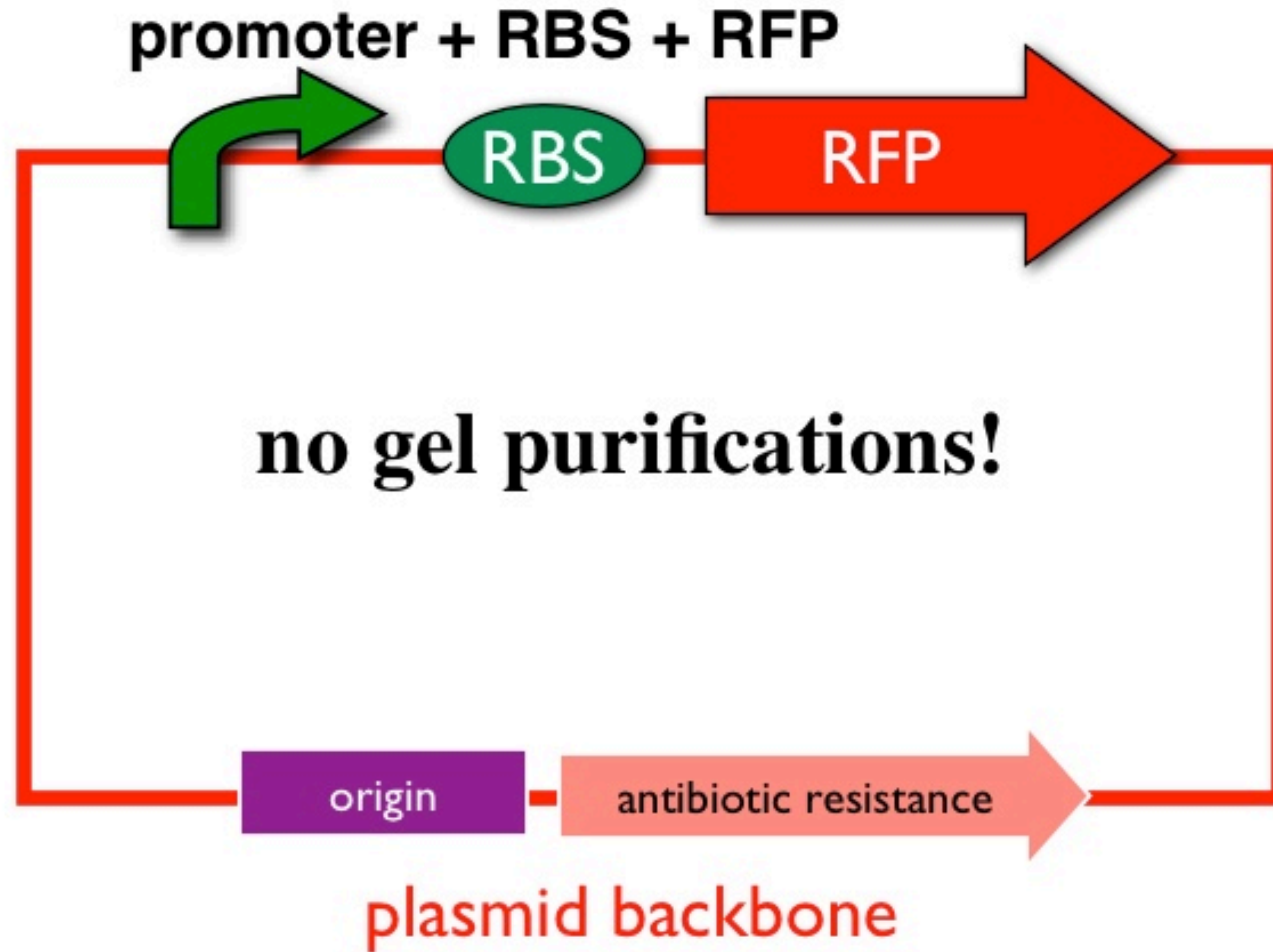
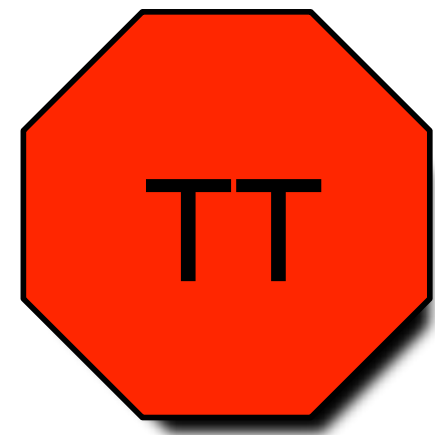
GGA Ligation Method



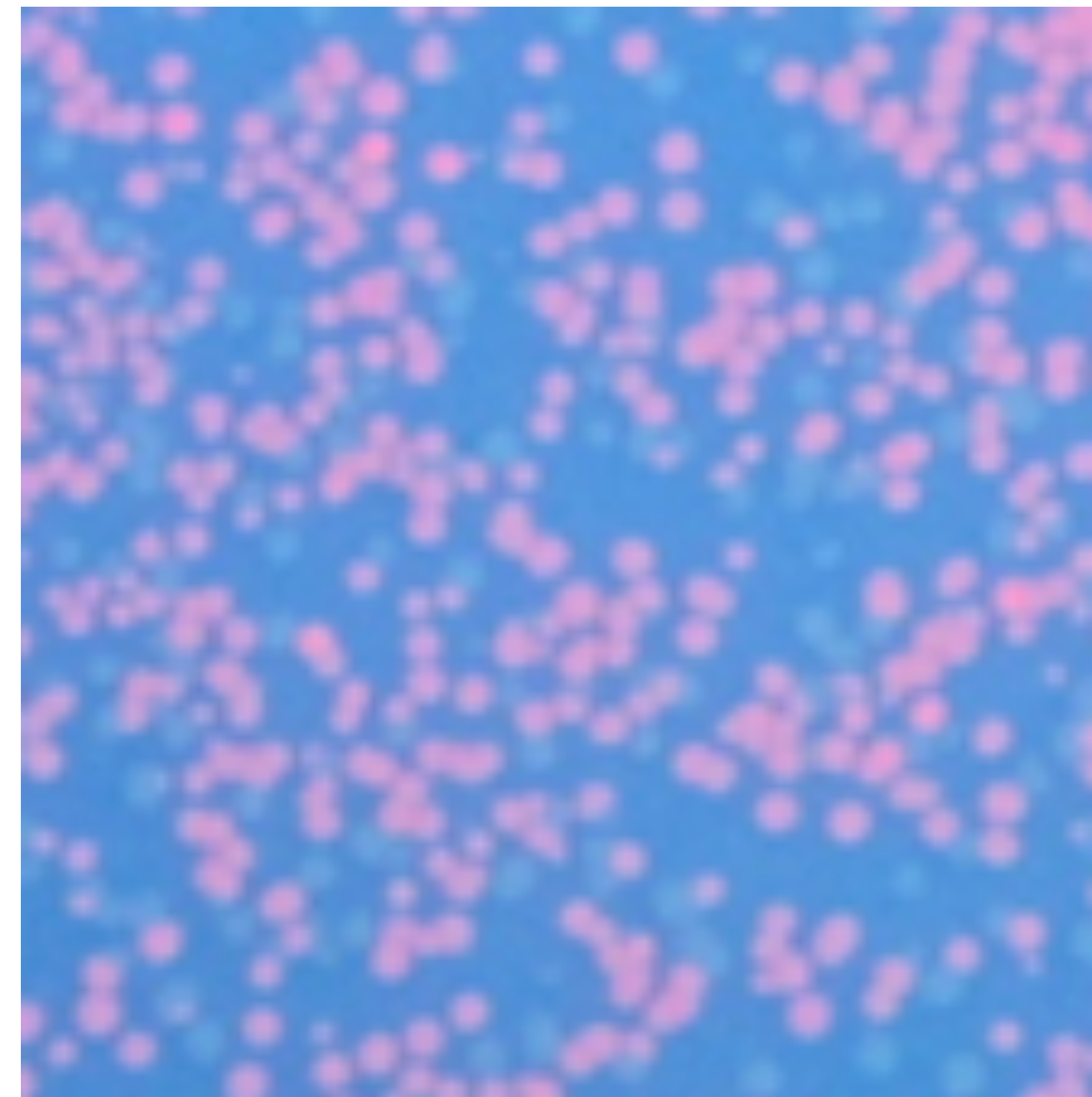
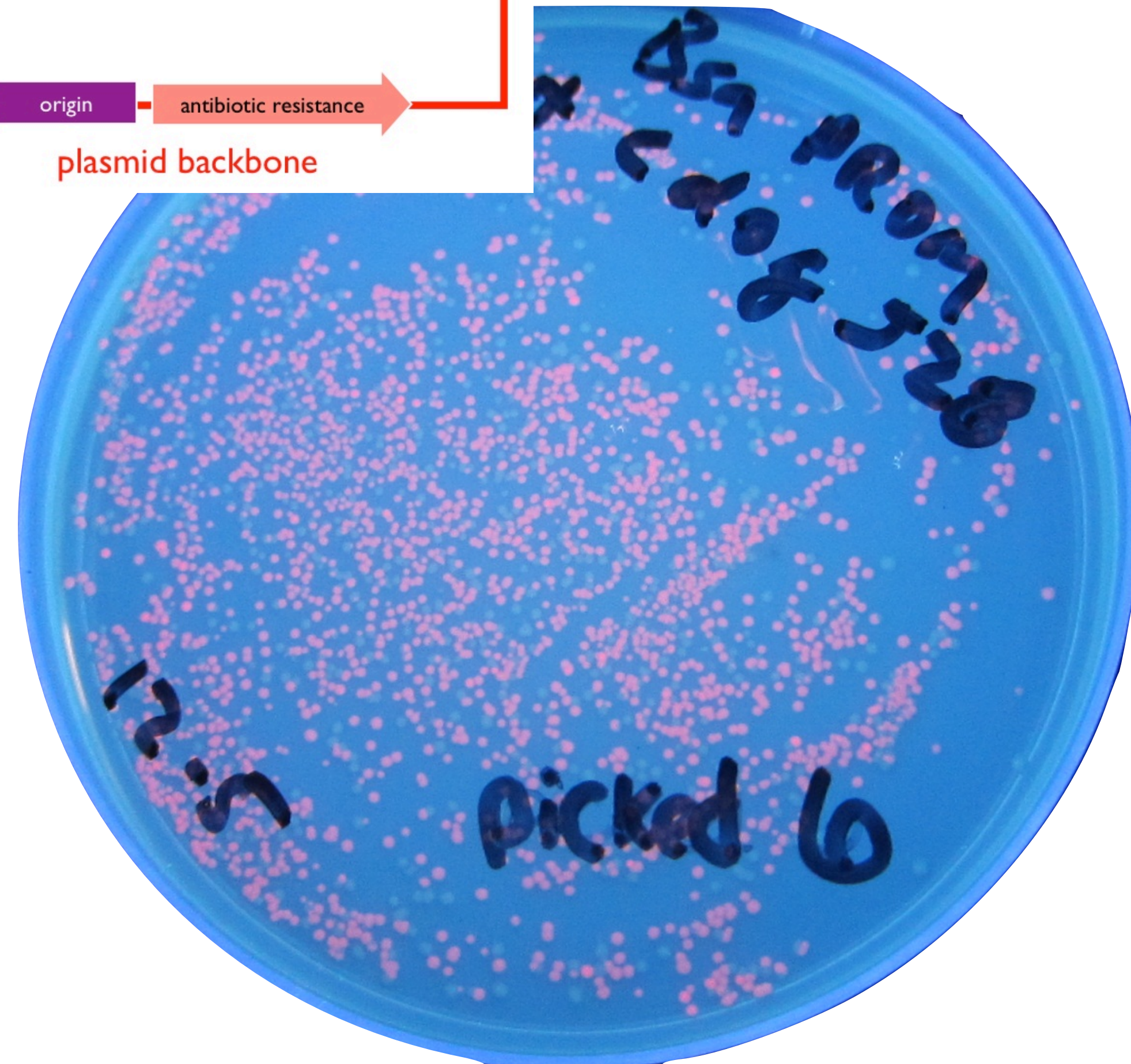
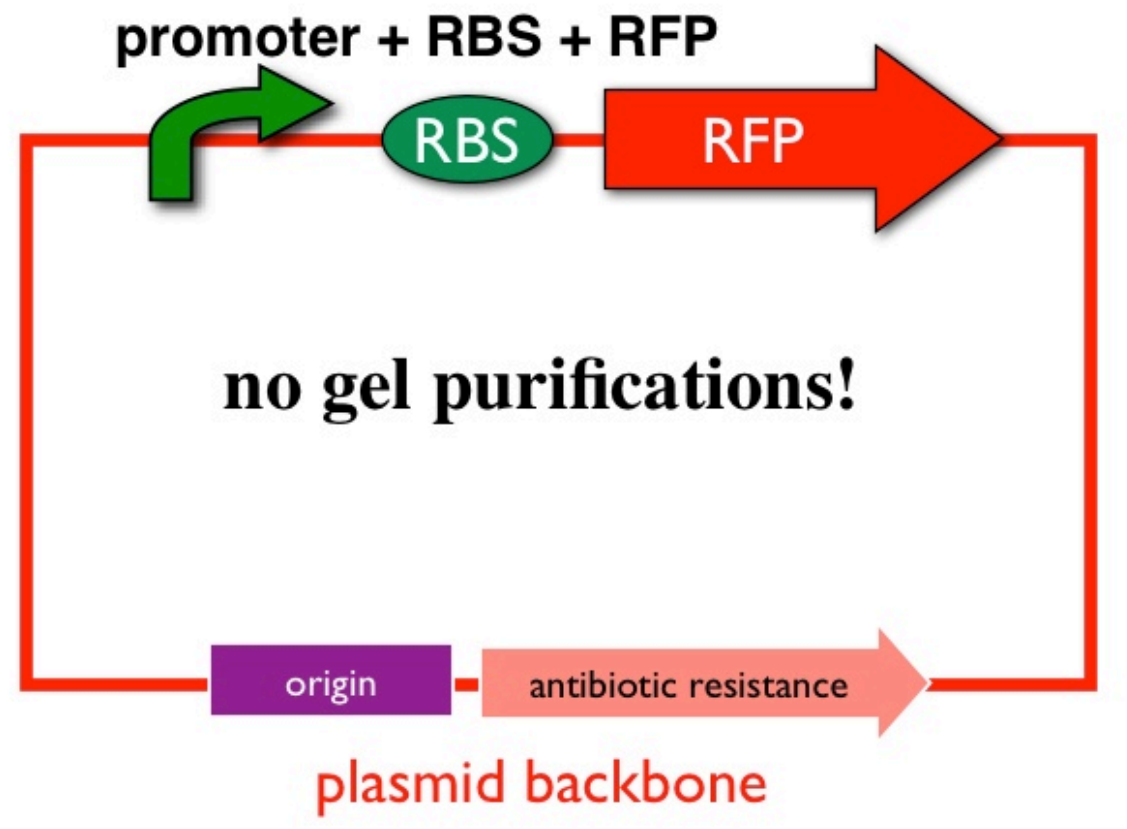
GGA Ligation Method



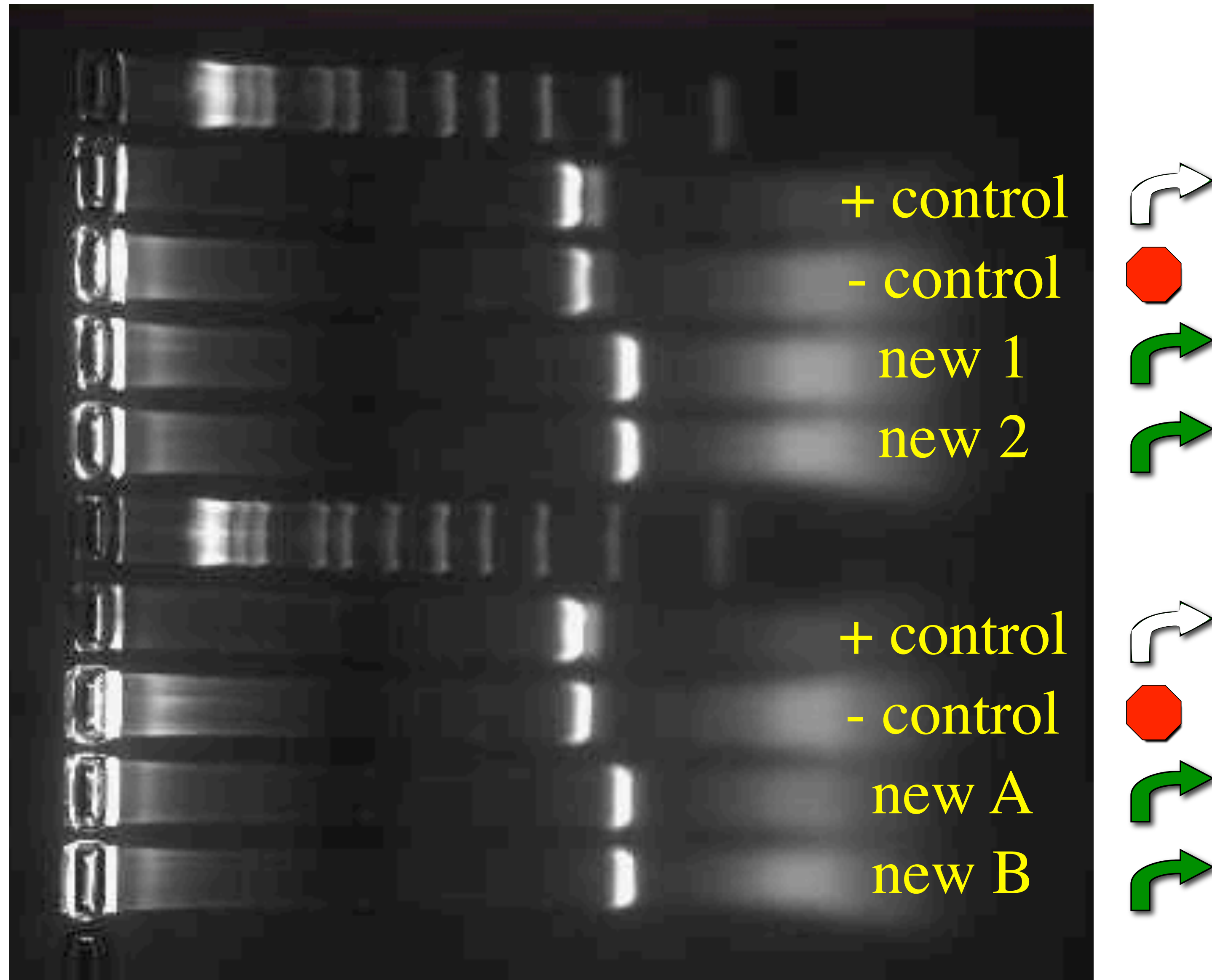
GGA Ligation Method



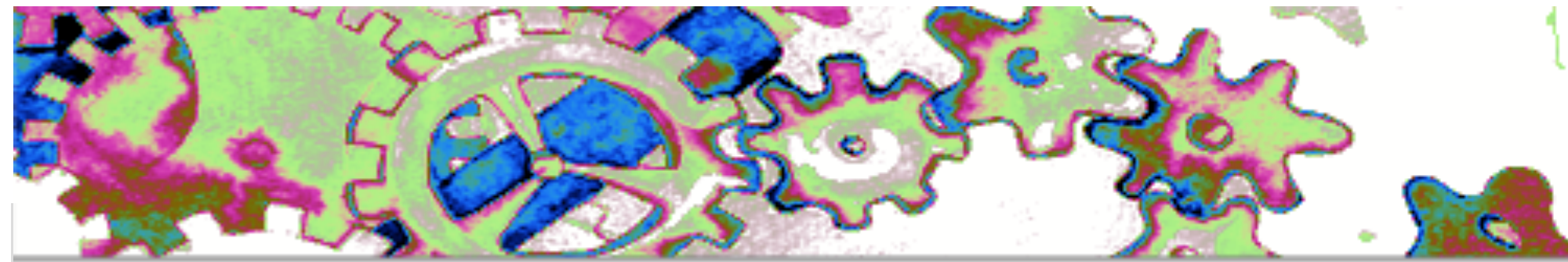
GGA Ligation Method



Student Sample, September 2012



Student Sample, September 2012

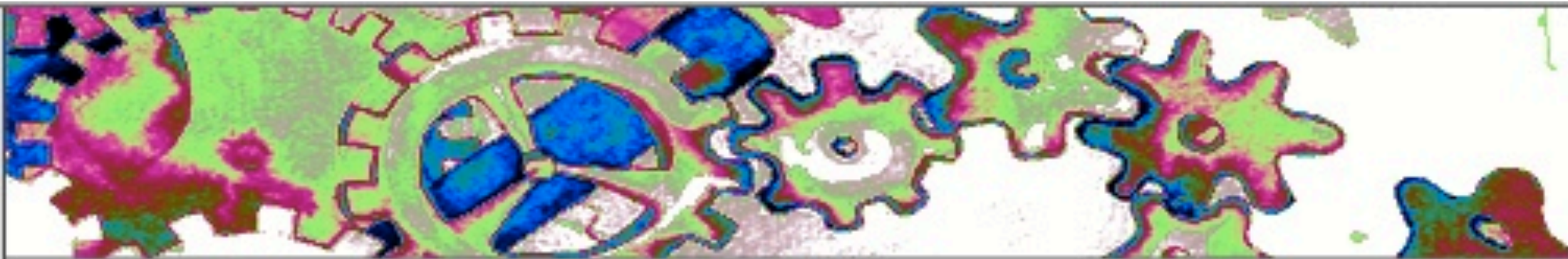


Registry of Standard Biological Parts

	BBa_J100067	Regulatory	fadB promoter (long sequence)	Meredith Nakano	85
	BBa_J100068	Regulatory	fadB promoter (short sequence)	Meredith Nakano	61
	BBa_J100069	Reporter	Superfolder GFP	Rebecca Evans	770
	BBa_J100070	Coding	Superfolder GFP	Rebecca Evans	720
	BBa_J100071	Regulatory	cadA promoter	Ben Clarkson	334
	BBa_J100072	Regulatory	LcpxP promoter--Long cpxP promoter	Ben Clarkson	392
	BBa_J100073	Regulatory	ScpxP--Short cpxP promoter	Ben Clarkson	94
	BBa_J100074	Regulatory	Long pLux Promoter	Betsy Gammon	197
	BBa_J100075	Regulatory	CydAP1 Long Promoter	Betsy Gammon	158
	BBa_J100076	Regulatory	CydAP1 Short Promoter	Betsy Gammon	151
	BBa_J100077	Composite	J100068:K0903005	Meredith Nakano	793
	BBa_J100078	Composite	J100067:K0903005	Meredith Nakano	817
	BBa_J100079	Device	Riboswitch and GFP	Rebecca Evans	879
	BBa_J100080	Device	Riboswitch and GFP	Rebecca Evans	882
	BBa_J100081	Reporter	J100071+E0240	Ben Clarkson	334
	BBa_J100082	Reporter	J100072+E0240	Ben Clarkson	1276
	BBa_J100083	Composite	LuxI Long + RBS + GFP	Betsy Gammon	1081
	BBa_J100084	Composite	CydAP Long + RBS + GFP	Betsy Gammon	1042
	BBa_J100085	RNA	short CRISPR sequence with GFP target spacer	Caroline Vrana	240
	BBa_J100086	Composite	CydAP Short Promoter + RBS + GFP	Betsy Gammon	1035
	BBa_J100087	Reporter	J100073+E0240	Ben Clarkson	978
	BBa_J100088	Generator	J100071+J10063	Ben Clarkson	2965
	BBa_J100089	Generator	J100072+J10063 (LcpxP+LRE, Luciferase)	Ben Clarkson	3023
	BBa_J100090	Regulatory	CRISPR sequence with GFP and AmpR targets	Caroline Vrana	412
W	BBa_J100092	Regulatory	Constitutive promoter for M1-162	Natalie Spach	50
?	BBa_J100093	Regulatory	rrnB P1 promoter	Kayla McAvoy	60
?	BBa_J100094	Regulatory	Lac promoter E. Coli	Cameron Bard	44
?	BBa_J100095	Regulatory	malE1 Maltose induced promoter.	Pooja Potharaju	65
	BBa_J100096	Regulatory	PBAD Promoter from araE Gene	Elizabeth Brunner	27
W	BBa_J100097	Regulatory	Anhydrotetracycline inducible promoter with Bsal sticky ends	Sarah Kim	55
	BBa_J100098	DNA	Promoter for the argF gene	Erin Nieuwma	44
W	BBa_J100099	Regulatory	A promoter (CydAB) activated by the FNR enzyme	Phoebe Parrish	64



Student Sample, September 2012



Registry of Standard Biological Parts


[Go](#) [Search](#)

[page](#) [discussion](#) [view source](#) [history](#) [Log in / create account](#)

[BBa J100099 Main Page](#) [Part Design](#) [Physical DNA](#) [Hard Information](#) [Experience](#) [Tools](#)

Part:BBa_J100099

Designed by Phoebe Parrish Group: Campbell_M_Lab (2012-09-13)

 Regulatory DNA Planning
Experience: Works [Get This Part](#)

A promoter (CydAB) activated by the FNR enzyme

The promoter, CydAB, was found to be activated by the FNR enzyme, which is induced by the presence of $(\text{NH}_4)_2\text{Fe}(\text{SO}_4)_2$ and ascorbate. The oligo includes both CydAB, the FNR binding site, and the sticky ends needed for the Golden Gate Assembly method.

Sequence and Features

Format:	Subparts	Ruler	SS	DS	Search:	Length: 64 bp	Context: Part only	Get selected sequence		
1	11	21	31	41	51	61	71	81	91	
1	ggaattgata tttatcaatg tataagtctt ggaaatgggc atcaaaaaga gataaattgt tctc									
	~~~~~ FNR binding			~~~~~ -35		~~~~~ -10				

Assembly Compatibility: 10 12 21 23 25

Jeffrey Green. 1993. "Activation of FNR-dependent transcription by iron: An in vitro switch for FNR." FEMS Microbiology Letters 113 (1993) 219-222

[\[edit\]](#)

# Student Sample, September 2012

## Part:BBa_J100099:Experience

Designed by Phoebe Parrish Group: Campbell_M_Lab (2012-09-13)

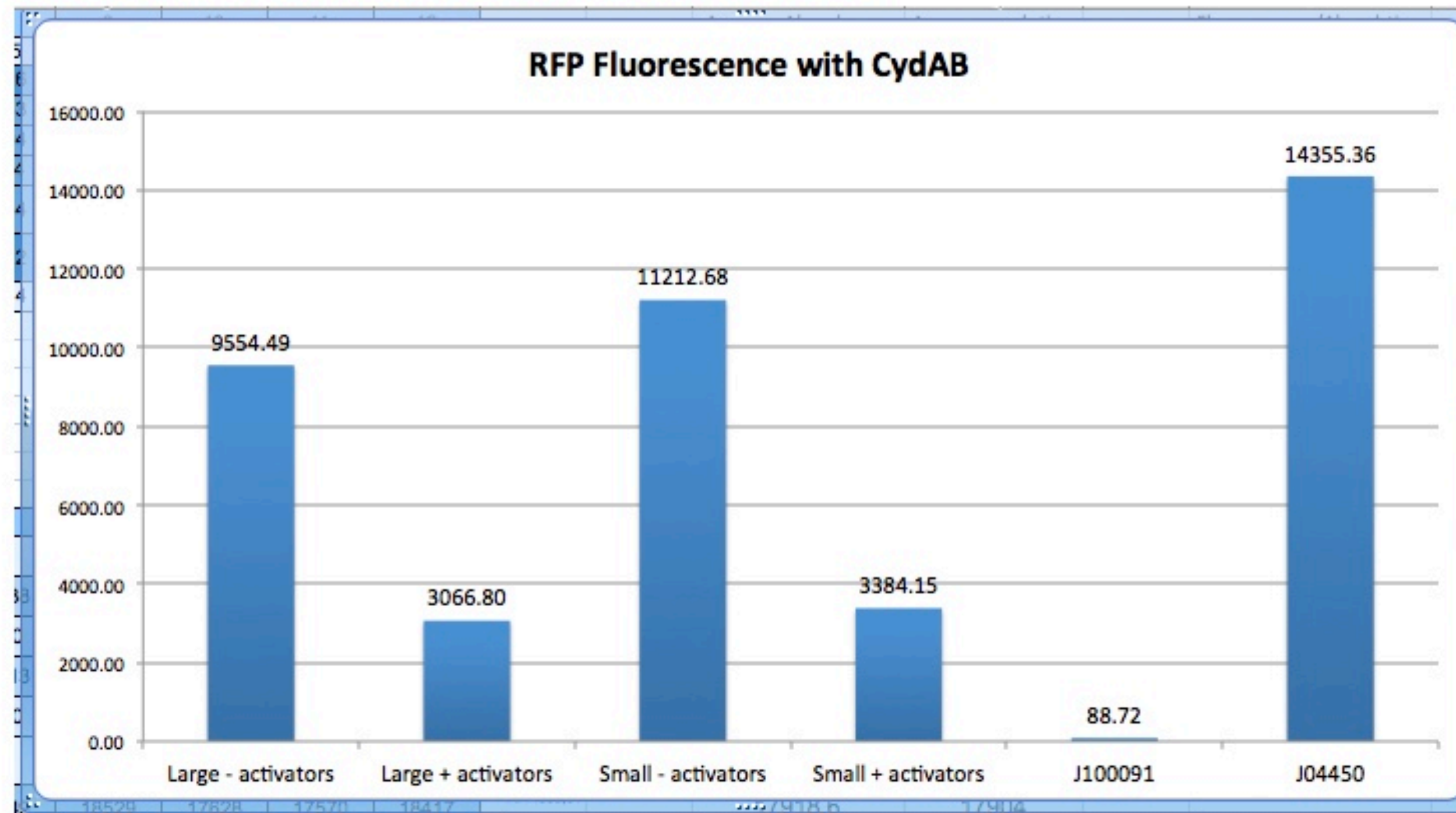


DNA Planning  
Experience: Works  
[Get This Part](#)

This experience page is provided so that any user may enter their experience using this part. Please enter how you used this part and how it worked out.

### Applications of BBa_J100099

We pipetted 200 microliters of one solution containing E coli cells from a small colony and the activators, one with cells from a small colony and no activators, one containing cells from a large colony and the activators, and one containing cells from a large colony and no activators. We also did a positive control with E coli cells containing a known promoter that causes red fluorescence (J04450) and a negative control with cells containing a the transcriptional terminator that does not cause red fluorescence (J100091). We tested both fluorescence of our samples using a fluorometer and the light absorbance using a spectrophotometer. We measured the fluorescence and absorbance of five samples of each solution, including a control solution that just contained the growth medium. We averaged the values for each solution and subtracted the average fluorescence/absorbance of the control. We then divided the average fluorescence by the average absorbance for each solution. These values are displayed on the accompanying graph.



# Registry of Functional Promoters (RFP)

## Registry of Functional Promoters (V1.0)

### Welcome to the Registry of Functional Promoters

This Registry of Functional Promoters was developed by Bill Hatfield, Laurie J. Heyer, A. Malcolm Campbell at Davidson College and Todd Eckdahl of Missouri Western State University, through the support of HHMI grant 52006292 ([GCAT main page](#)) and is freely available for others to use though no support other than the user manual is available.

If you are already a Registered User of GCAT-alog , you do not need to Reregister

[LOGIN](#) [REGISTER AS NEW USER](#)

- For comments or questions about this website contact, [Malcolm Campbell](#)

[gcat.davidson.edu/RFP/](http://gcat.davidson.edu/RFP/)

# Registry of Functional Promoters (RFP)

**Registry of Functional Promoters (v1.0)**

**SEARCH**

---

**Search by Entry Number**

Entry Number  Use ", " for multiple entries, "-" for range

---

**Search Criteria**

OR  AND  Promoter Name

OR  AND  Part Number

OR  AND  Sequence

OR  AND  Length

OR  AND  Criterion

OR  AND  Species of Origin:

OR  AND  Constitutive  Regulated

OR  AND  RBS Used for Testing:

OR  AND  ORF Used for Testing:

OR  AND  Plasmid Used for Testing:

OR  AND  *E.coli* Used for Testing:

OR  AND  Media Used for Testing:

OR  AND  Comparison Construct:

OR  AND  Comparison Plasmid:

OR  AND  *E.coli* Used for Comparison Construct:

OR  AND  Media Used for Comparison Construct:

OR  AND  Fold Difference From Comparison:

OR  AND  Comment

OR  AND  Direction: Forward  Reverse

OR  AND  Status: Works  Not Working  Ifv

[gcat.davidson.edu/RFP/](http://gcat.davidson.edu/RFP/)



# Registry of Functional Promoters (RFP)

## Registry of Functional Promoters (v1.0)

### SEARCH PROMOTER RESULTS

Entry No.	Promoter Name	Part Number	Sequence	Length	Citation	Species of Interest	Constitutive/Regulated	Inducible/Repressible	Regulator	RBS Used for Testing	ORF Used for Testing	Plasmid Used for Testing
1	TetR Repressible Promoter	<a href="#">R0040</a>	tccctatcagtgatagagattgacatccctatcagtgatagagatactgagcac	54			Regulated	Repressible	TetR			pSI
2	56 bp LacI Promoter	<a href="#">K091110</a>	cgttgacaccatcgaatggcgcaaaaccttgcgggatggcatgatagcgccggg	56			Constitutive					
3	200 bp LacI Promoter	<a href="#">R0010</a>	caatacgcaaaccgctctccccgcggttgccgattcattaatgcagctggcac gacaggttcccactggaaagcgggcagtgagcgcaacgaattaatgtgagtt agctcactcattaggcaccccaggctttacactttatgcttccggctcgtatgtgtg ggaattgtgagcggataacaattcacaca	200			Constitutive					
4	LuxR & HSL Regulated Lux promoter	<a href="#">R0062</a>	acctgtaggatcgtacaggttacgcaagaaaatggtttgtatagtcgaataaa	55			Regulated	Repressible				
5	Backwards 200 LacI Promoter (right to left)	<a href="#">J31013</a>	tgtgtgaaattgtatccgctcacaattccacacaacatacagccggaagcataaa gtgtaaagcctggggtgcctaagtgagtgactaacacattaatgcggttgcgctc actgccgctttccagtcgggaaacctgtgcccagctgcattaatgaatcgccca acgcgcggggagagggcgtttgcgtattg	200			Regulated	Repressible				
6	OmpC Promoter	<a href="#">K199017</a>	tttacatttgaaacatctatagcgataaatgaaacatcttaaagtttagtatcatatc gtgttgattattctgcattttggggagaatggact	99			Constitutive					
7	23K series very strong constitutive Promoter	<a href="#">J23100</a>	ttgacggctagctcagtcctaggtacagtgctagc	35			Constitutive					

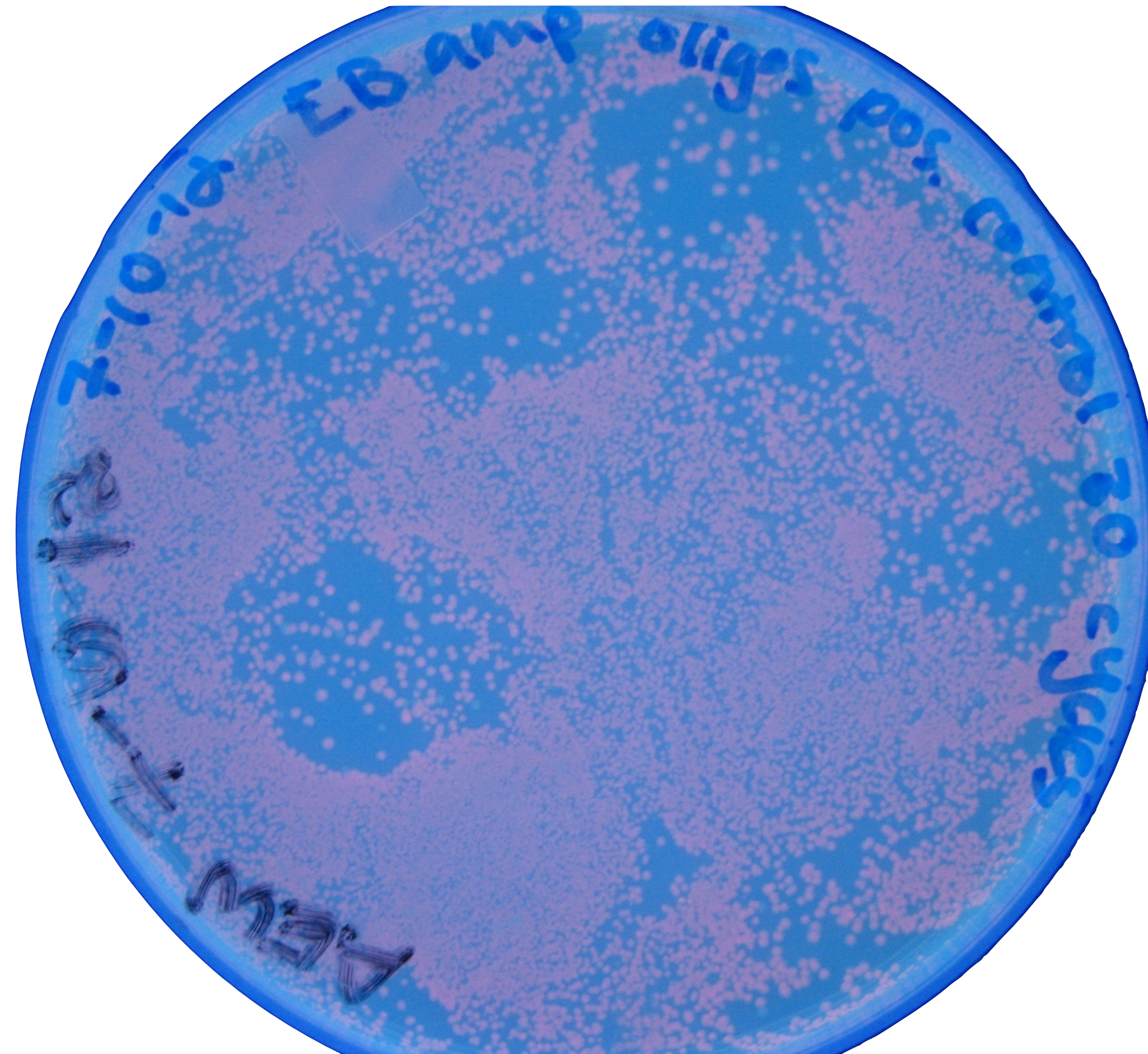
To Edit an Entry, Enter the Entry # and press "Edit Entry"

To Delete an Entry, Enter the Entry # and press "Delete Entry"

[Search Again](#)

# Testing Known Promoters: Ptac

5' CGACGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 3'  
3' CTCGACAAC TGTTAATTAGTAGCCGAGCATATTACACACCTCGCC 5'

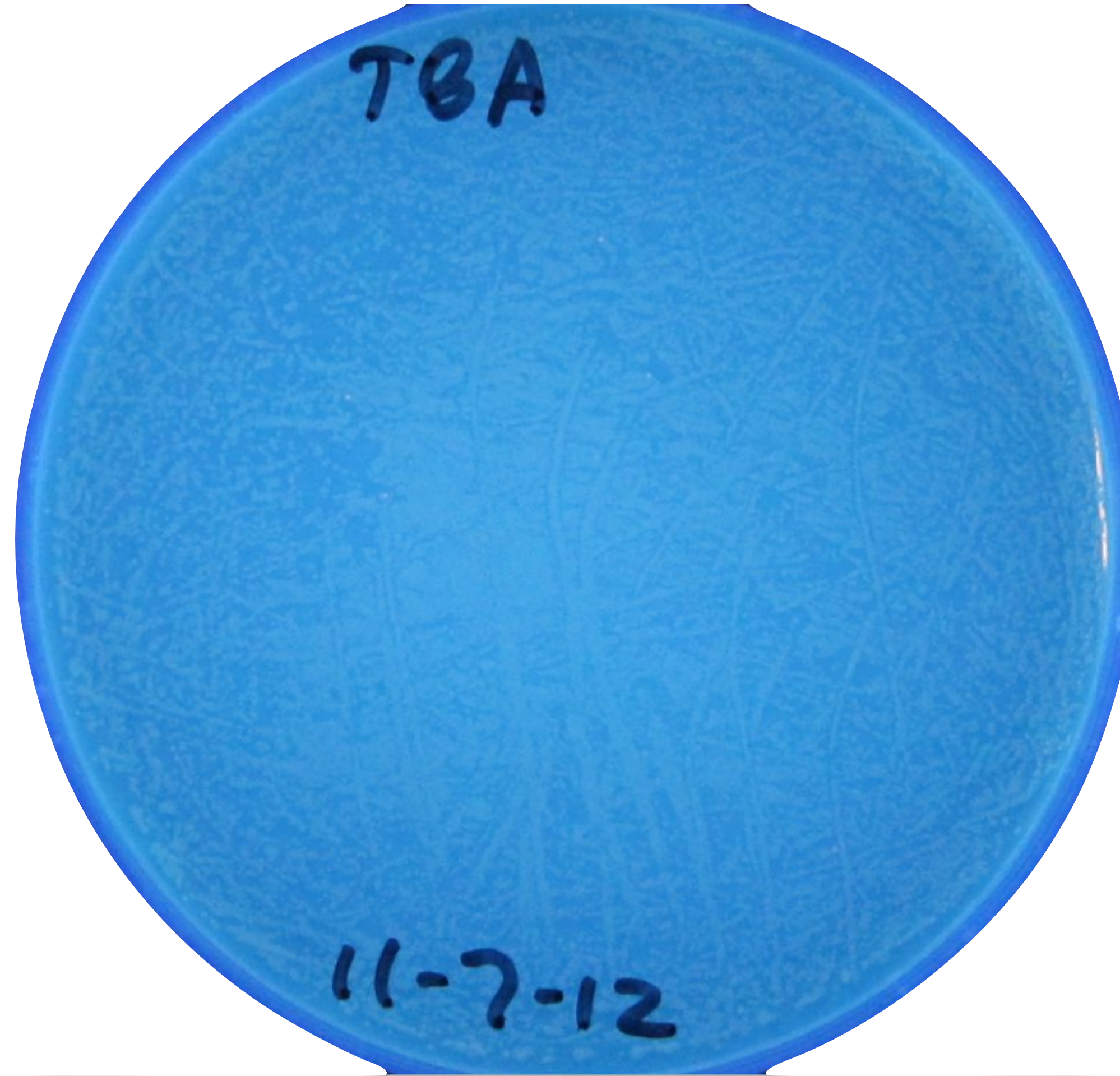


# Student Sample, November 2012

-35      **ATAA (deleted)**      -10

5' CGACGAGCTG**TTGACA**-----ATCATCGGCTCG**TATAAT**GTGTGGA      3'

3'      CTCGAC**AACTGT**-----TAGTAGCCGAGC**ATATTAC**CACACCTCGCC      5'



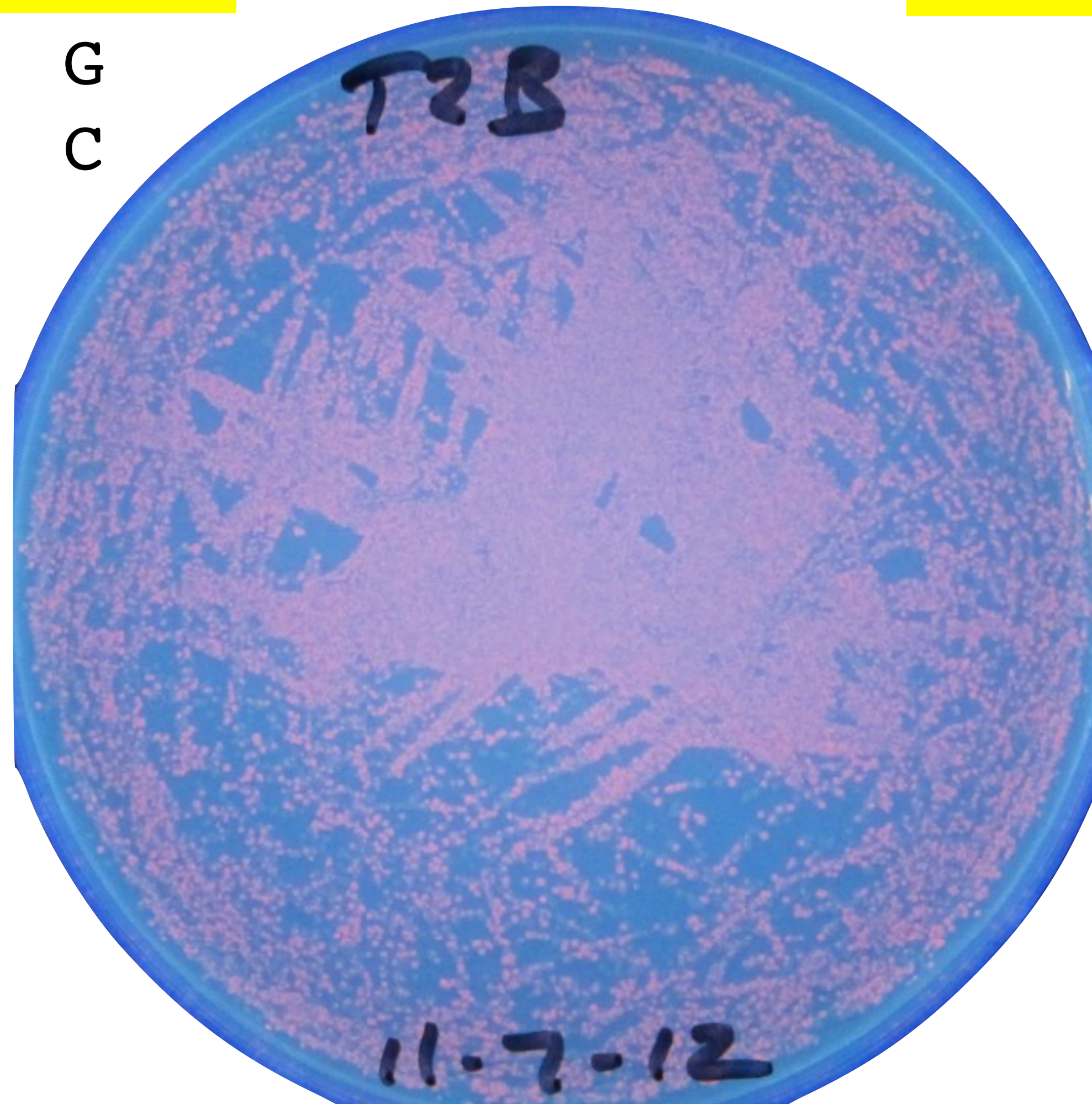
# Student Sample, November 2012

5' CGACGAGCTGTTtACAATTAATCATCGGCTCGTATAATGTGTGGA 3'  
3' CTCGACAAaTGTTAATTAGTAGCCGAGCATATTACACACCTCGCC 5'

-35

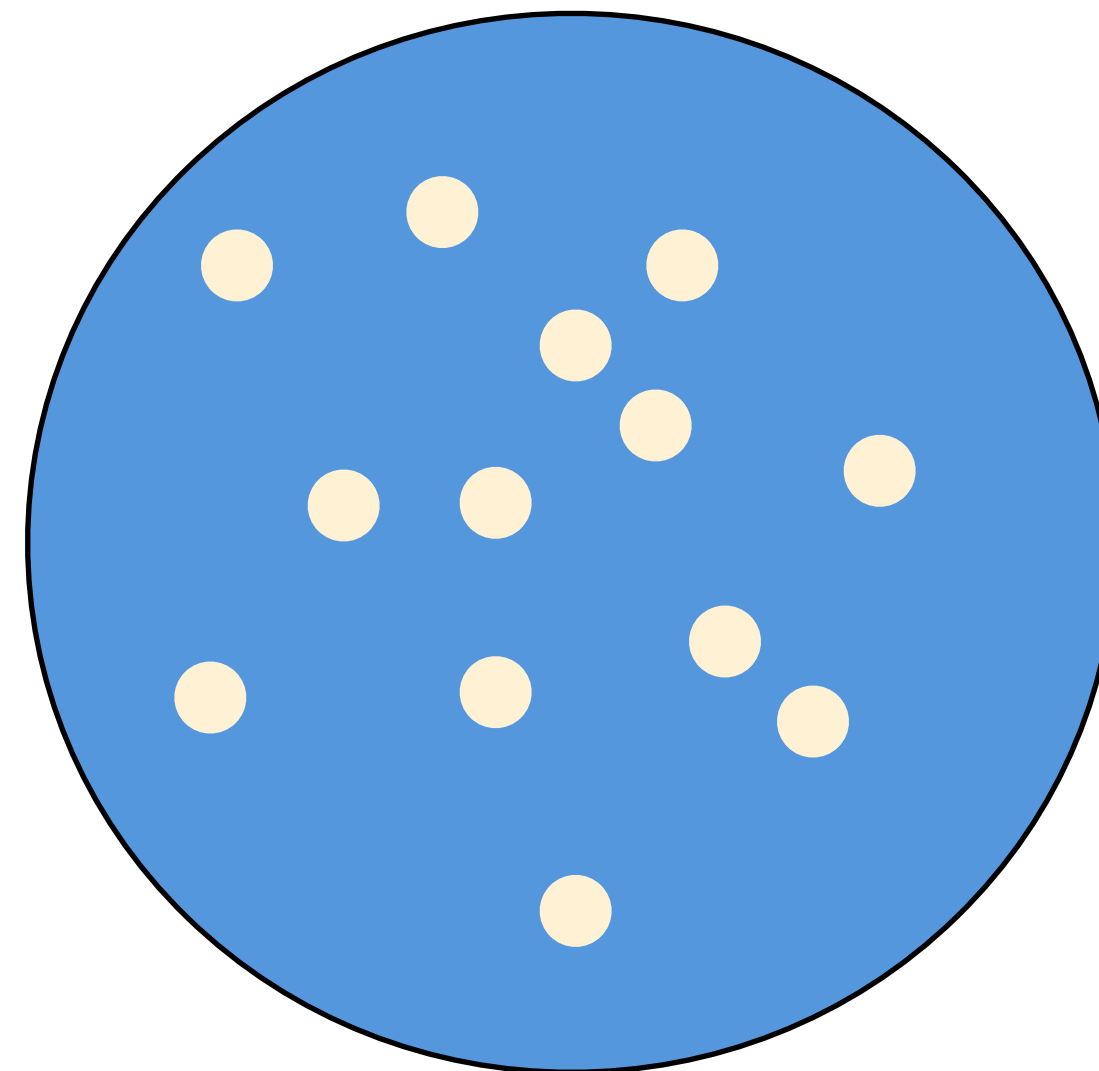
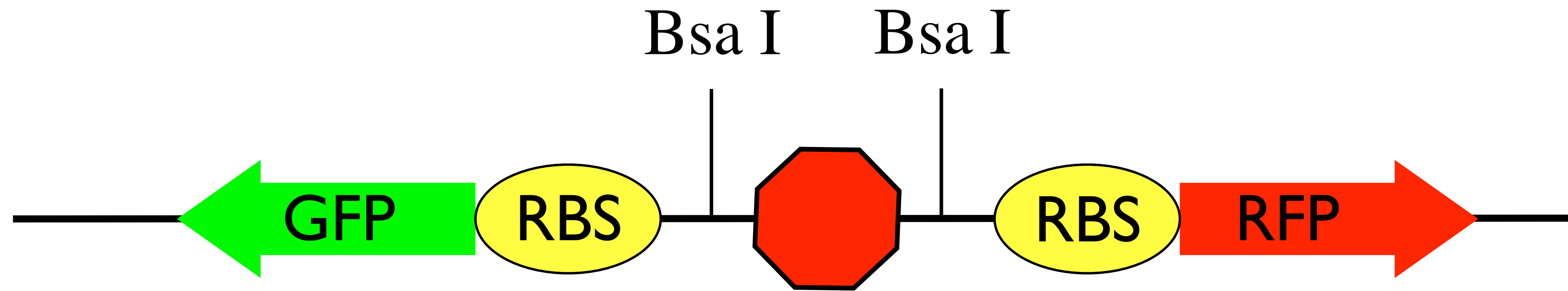
-10

G  
C



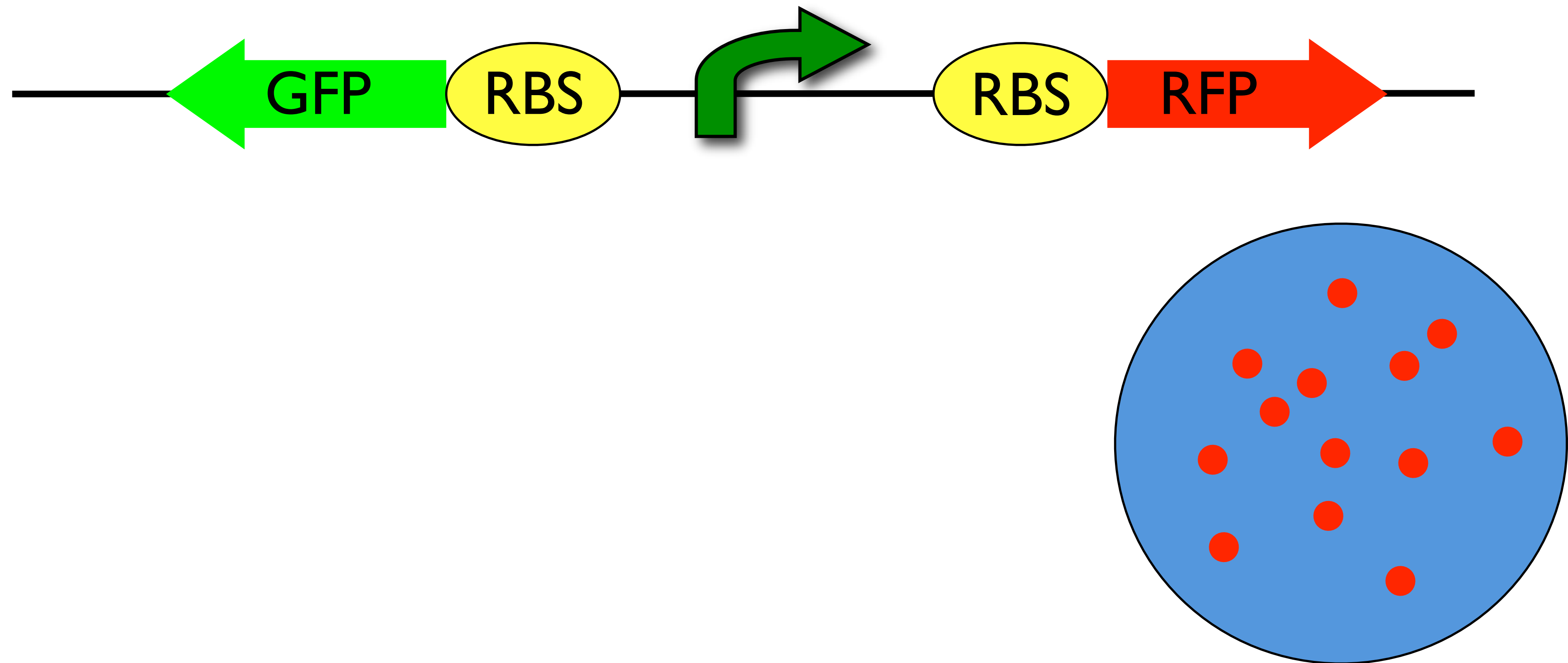
# New Versions of Plasmids

J119136



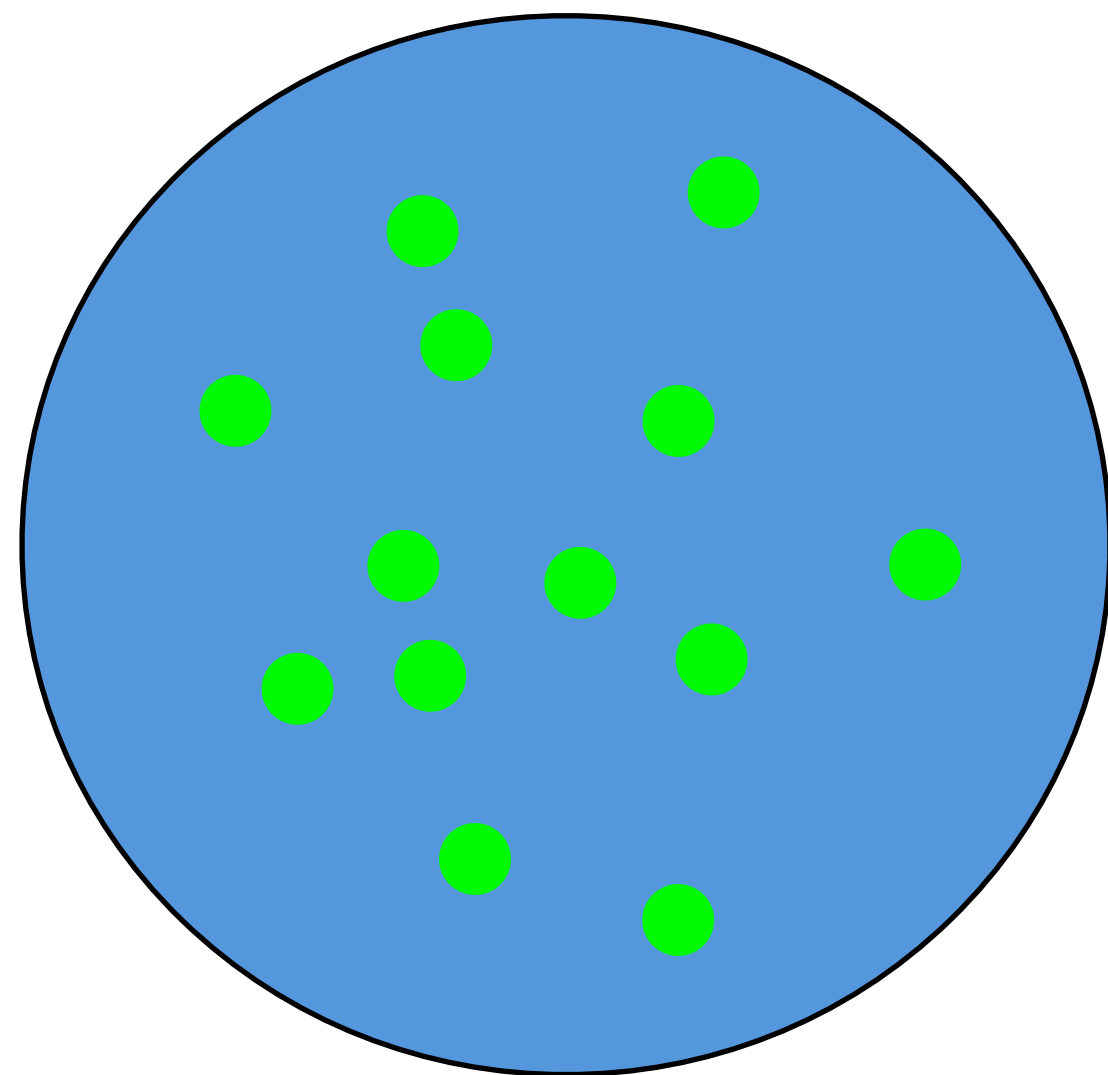
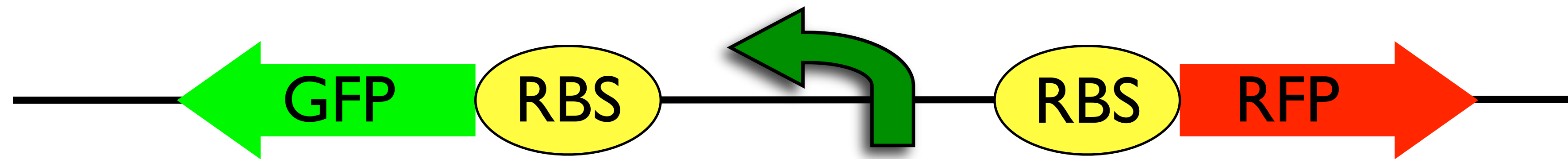
# New Versions of Plasmids

J119136



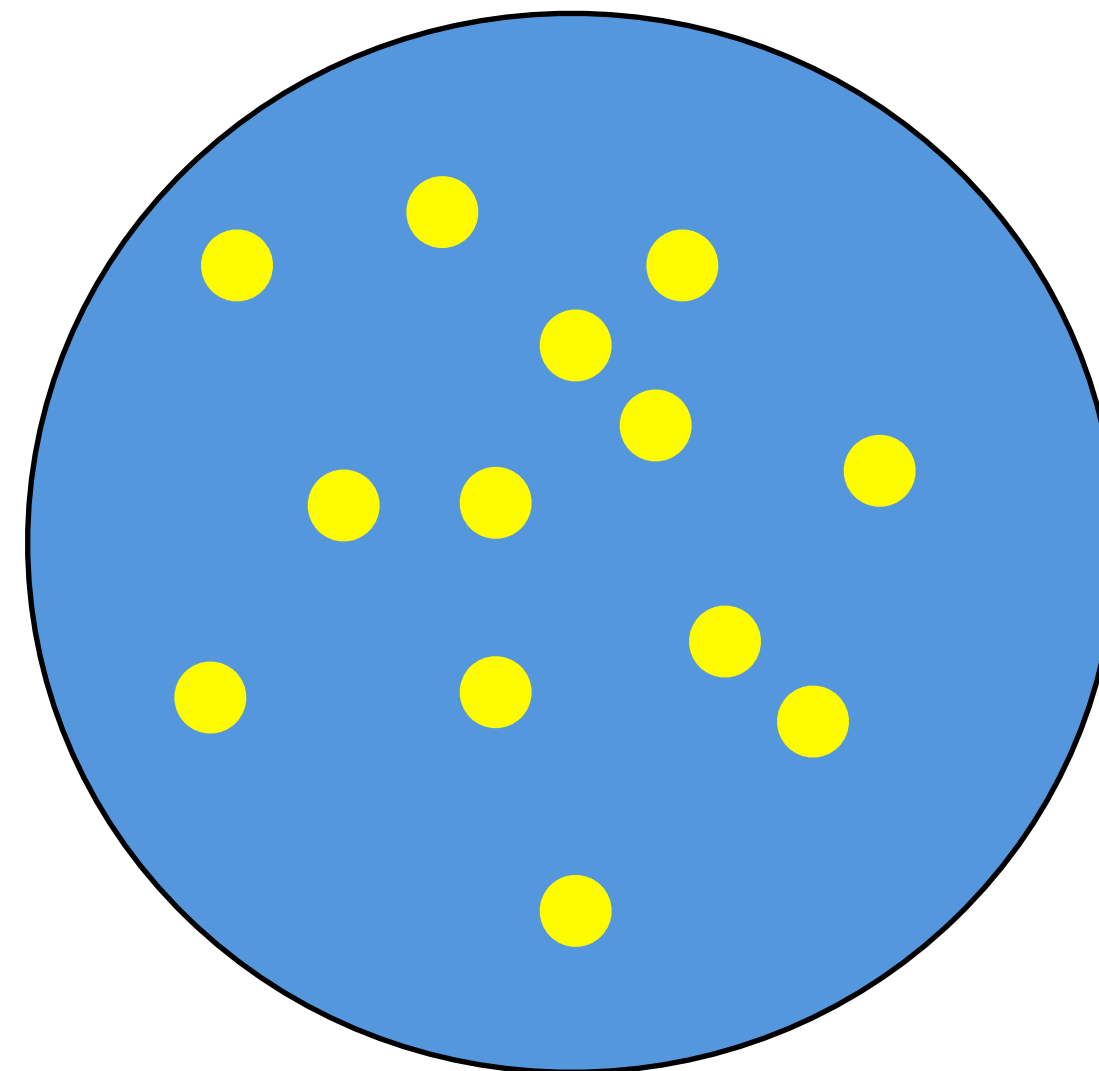
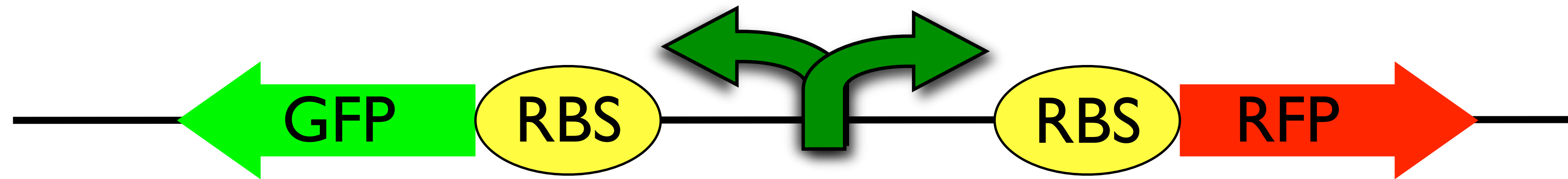
# New Versions of Plasmids

J119136



# New Versions of Plasmids

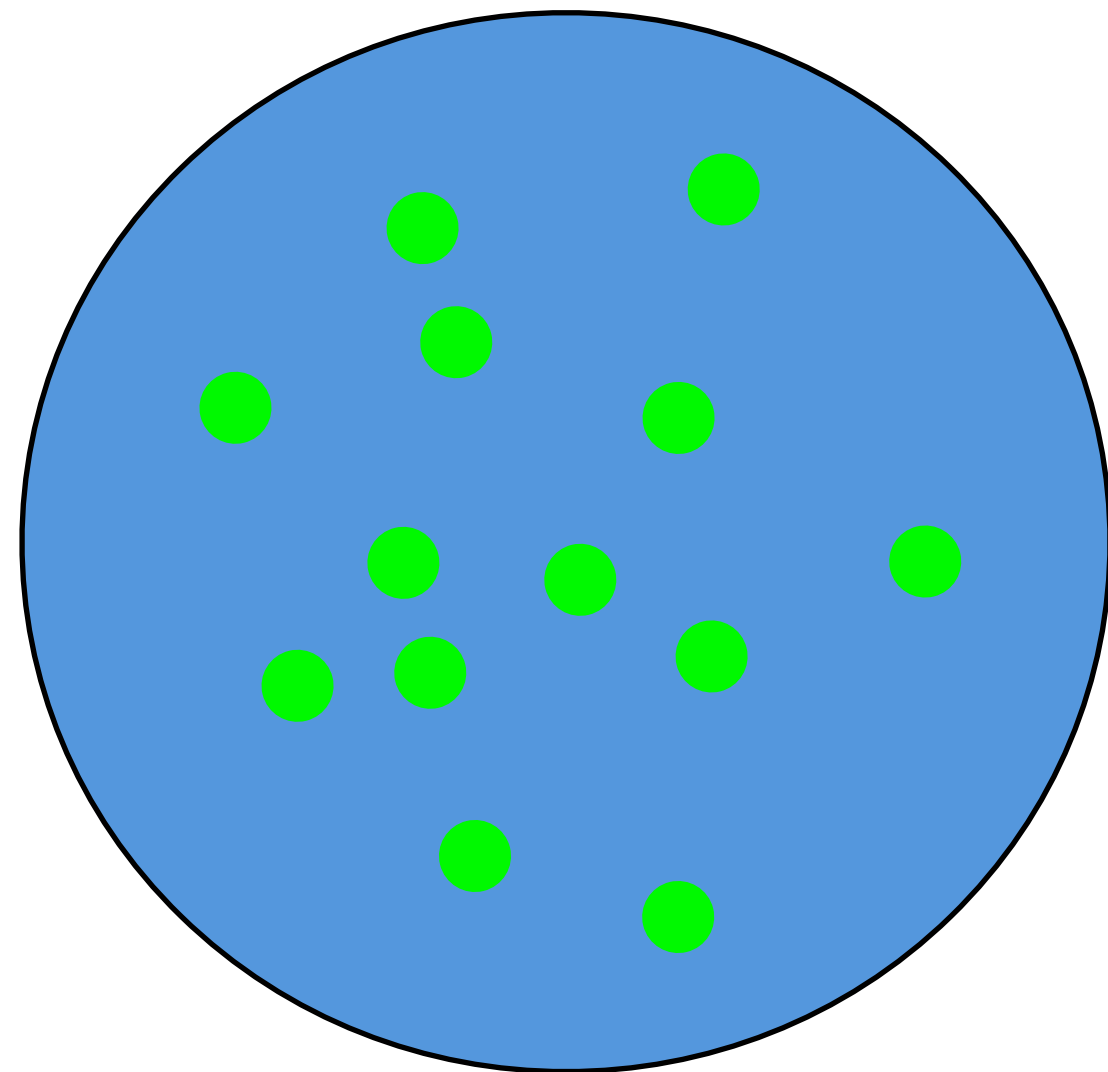
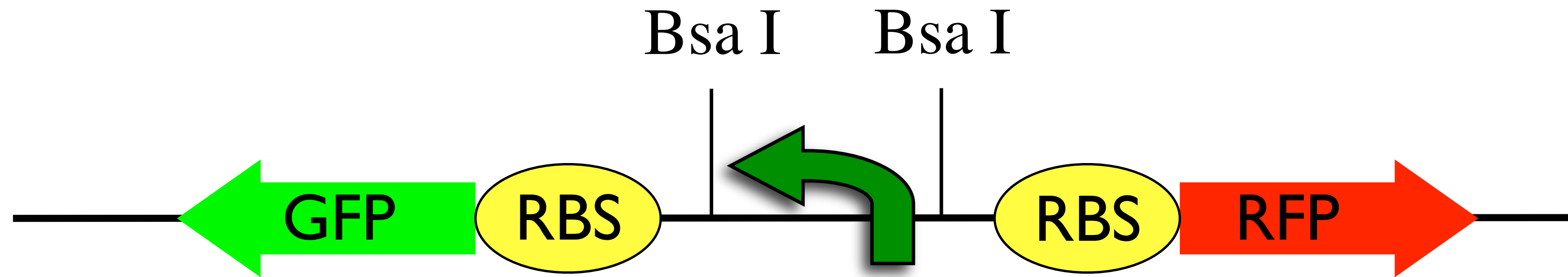
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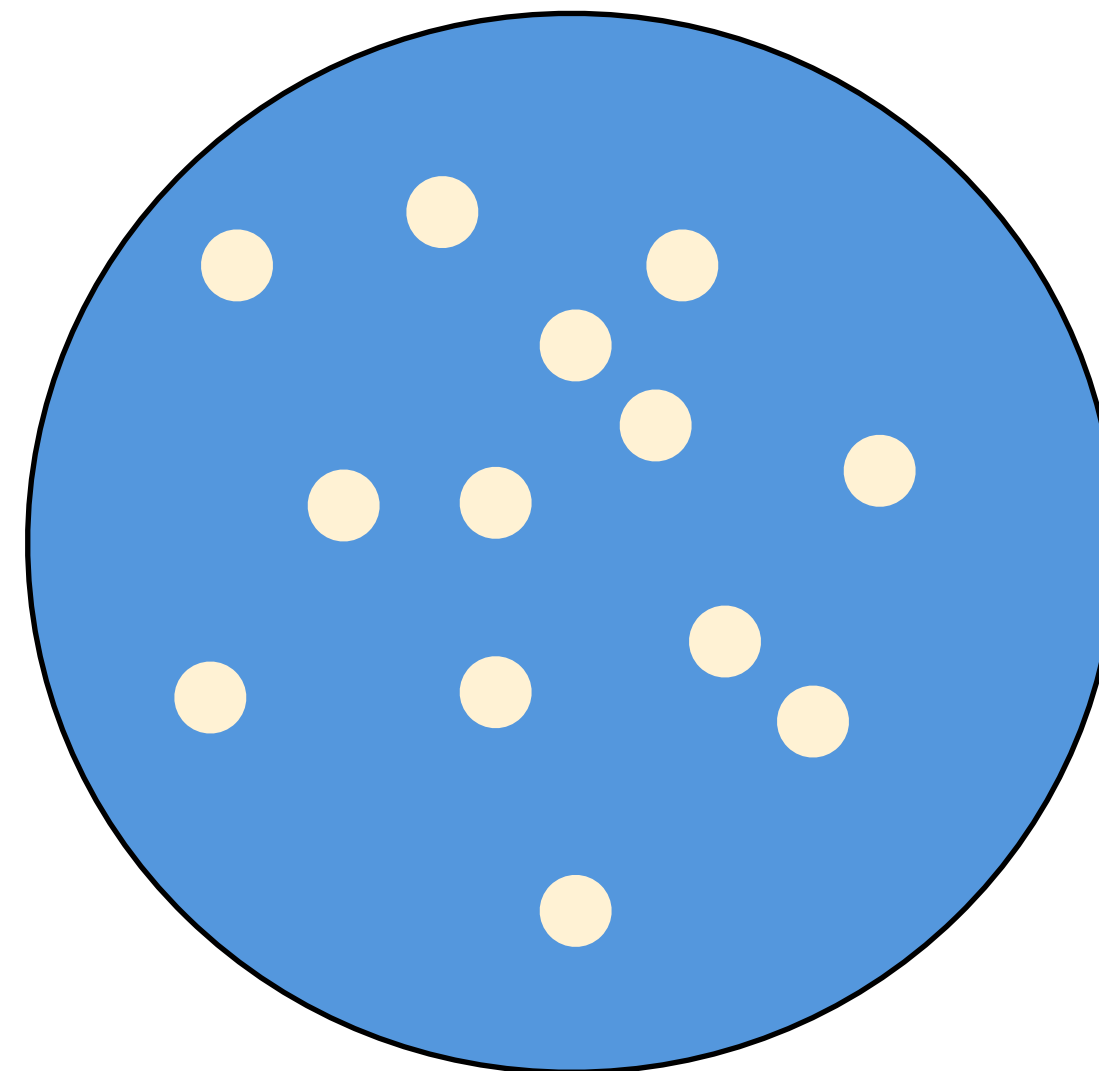
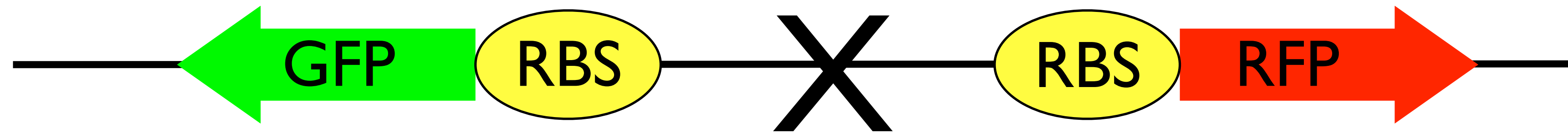
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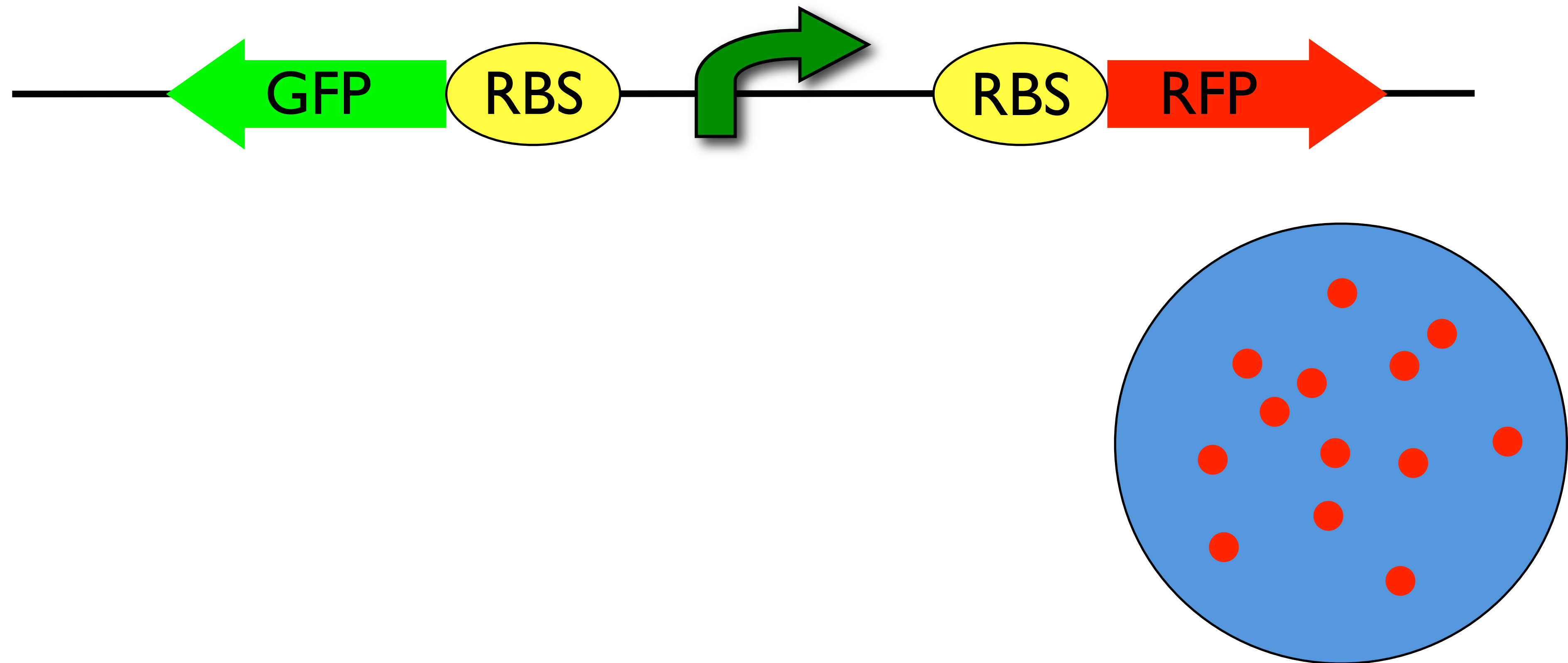
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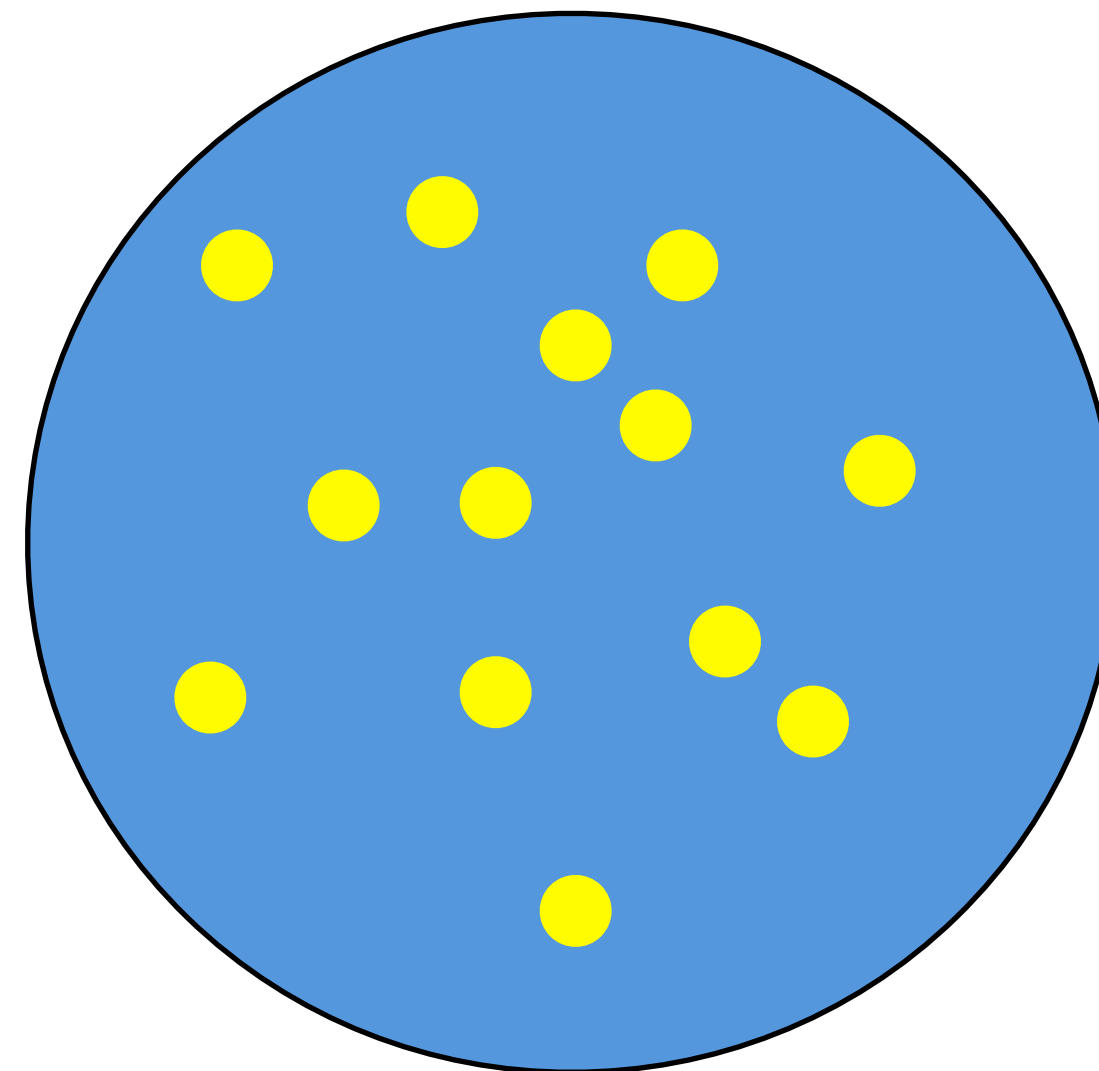
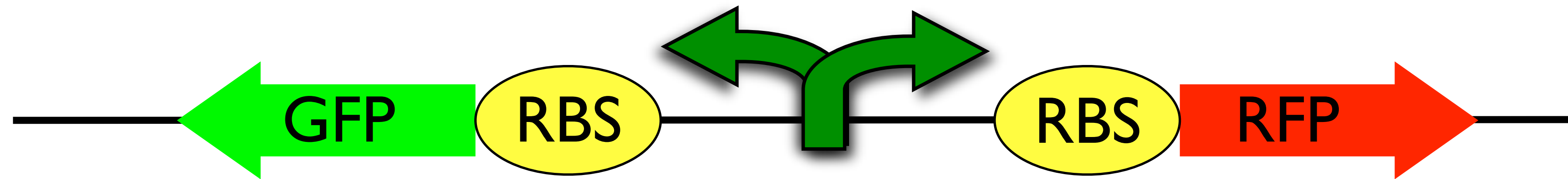
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J119137



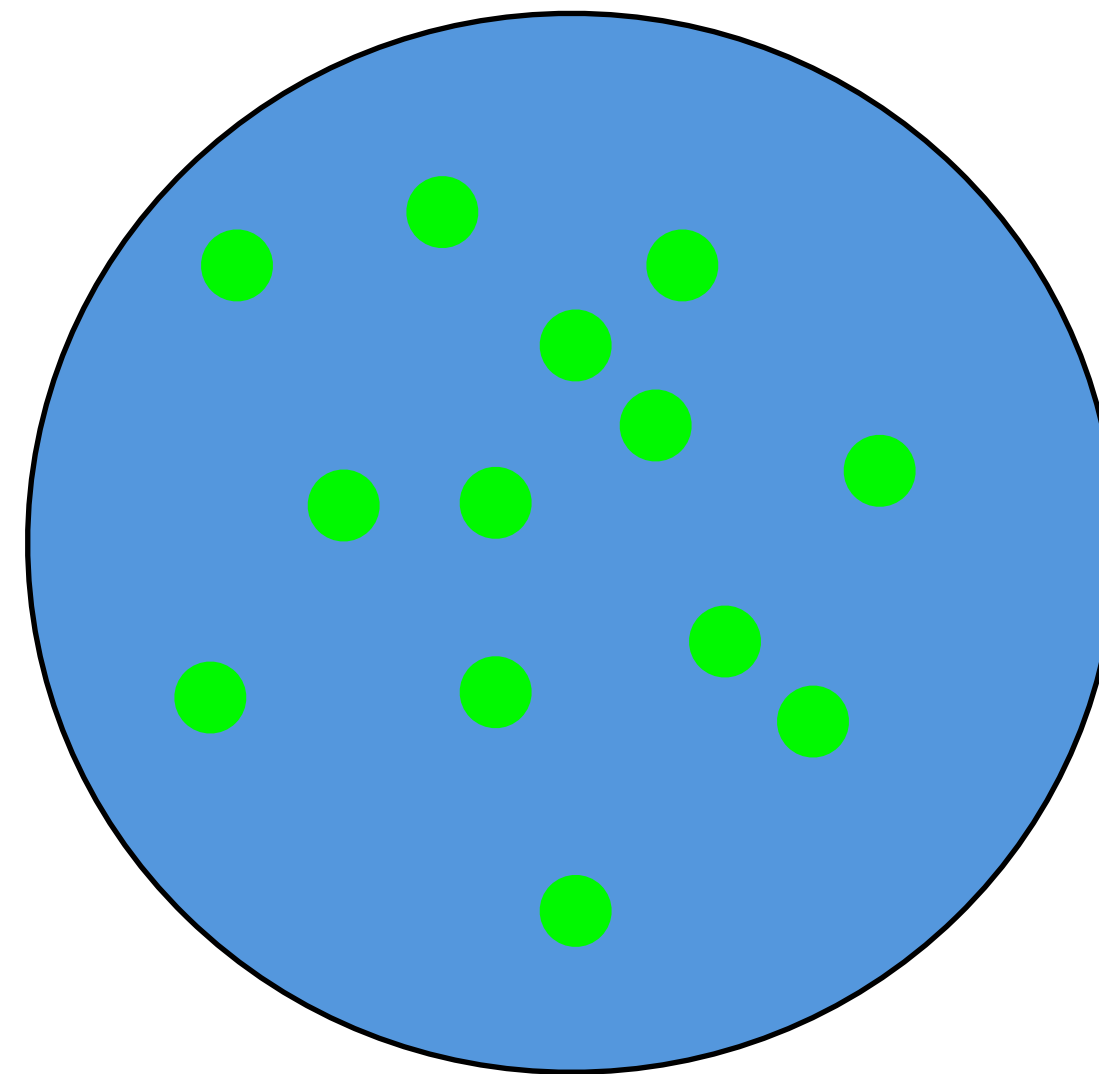
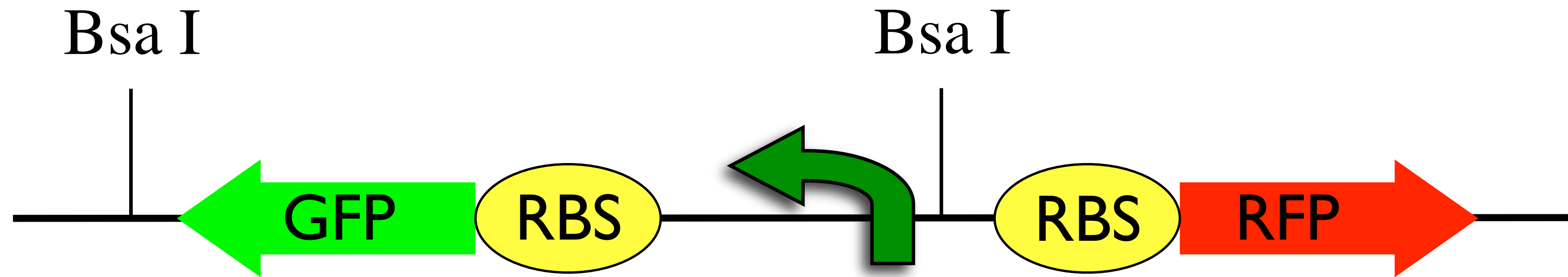
# New Versions of Plasmids

J119137



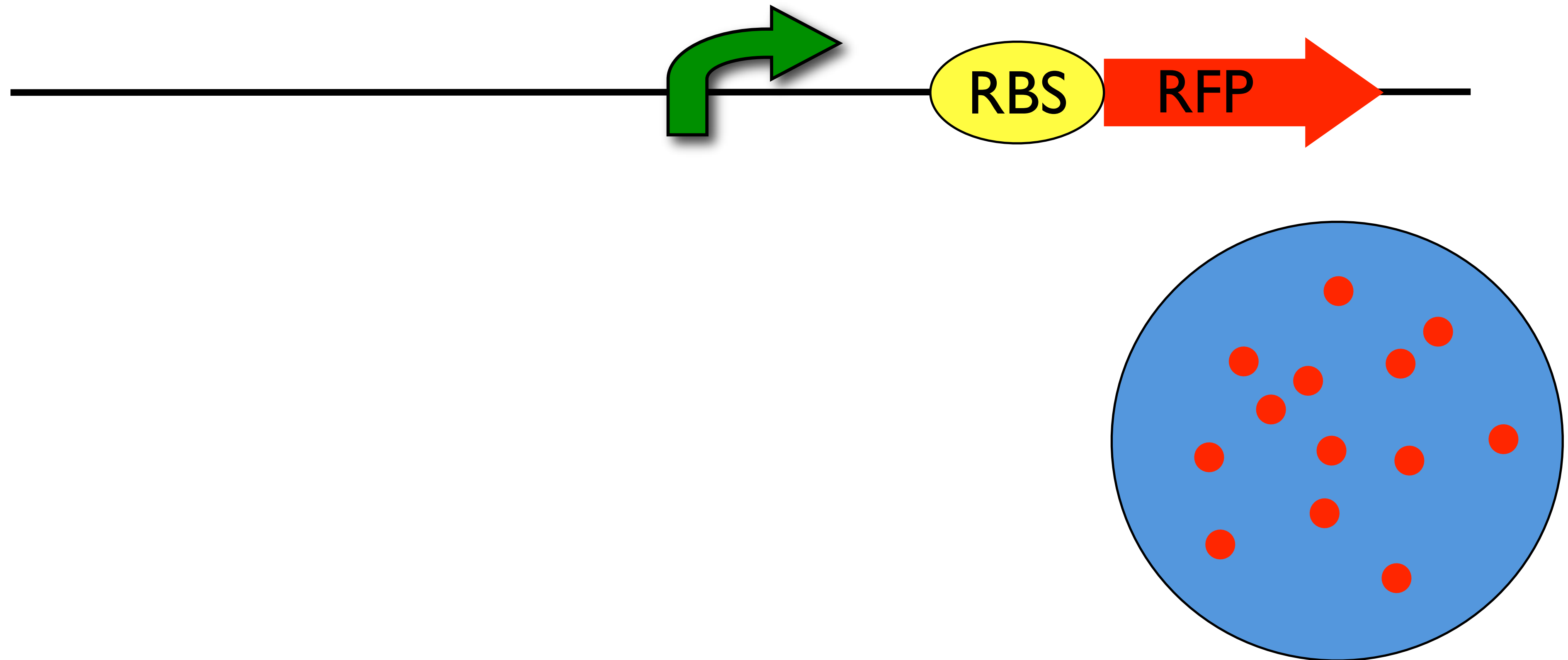
# New Versions of Plasmids

J119138



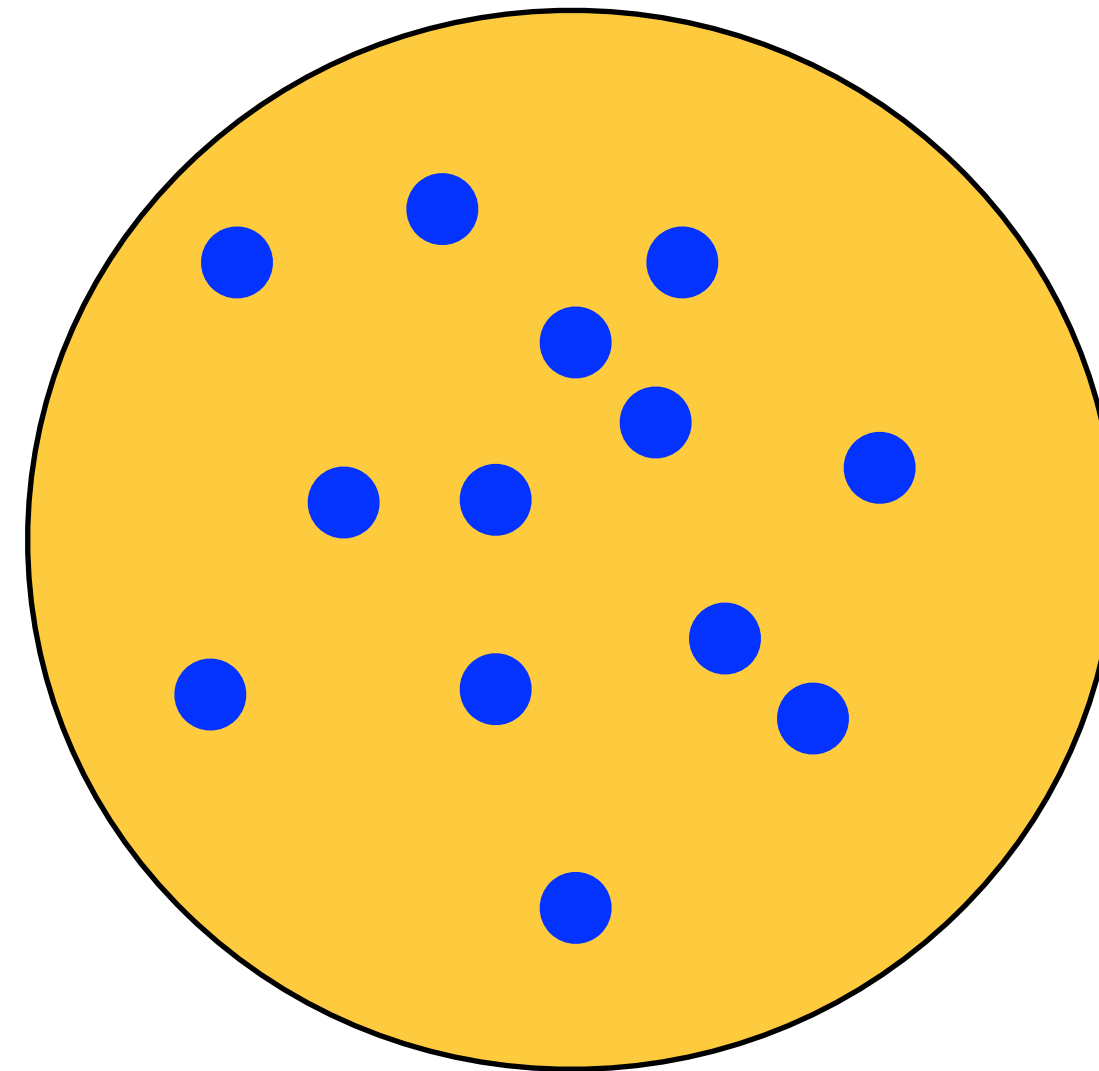
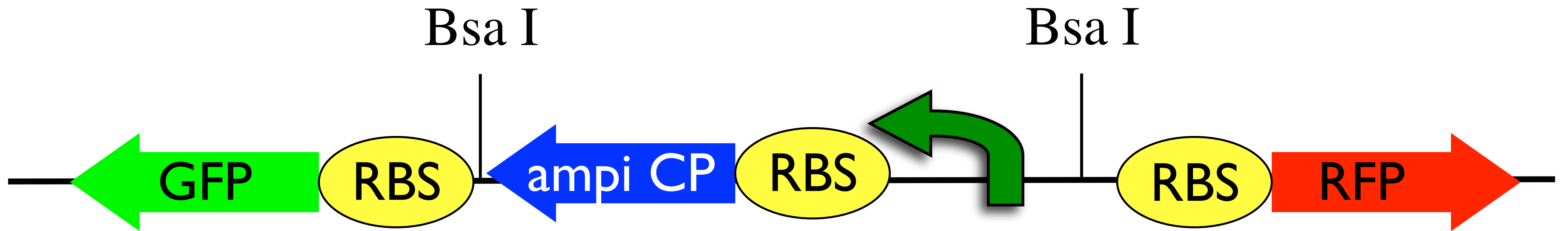
# New Versions of Plasmids

J119138



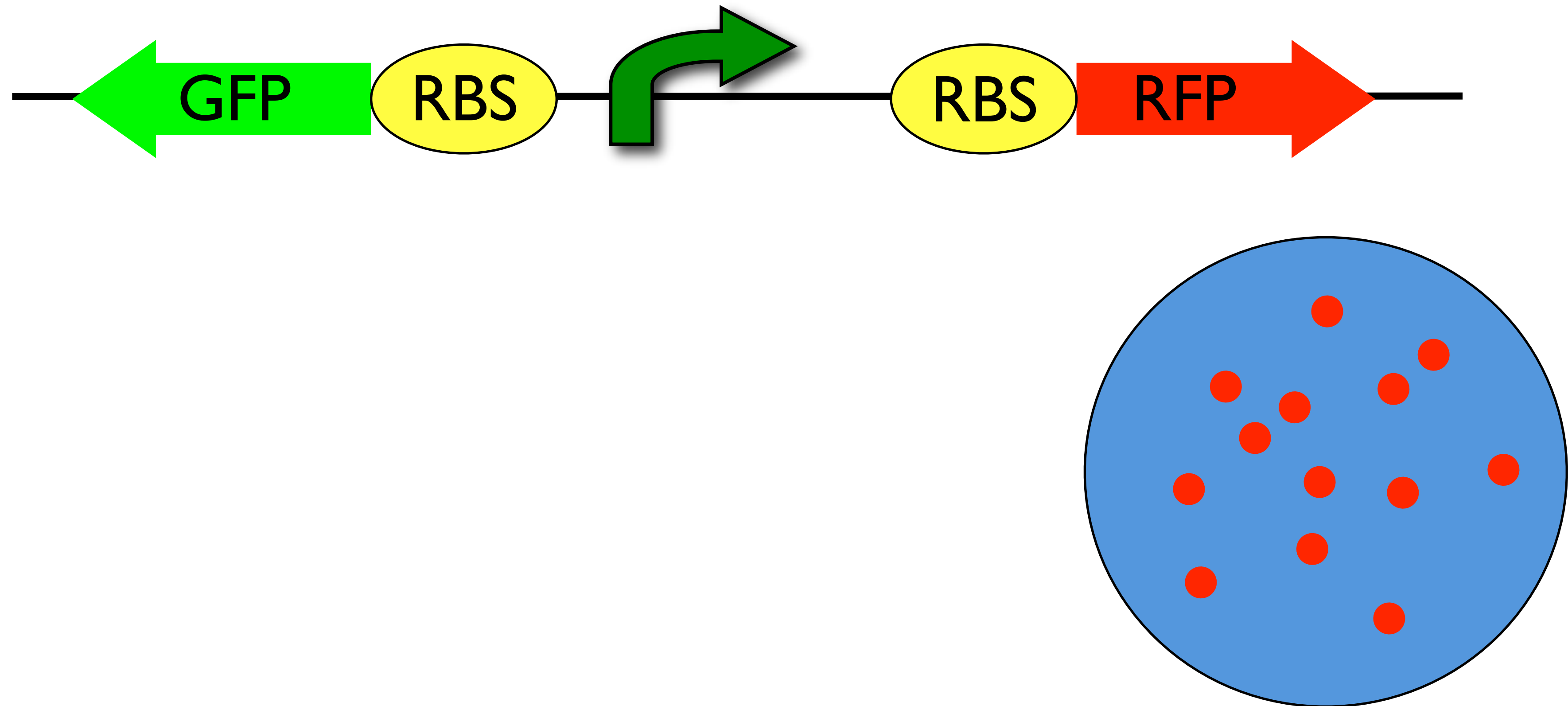
# New Versions of Plasmids

J119139



# New Versions of Plasmids

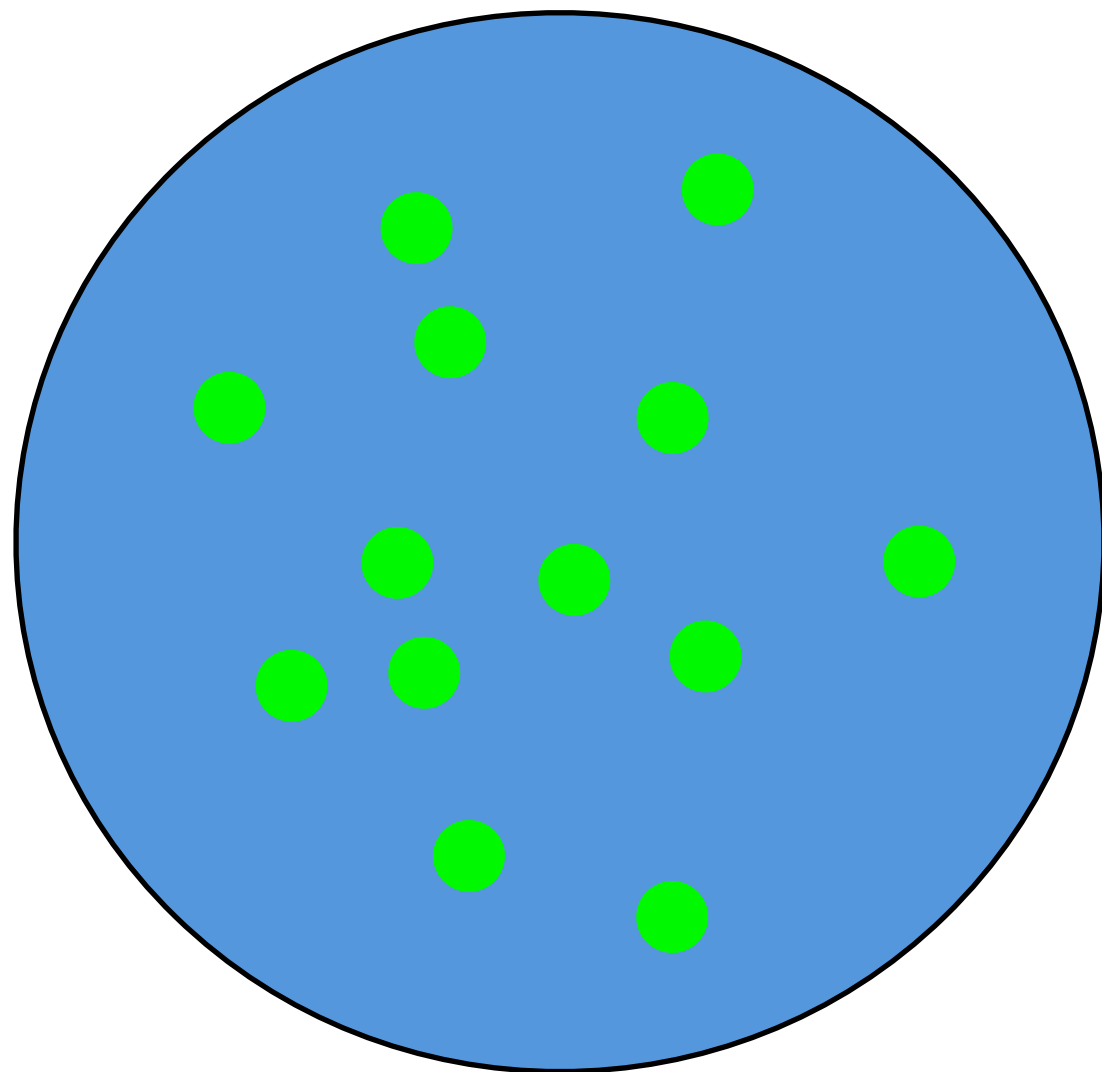
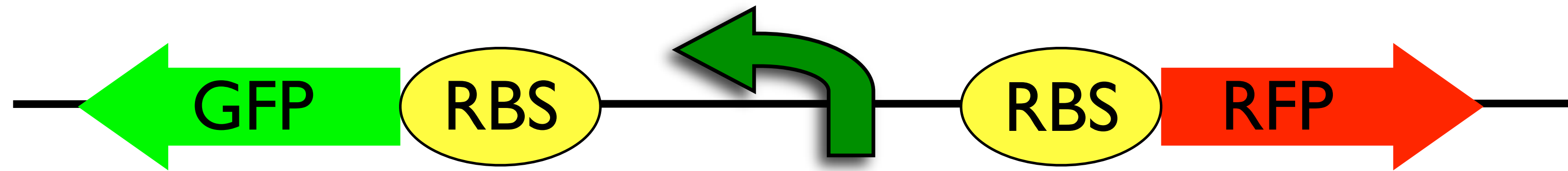
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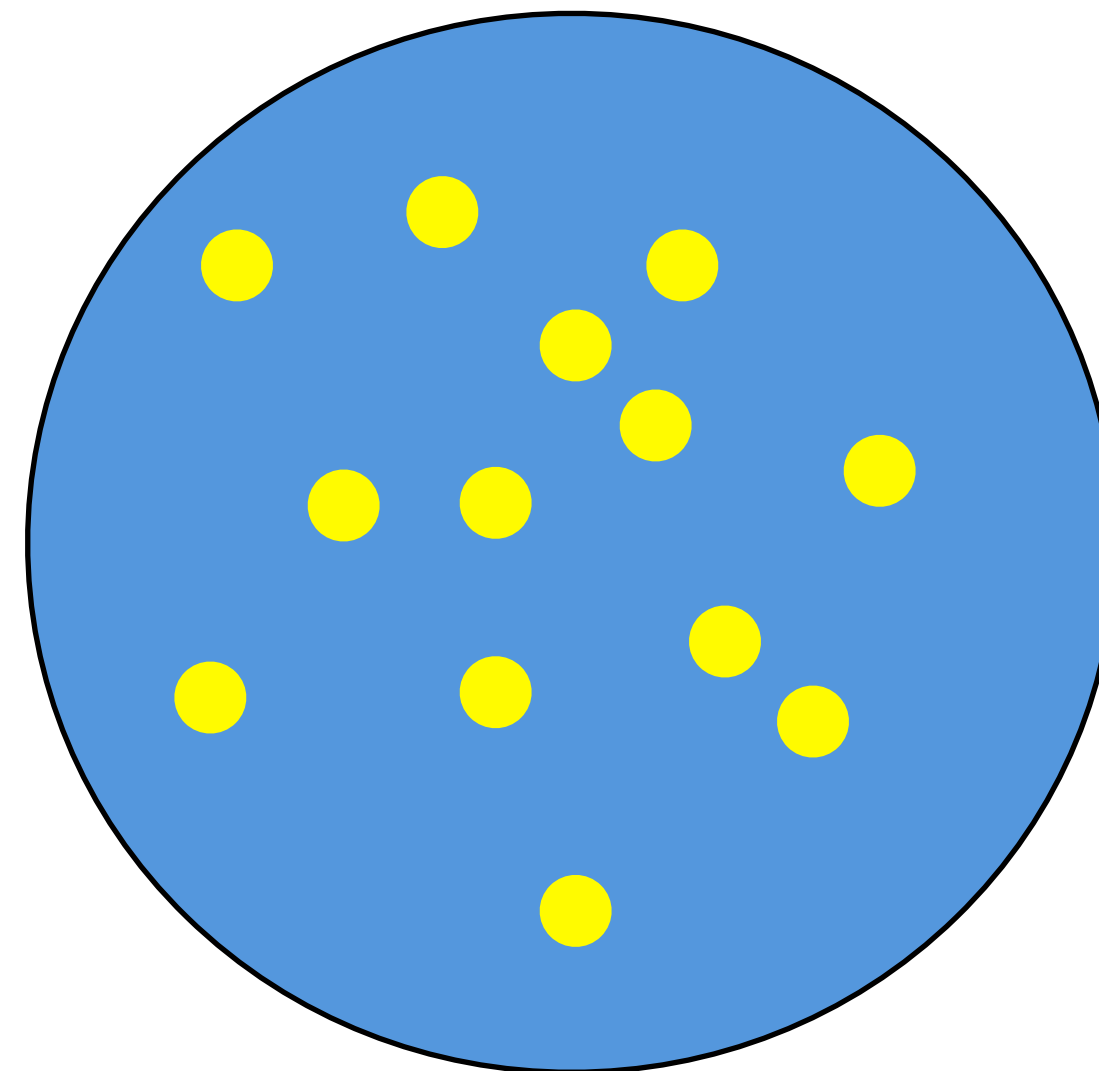
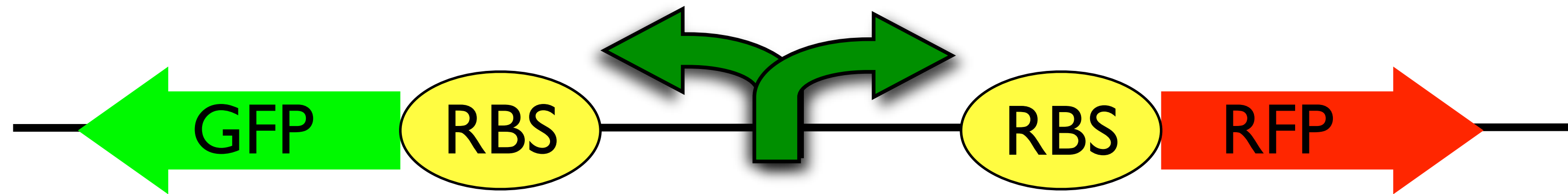
# New Versions of Plasmids

J119139



# New Versions of Plasmids

J119139



**Can undergraduates do  
cutting-edge research?**

# Collaborative 2012 Research Team



# Davidson 2012 Research Team



# Three Rules for Student Research

1. Everyone must learn.



# Three Rules for Student Research

1. Everyone must learn.

2. Everyone must have fun.



# Three Rules for Student Research

1. Everyone must learn.
2. Everyone must have fun.
3. We try to contribute to science.

**1. Research** [Open Access](#) [Highly accessed](#)  
51699 **Solving a Hamiltonian Path Problem with a bacterial computer**  
Accesses Jordan Baumgardner, Karen Acker, Oyinade Adefuye, Samuel Crowley, Will DeLoache, James Heard, Andrew T Martens, Nickolaus Morton, Michelle Ritter, Amber Shoecraft, Jessica Treece, Amanda Valencia, Mike Waters, A Malcolm Campbell, Laurie J Heyer, Jeffrey L Poet, Todd T Eck  
*Journal of Biological Engineering* 2009, **3**:11 (24 July 2009)  
[Abstract](#) | [Full text](#) | [PDF](#) | [PubMed](#) | [F1000 Biology](#) | [▶ Editor's summary](#)



JOURNAL OF BIOLOGICAL  
ENGINEERING

**2. Research** [Open Access](#) [Highly accessed](#)  
42125 **Engineering bacteria to solve the Burnt Pancake Problem**  
Accesses Karmella A Haynes, Marian L Broderick, Adam D Brown, Trevor L Butner, James O Dickson, W Lance Harden, Lane H Heard, Eric L Jessen, Kelly J Malloy, Brad J Ogden, Sabriya Rosemond, Samantha Simpson, Erin Zwack, A Malcolm Campbell, Todd T Eckdahl, Laurie J Heyer, Jeffrey L Poet  
*Journal of Biological Engineering* 2008, **2**:8 (20 May 2008)  
[Abstract](#) | [Full text](#) | [PDF](#) | [PubMed](#) | [1 comment](#) | [▶ Editor's summary](#)

**25 undergraduate co-authors**

**3. Methodology** [Open Access](#) [Highly accessed](#)  
27364 **Engineering BioBrick vectors from BioBrick parts**  
Accesses Reshma P Shetty, Drew Endy, Thomas F Knight  
*Journal of Biological Engineering* 2008, **2**:5 (14 April 2008)  
[Abstract](#) | [Full text](#) | [PDF](#) | [PubMed](#) | [Cited on BioMed Central](#)

**Papers of the year 2008 & 2009**



# Choose Projects Wisely

- design modular projects
- choose an inexpensive system
- avoid maintenance costs/time
- research groups  $\geq 4$  take less effort than  $\leq 3$



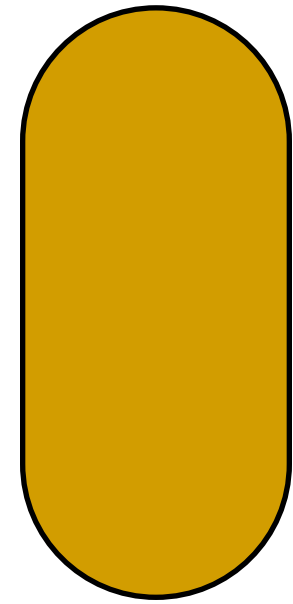
# Modular Programmed Evolution of *E.coli* for Optimization of Metabolic Pathways

Caroline Vrana, Ben Clarkson, Becca Evans, Betsy Gammon, Meredith Nakano, **Laurie J. Heyer, A. Malcolm Campbell**  
Davidson College, NC

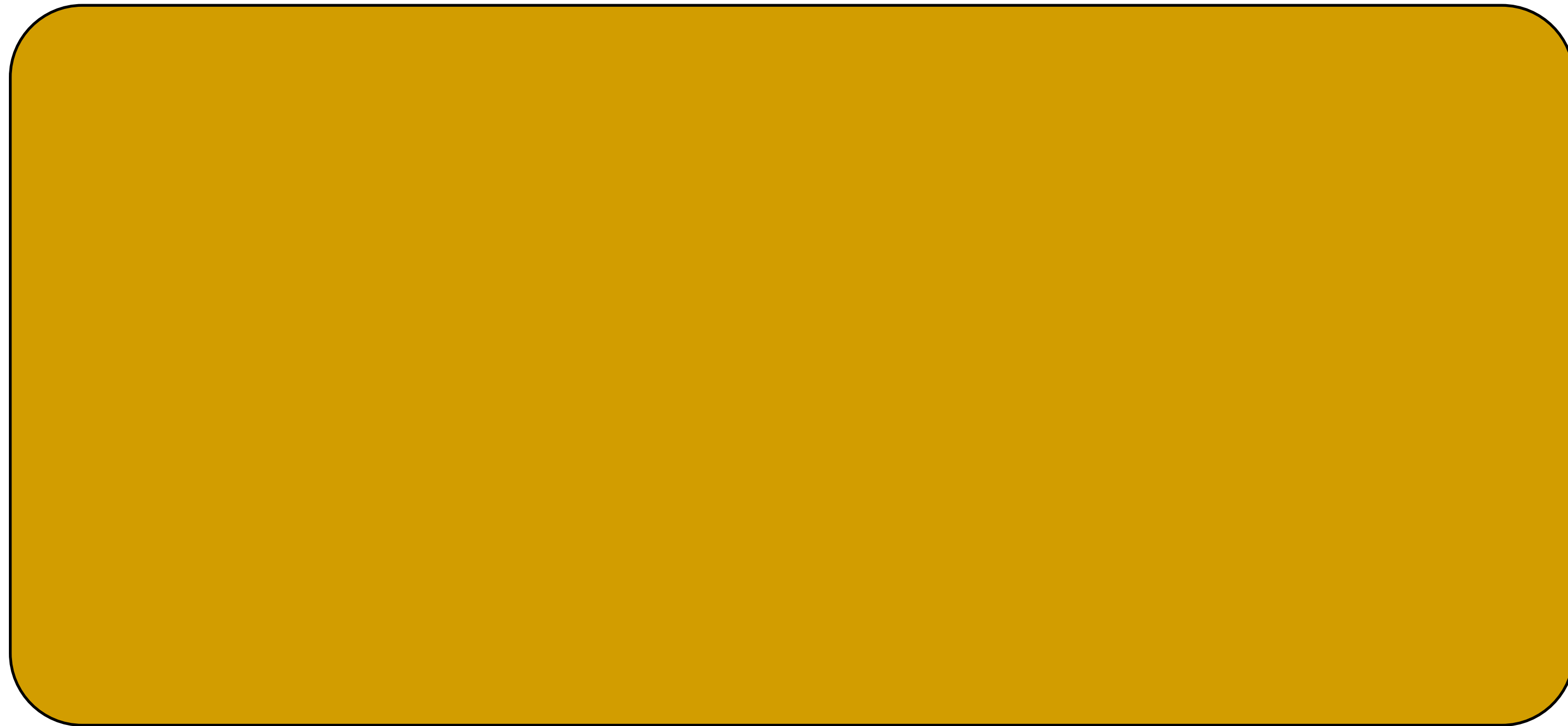
Caleb Carr, David Carr, Eddie Miles, Jerrad Morton, Sachith Polpitaya, Kamay Trueblood, **Jeffrey L. Poet, Todd T. Eckdahl**  
Missouri Western State University, MO



# Make *E. coli* Optimize Drug Production



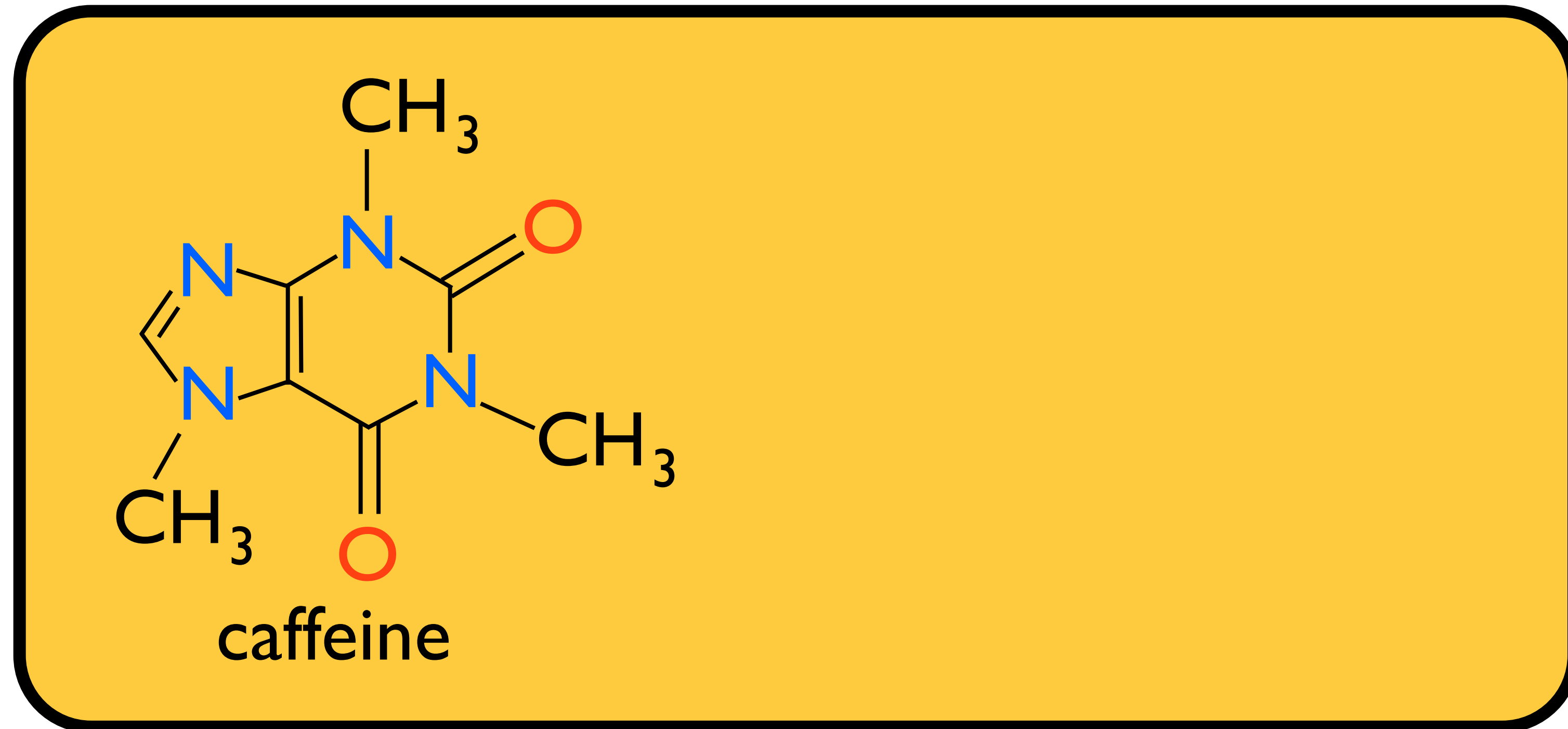
# Make *E. coli* Optimize Drug Production



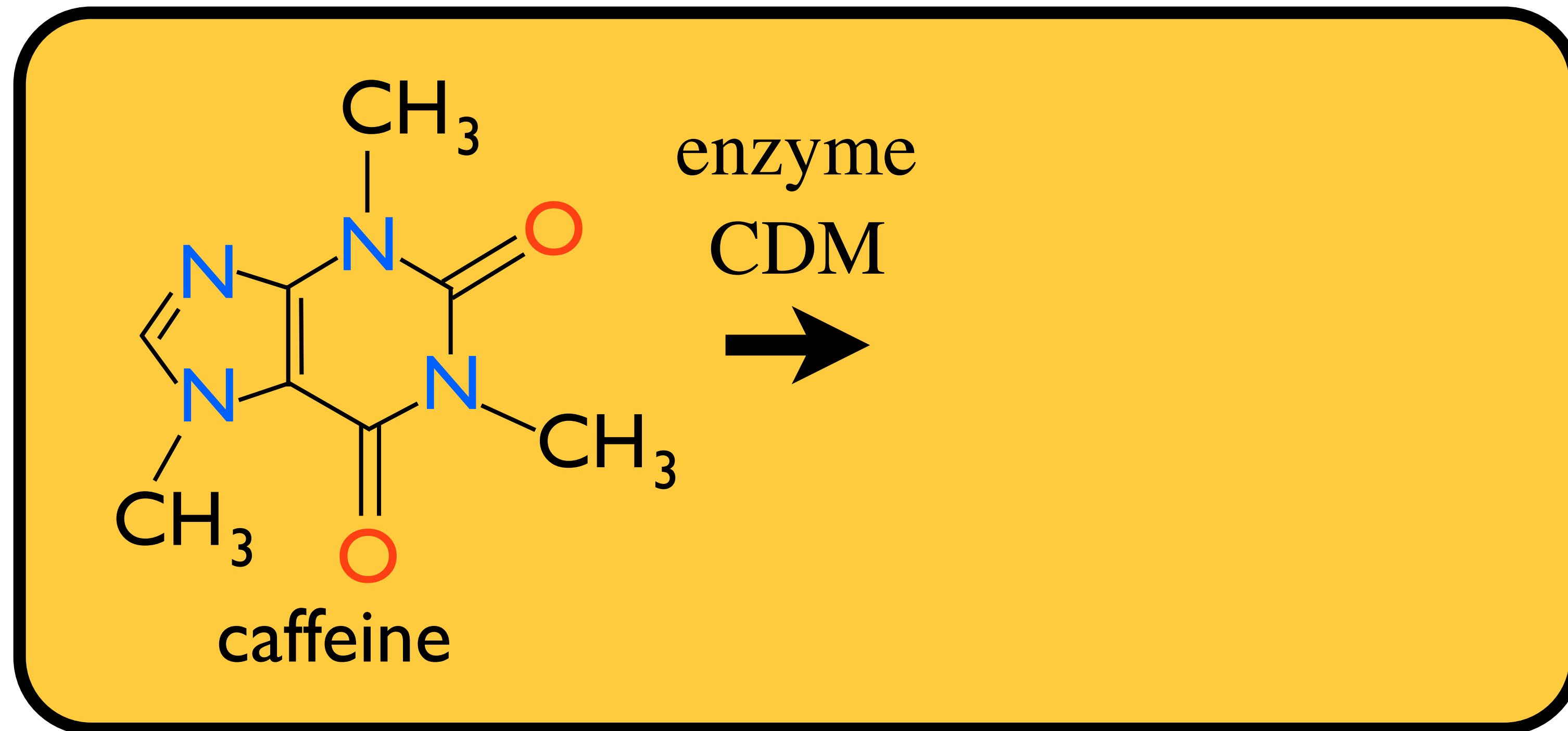
# Make *E. coli* Optimize Drug Production



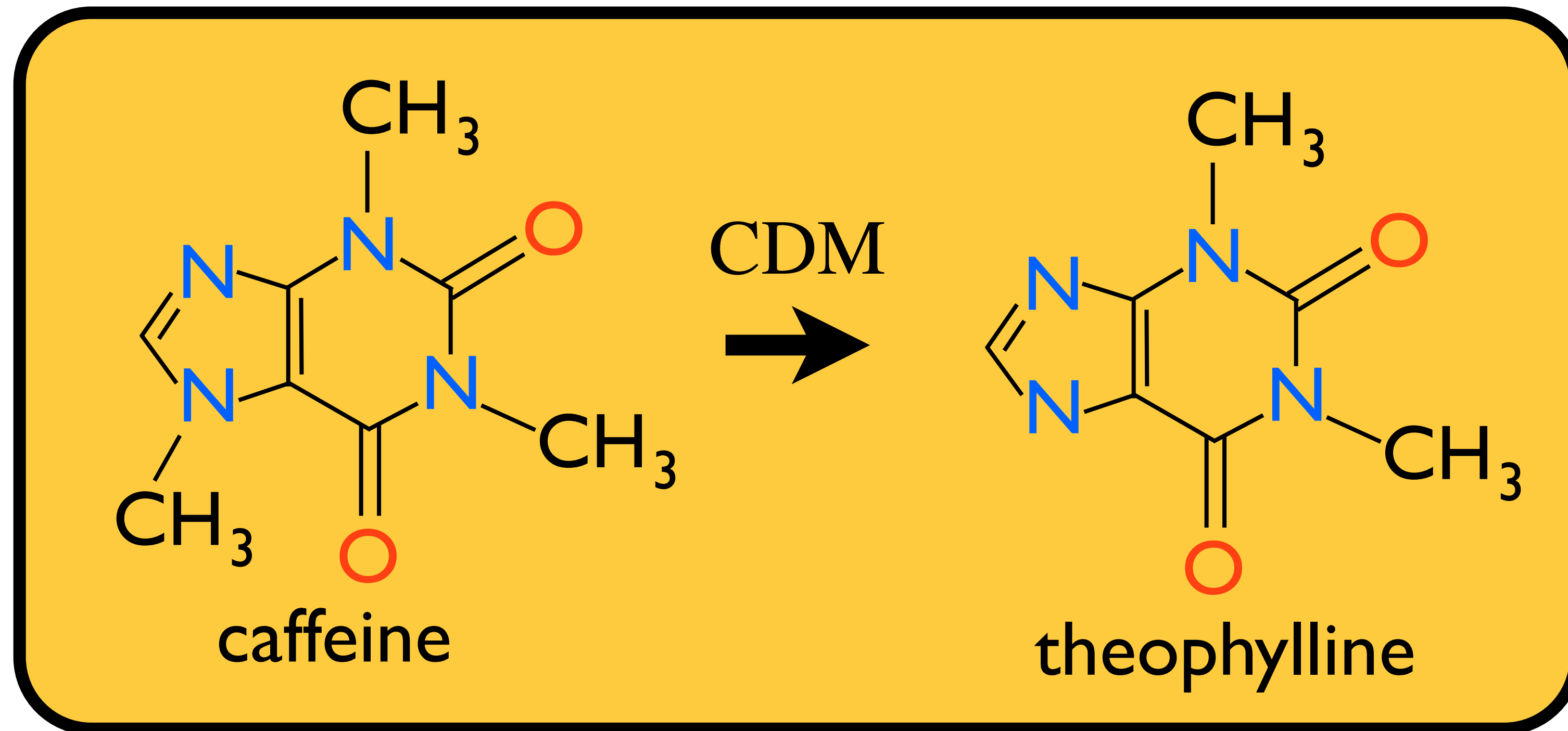
# Make *E. coli* Optimize Drug Production



# Make *E. coli* Optimize Drug Production



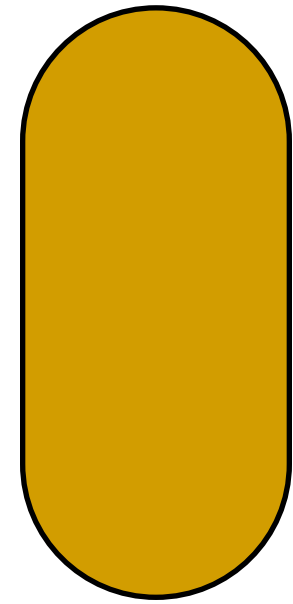
# Make *E. coli* Optimize Drug Production



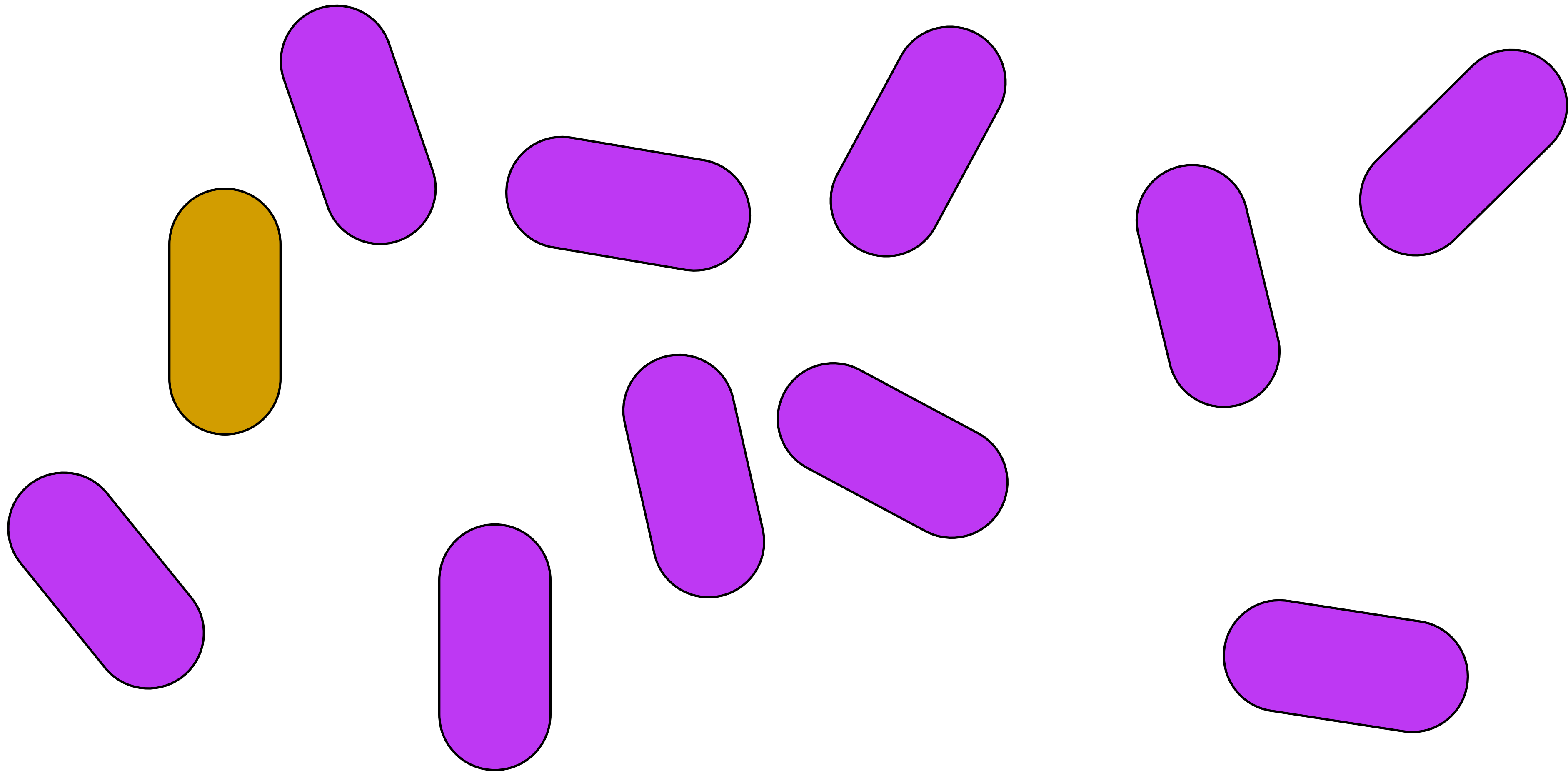
asthma medication



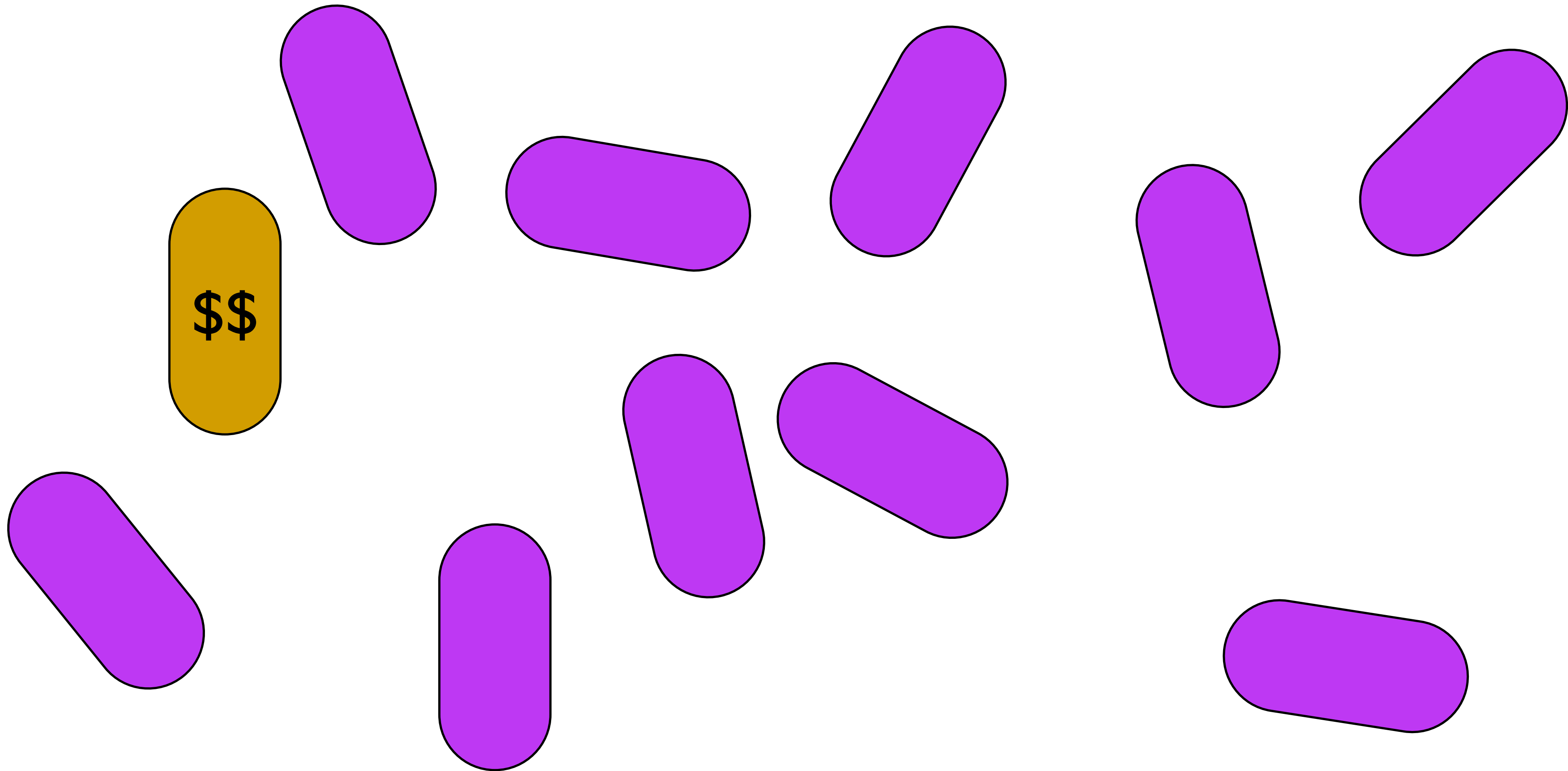
# What Makes Optimization Difficult?



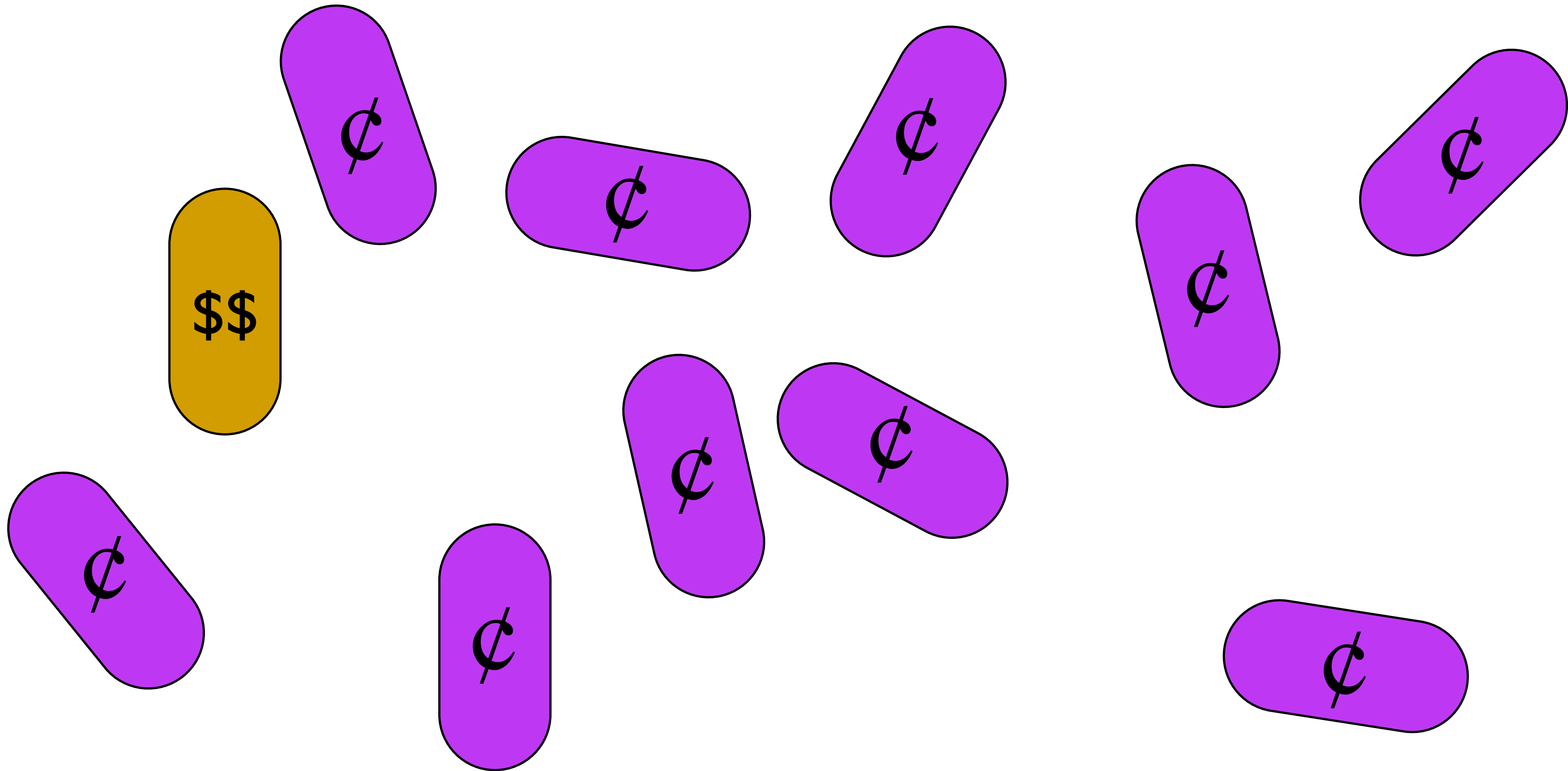
# What Makes Optimization Difficult?



# What Makes Optimization Difficult?



# Natural Selection



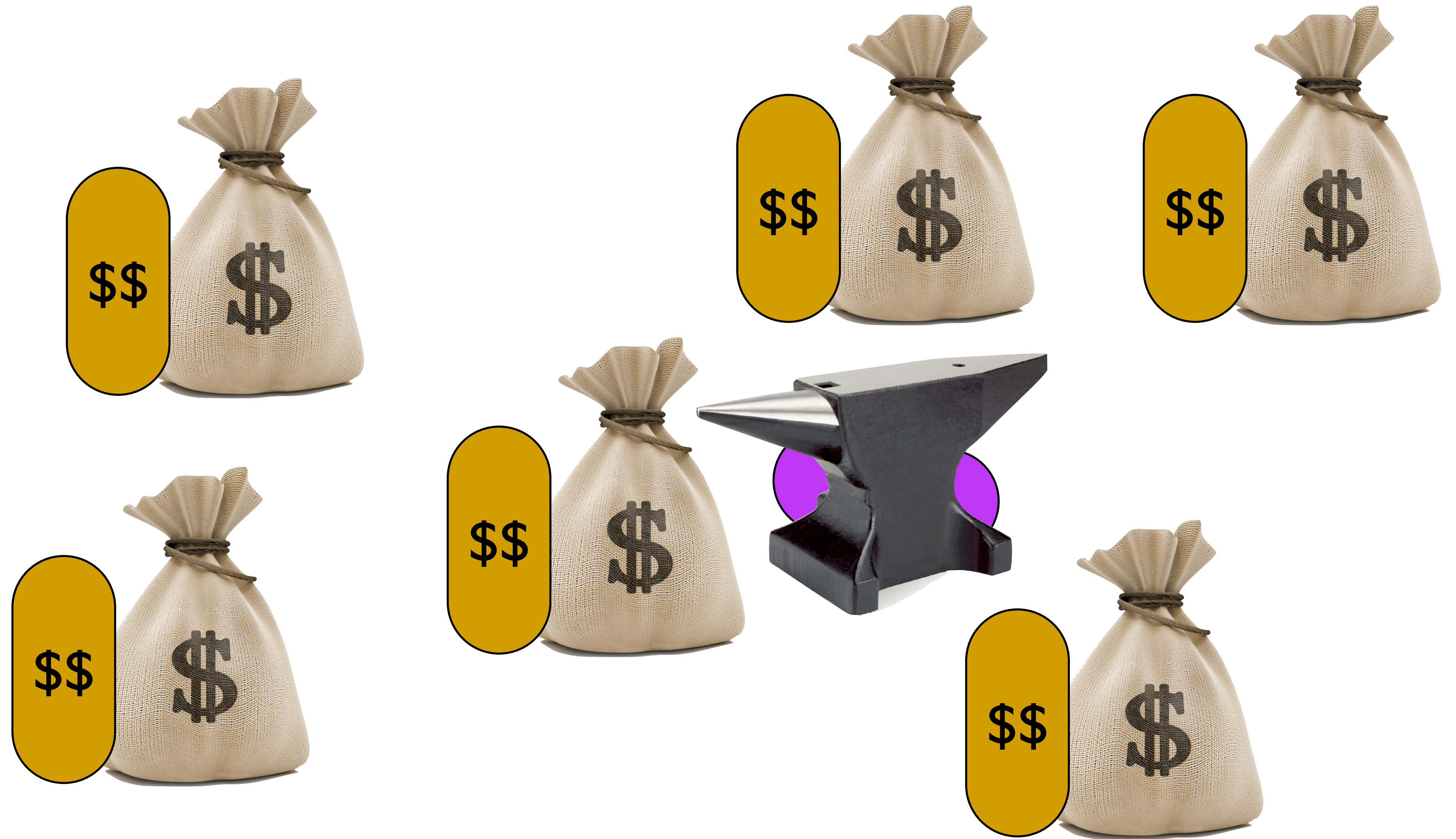
# Synthetic Selection



# Synthetic Fitness



# Synthetic Fitness



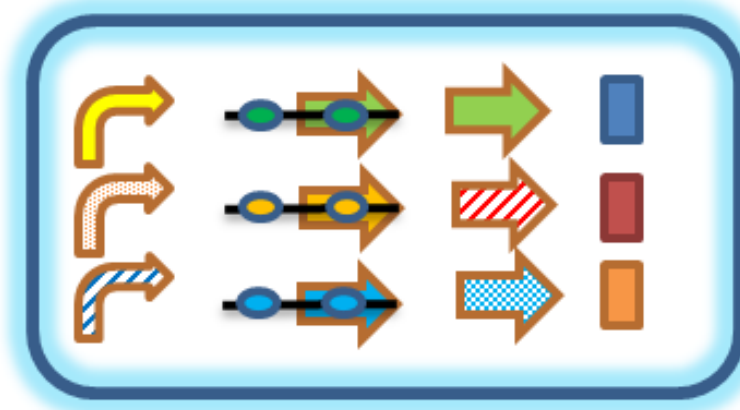
# Engineering Programmed Evolution



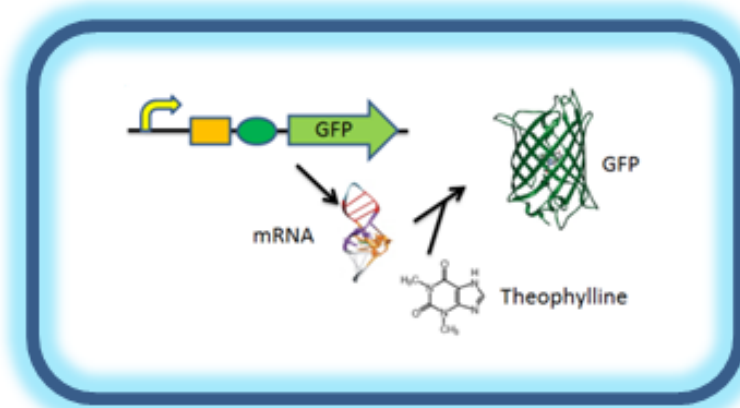
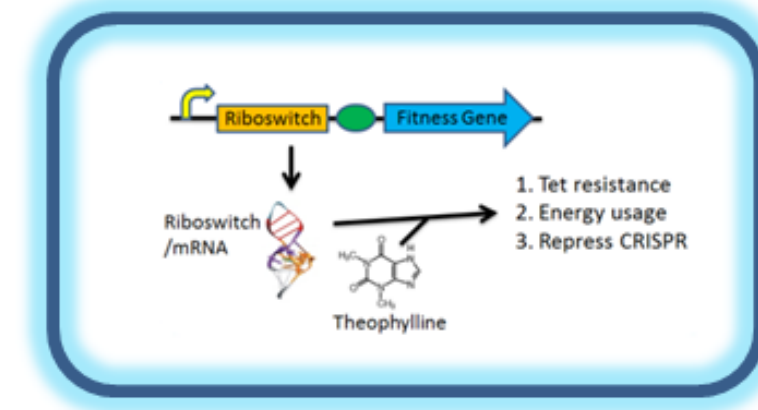


# Programmed Evolution

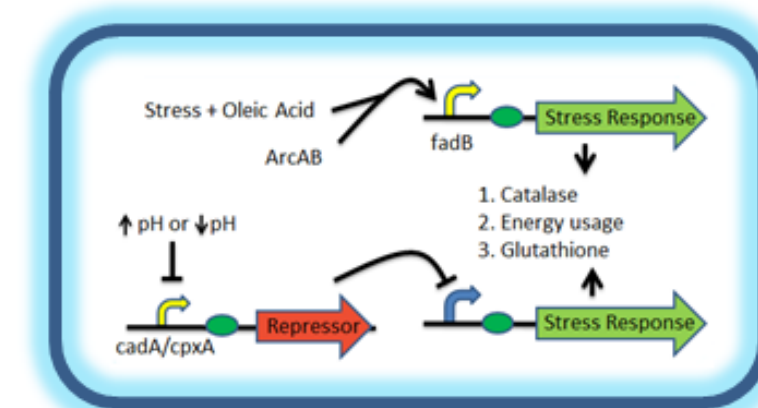
Combinatorics Module



Fitness Module



Biosensor Module



Stress Response Module

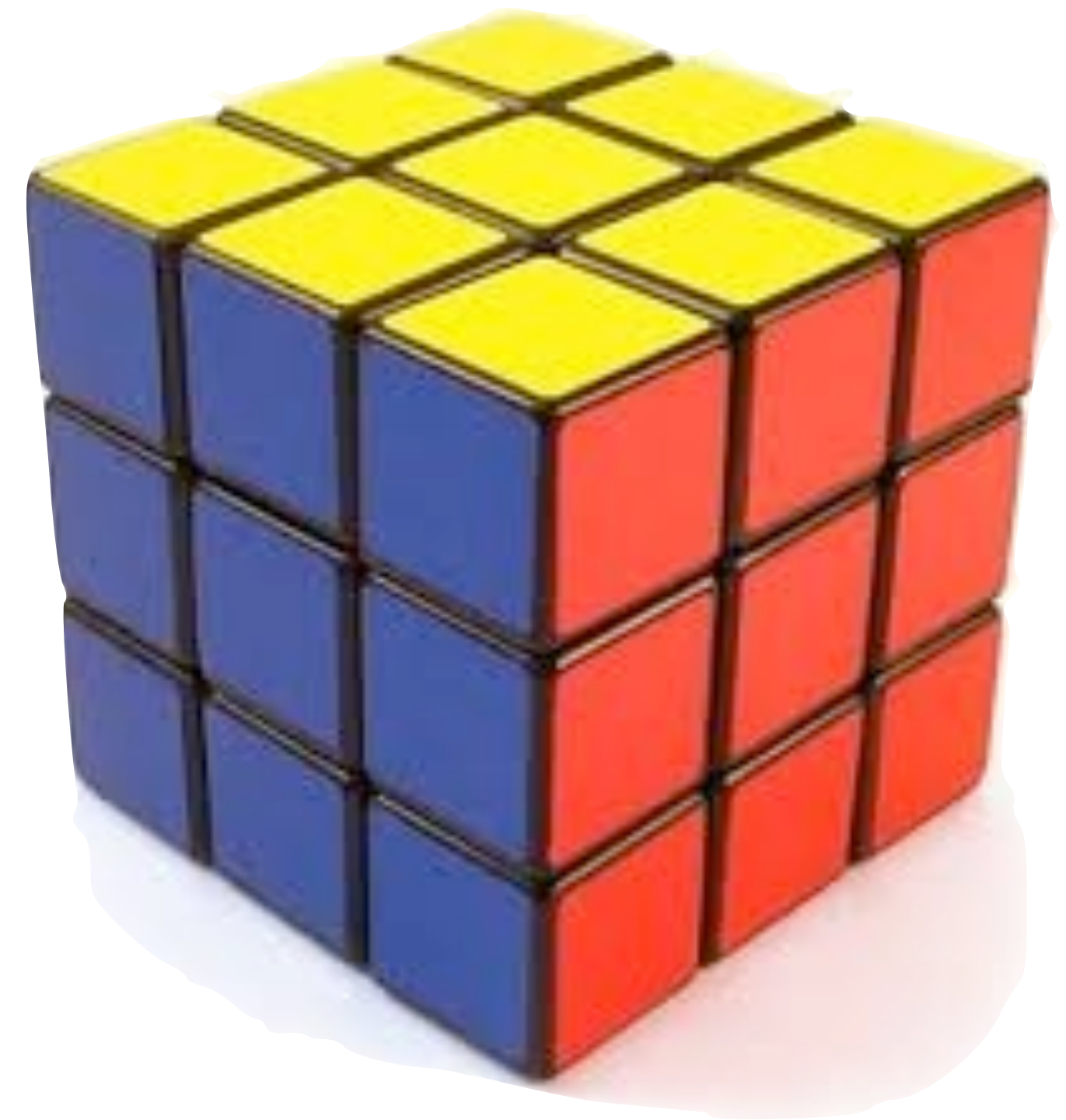


# Math Modeling of Programmed Evolution

metabolic flux =  $f(\text{promoter, RBS, alleles, degradation tags})$



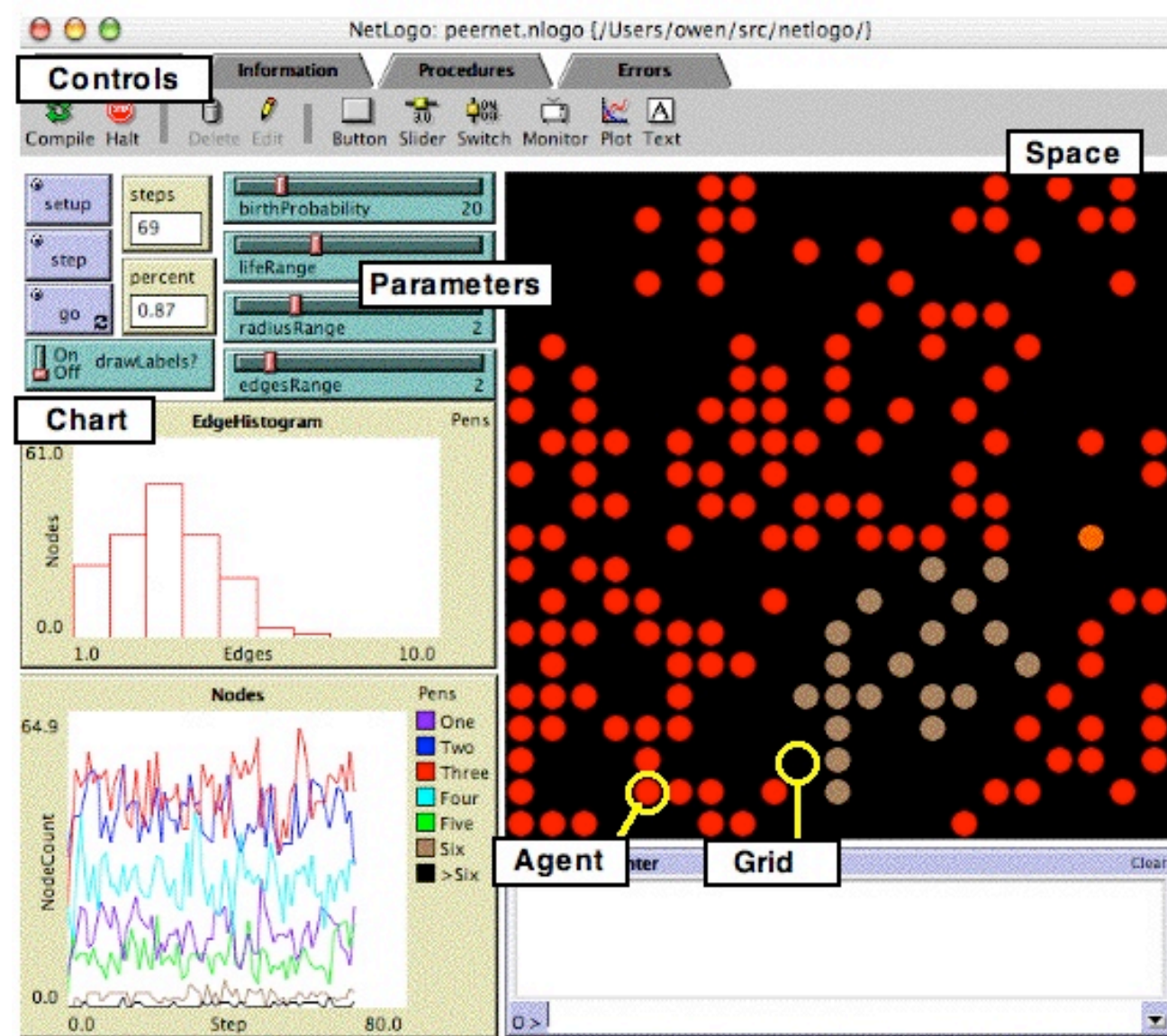
humans  
→  
bacteria



searching multi-dimensional space

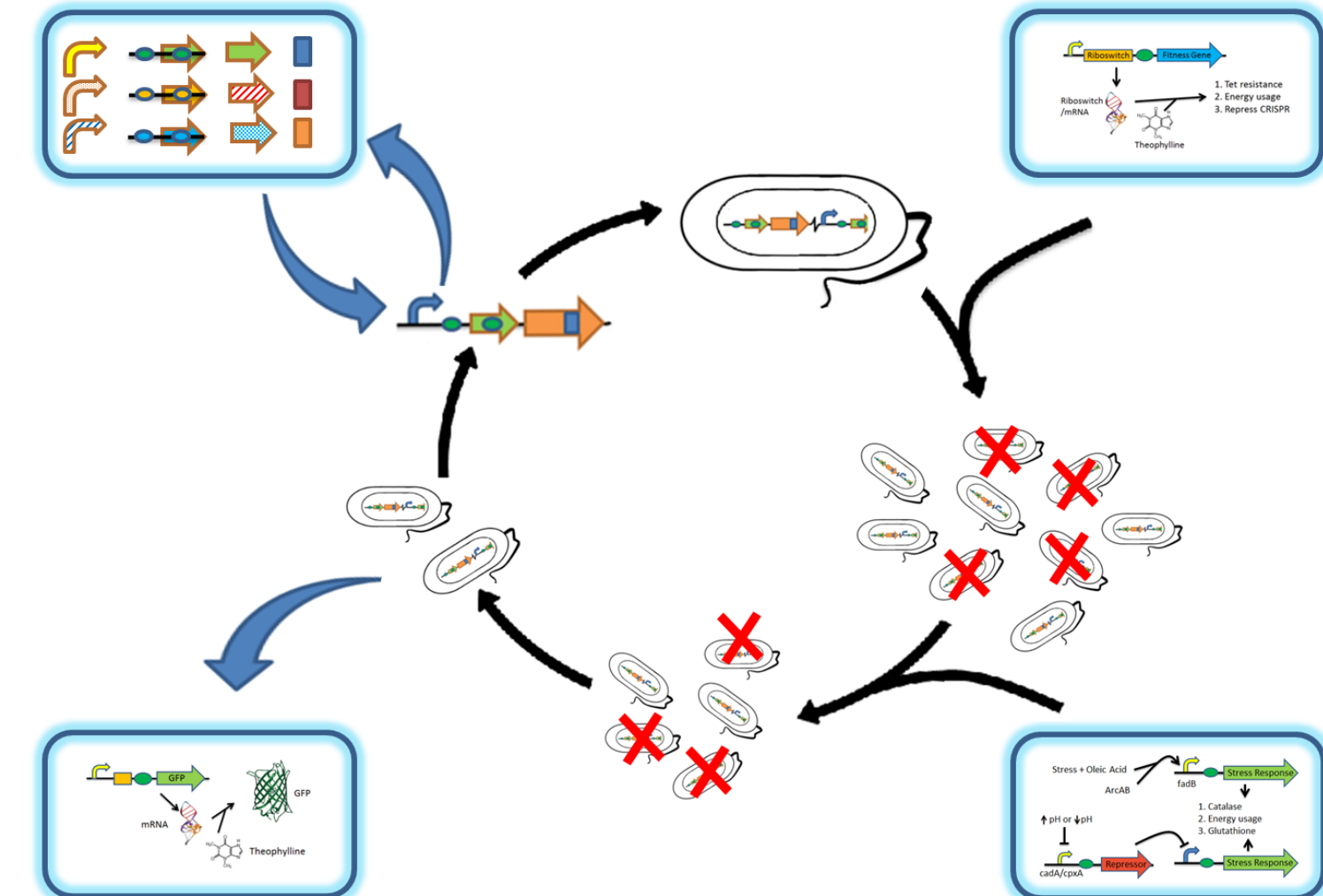
# Agent-Based Models of Programmed Evolution

NetLogo



Combinatorics Module

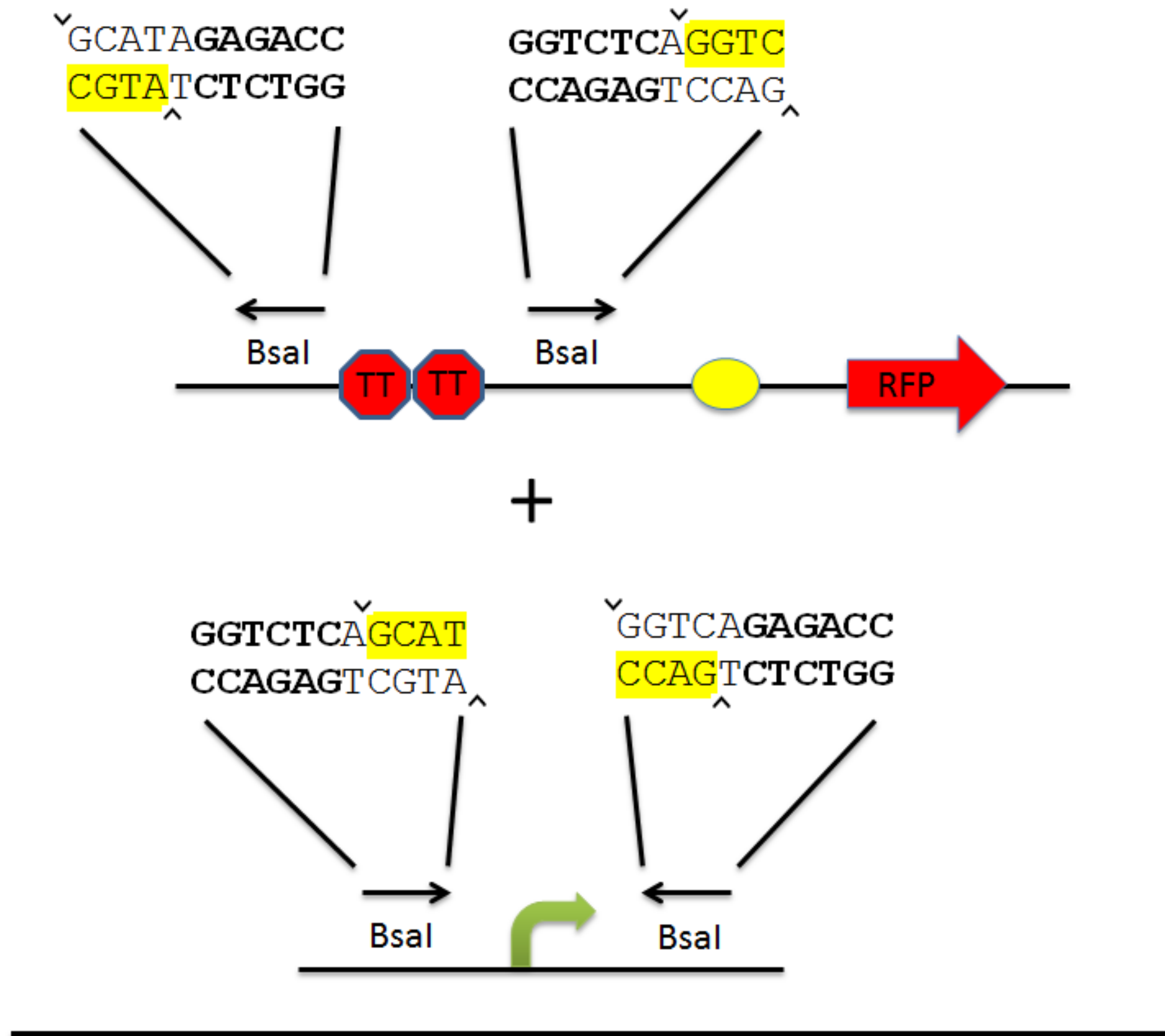
Fitness Module



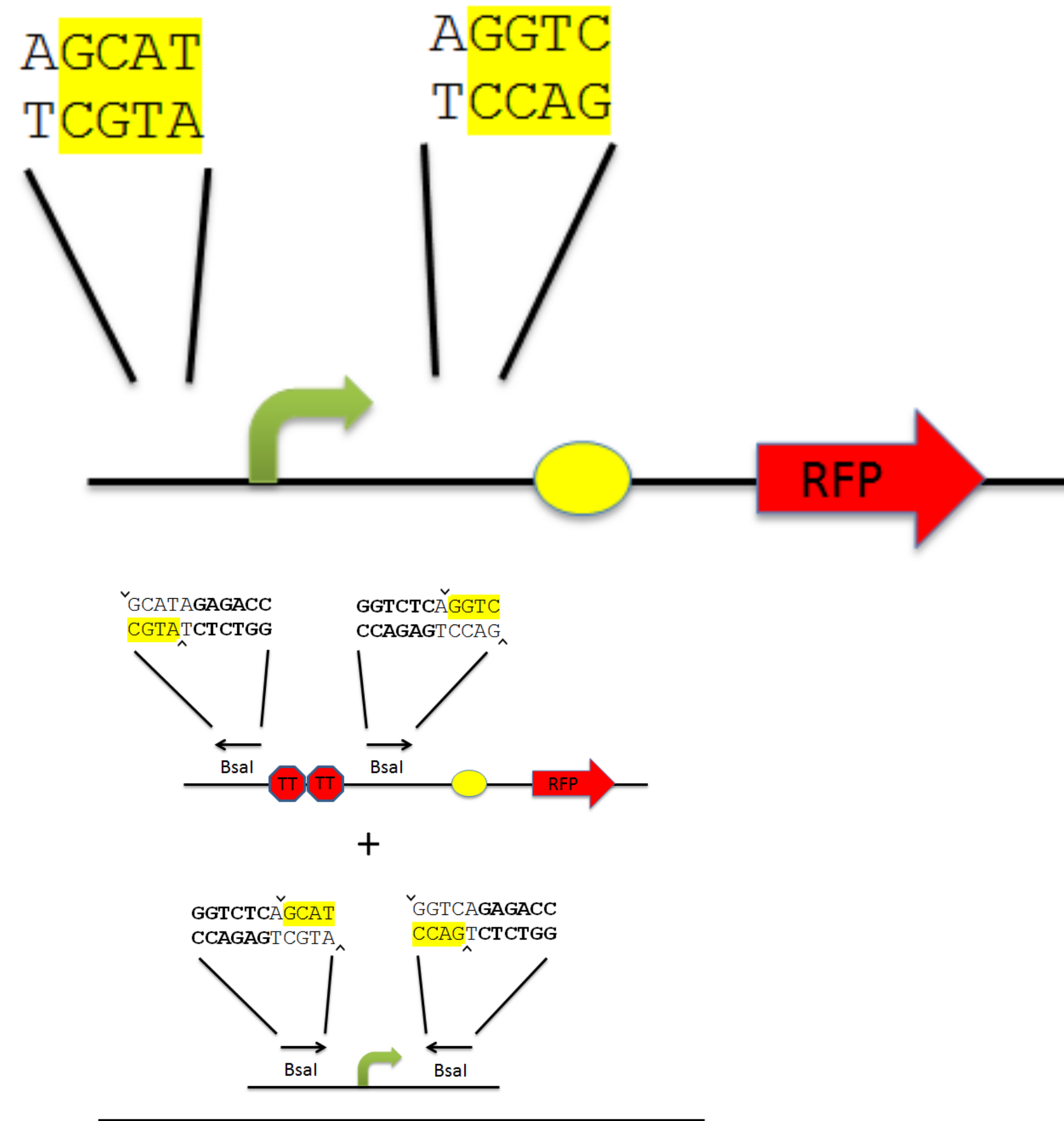
Biosensor Module

Stress Response Module

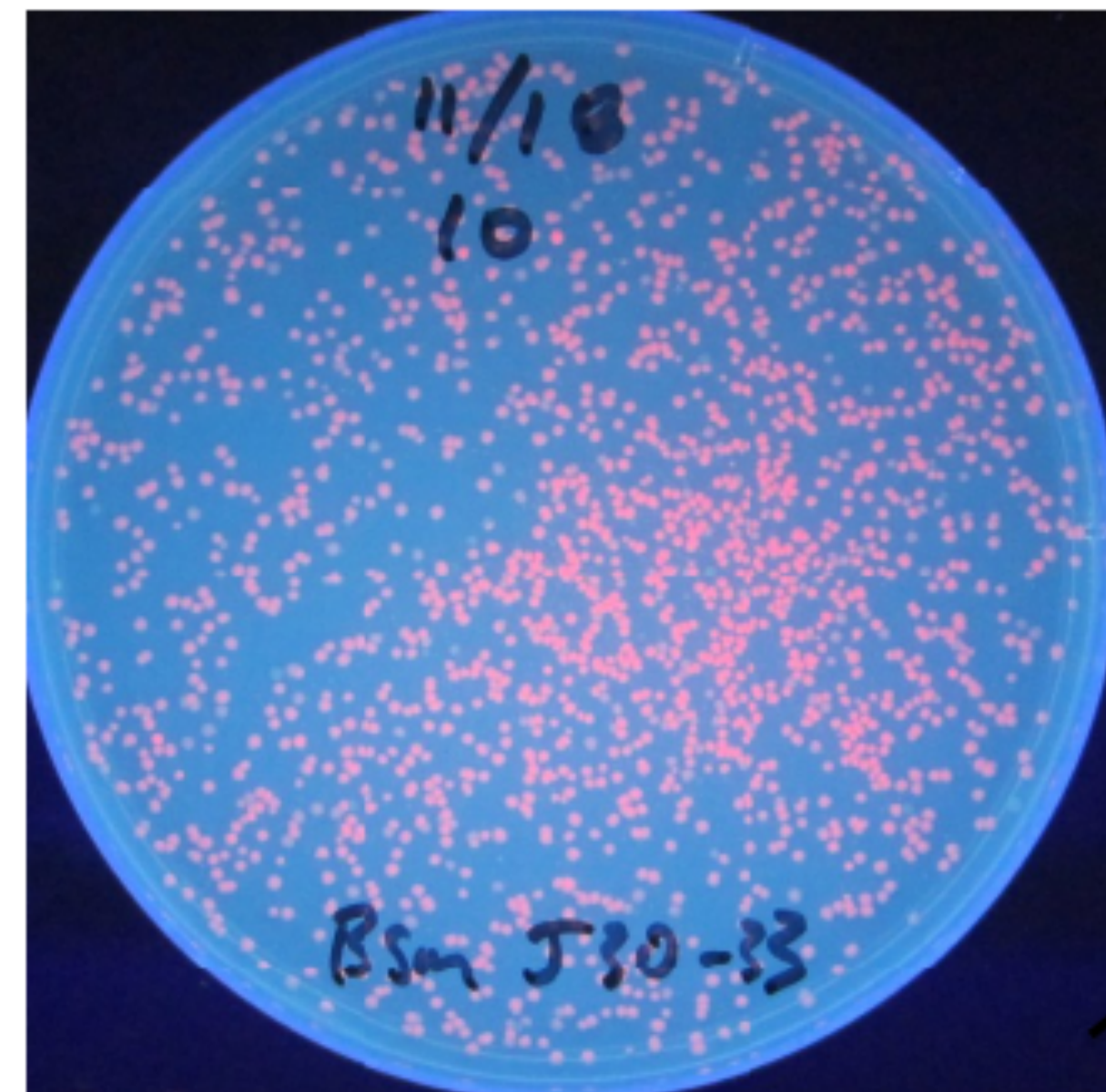
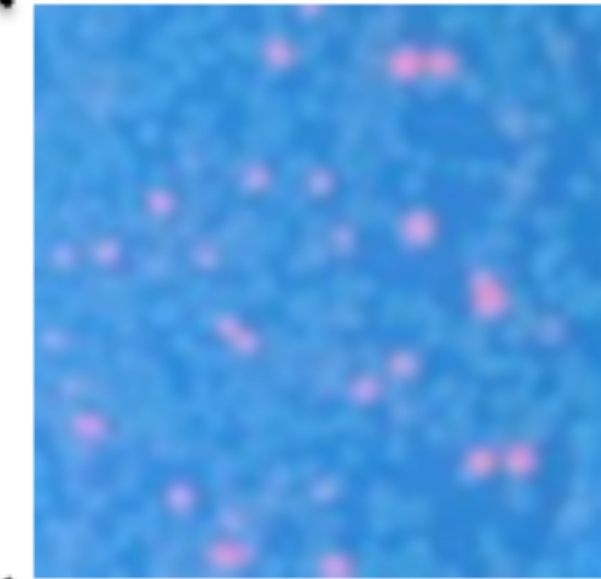
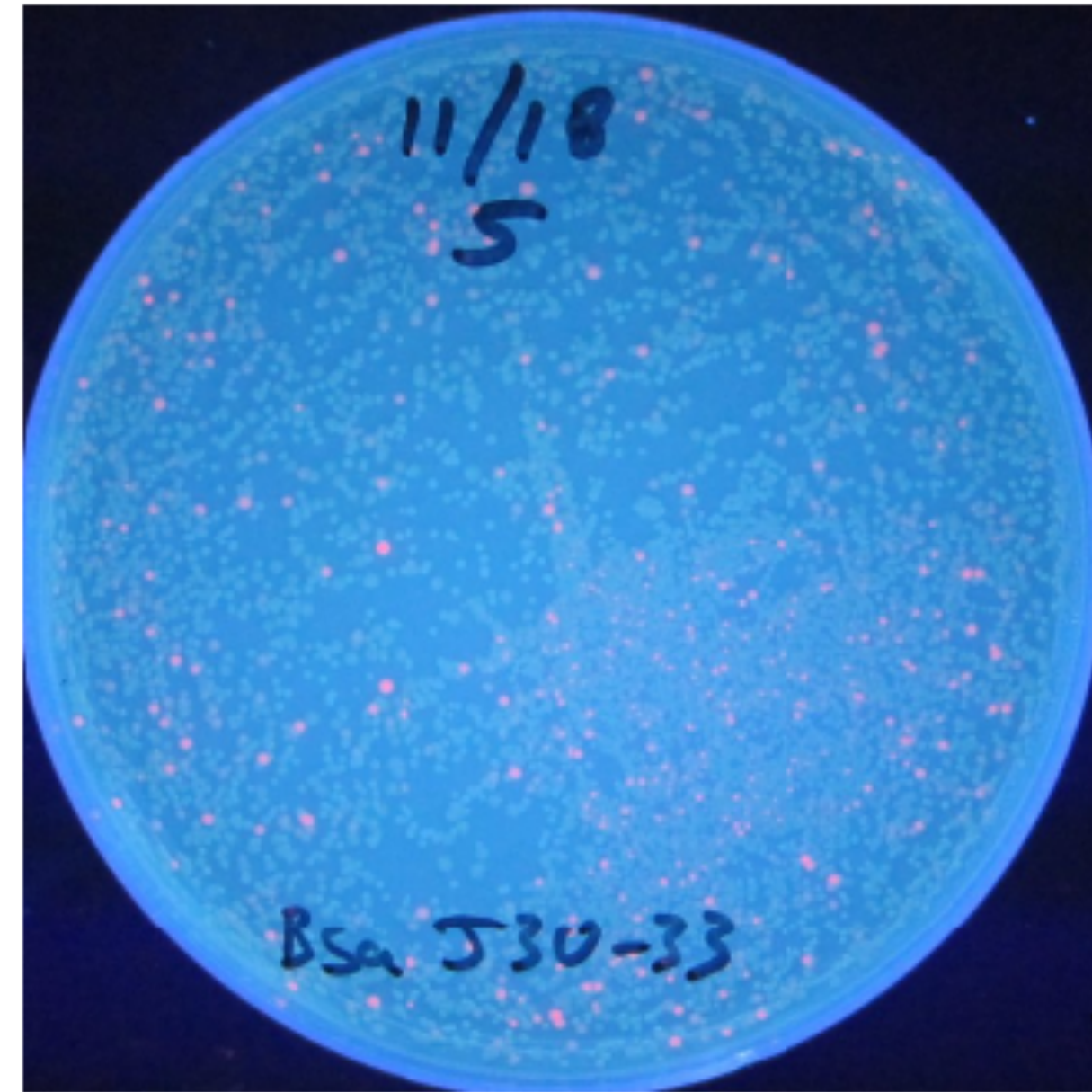
# Golden Gate Assembly of Parts



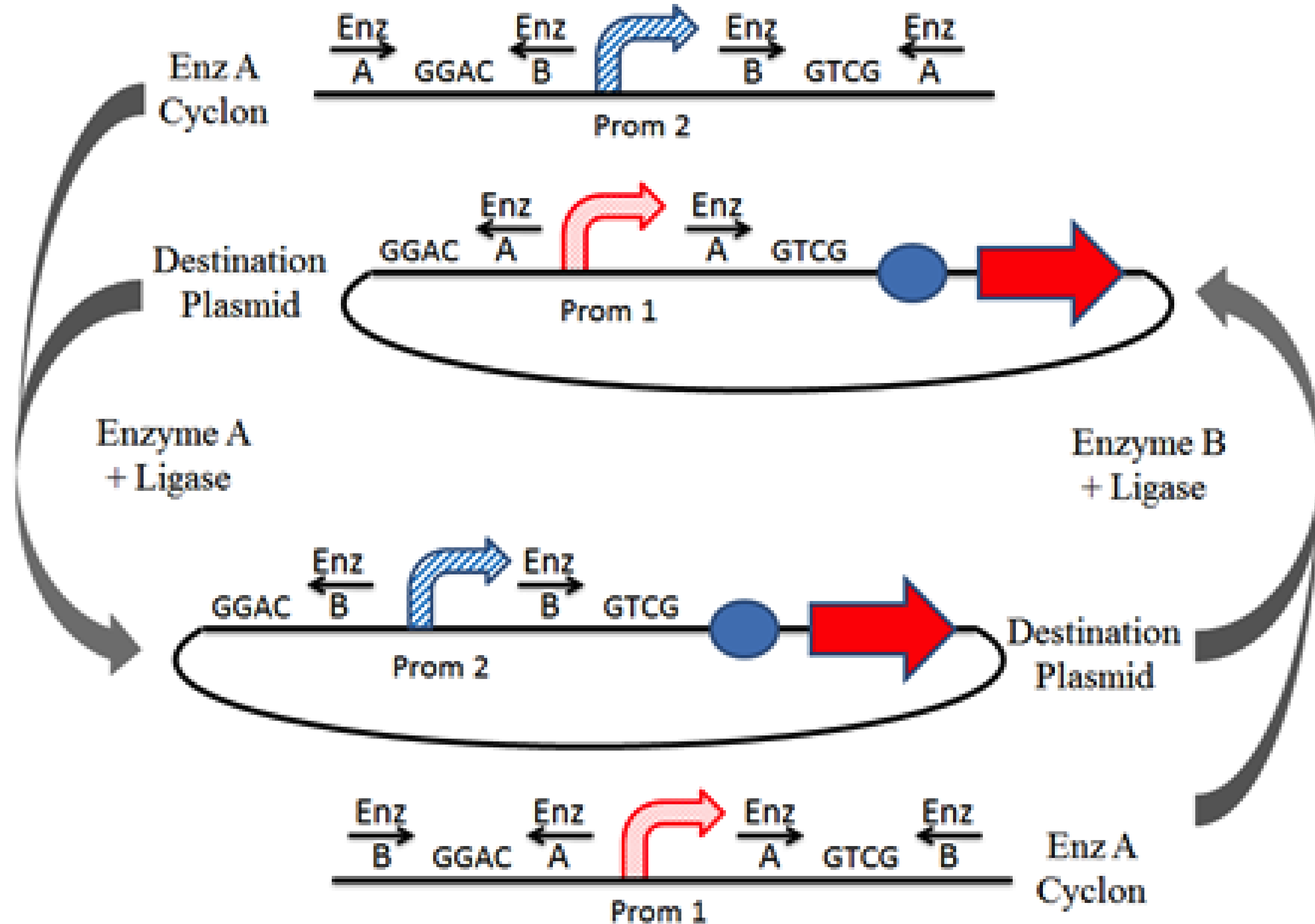
# Golden Gate Assembly of Parts



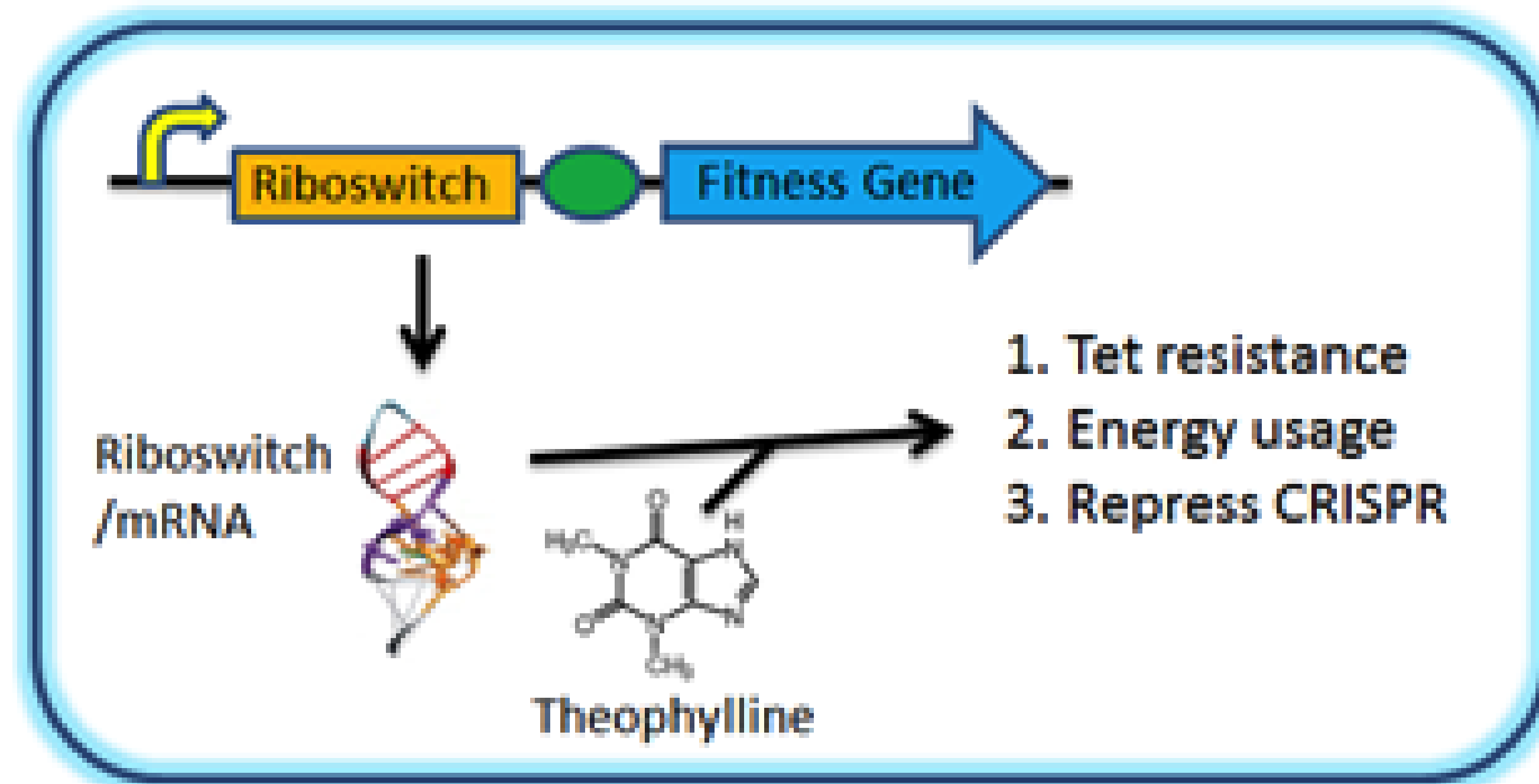
# Golden Gate Assembly Library of Promoters



# Cycling Golden Gate Assembly

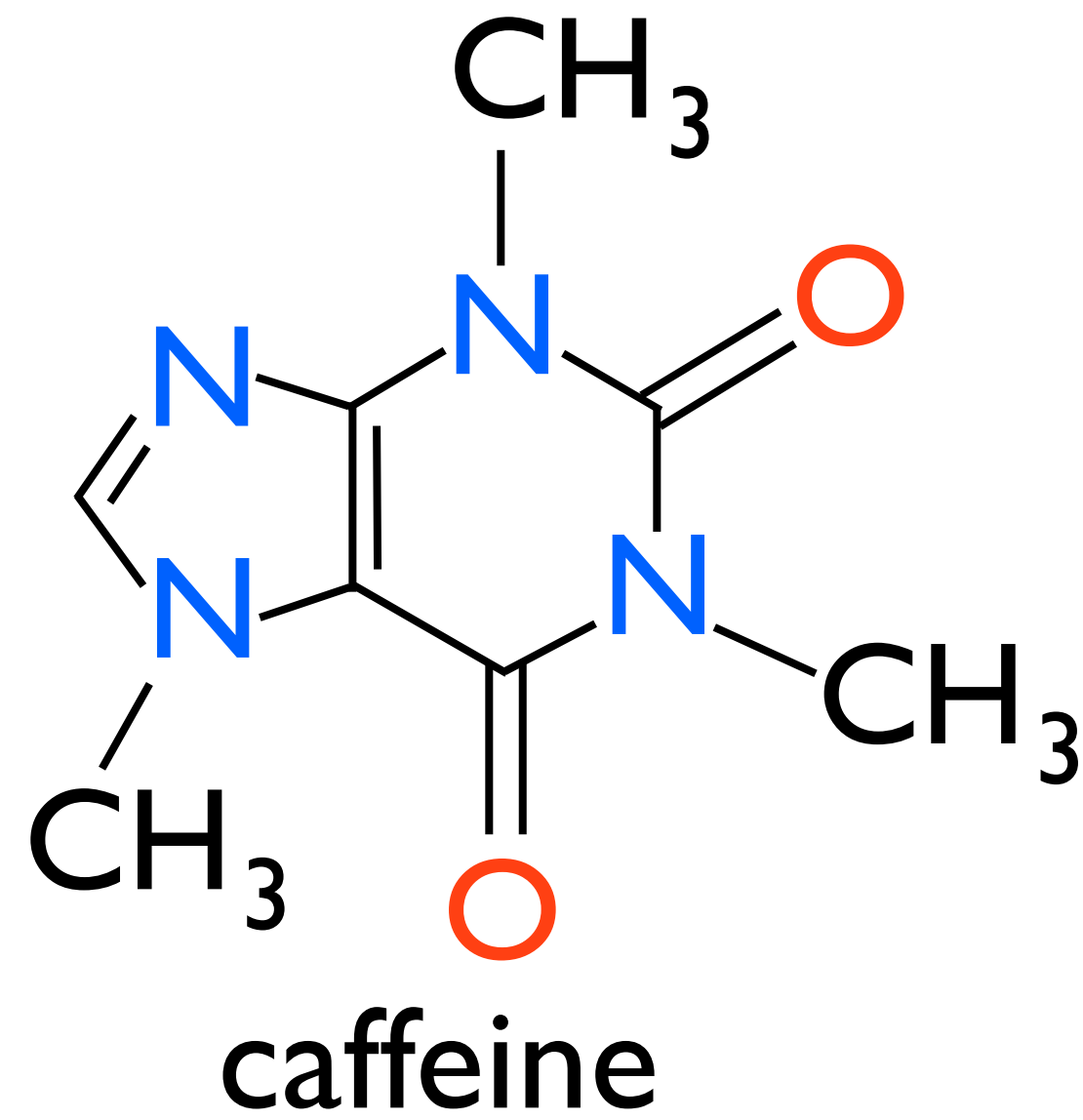


# Fitness Module

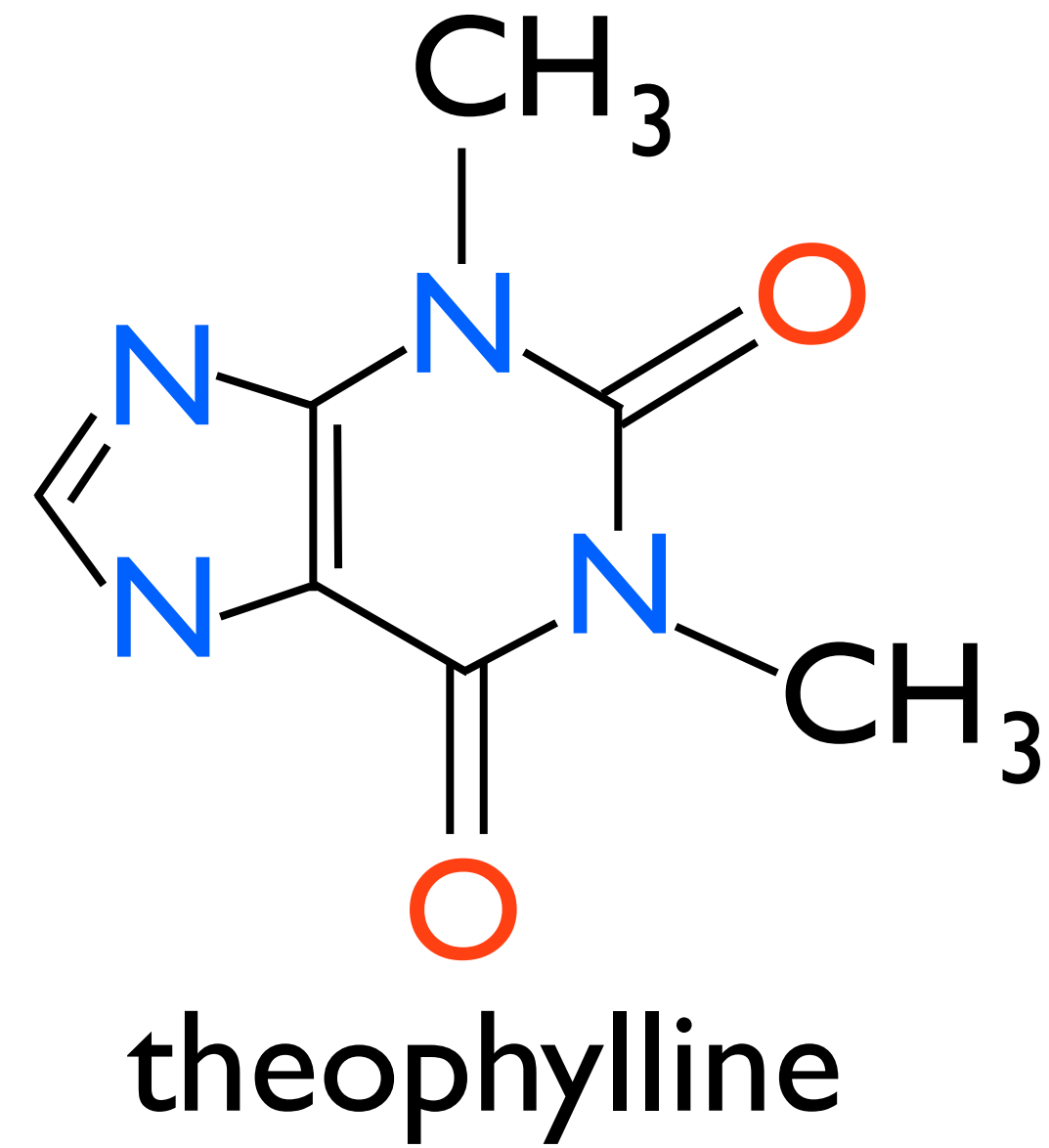




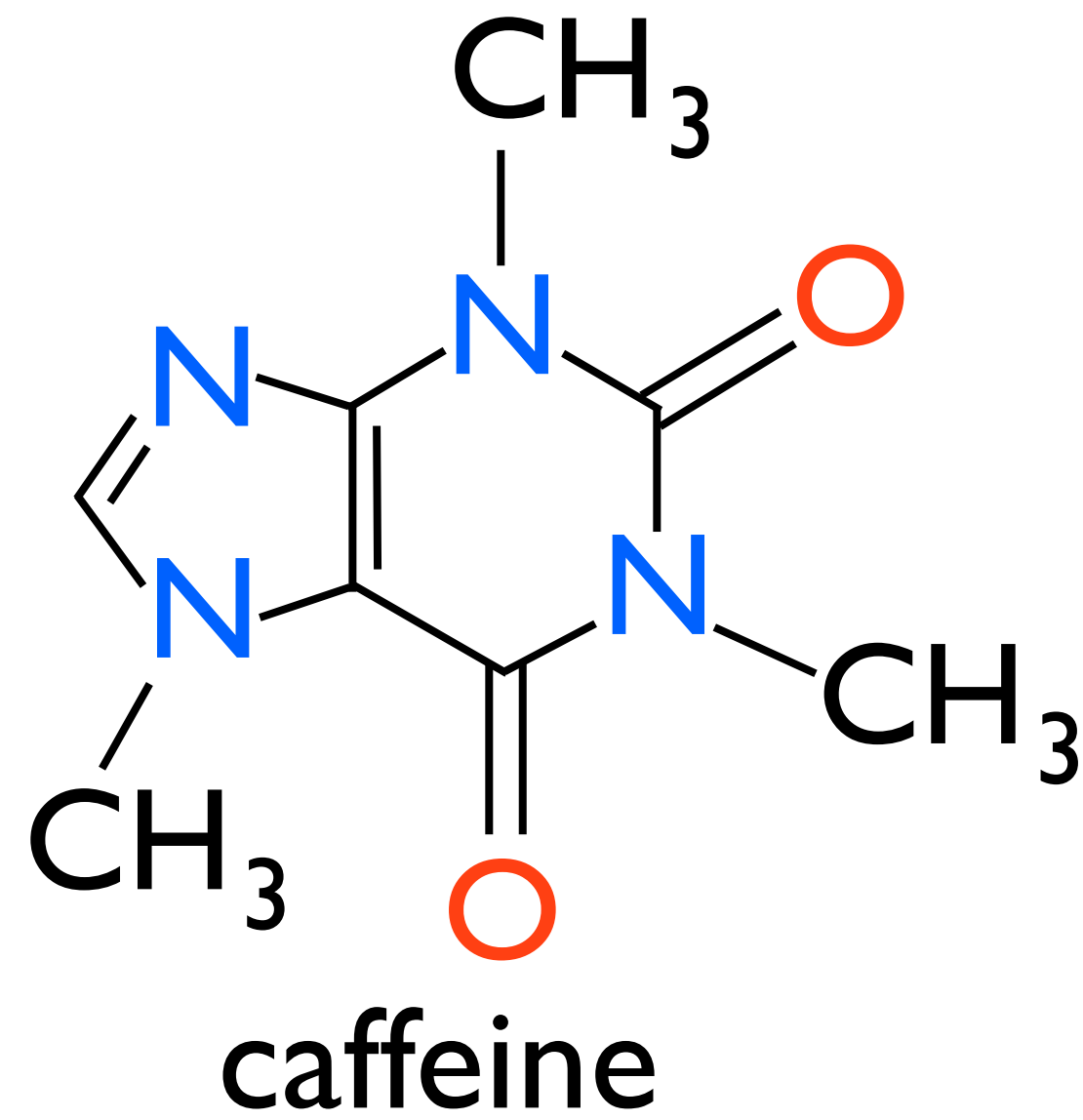
# How to Build a Fitness Module?



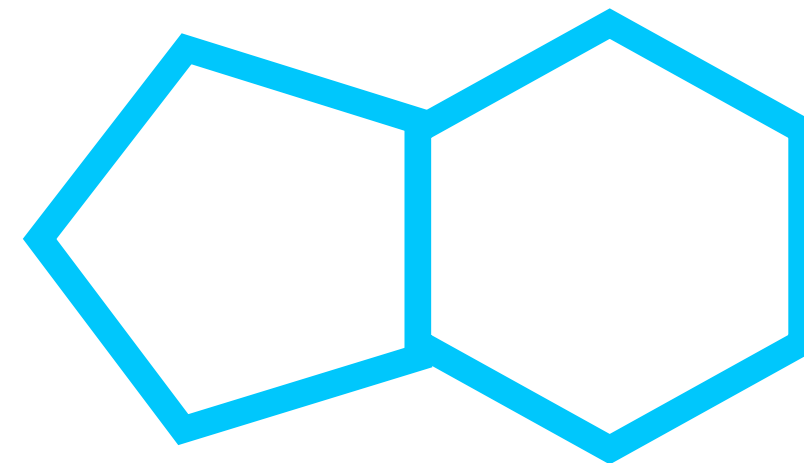
CDM  
➔



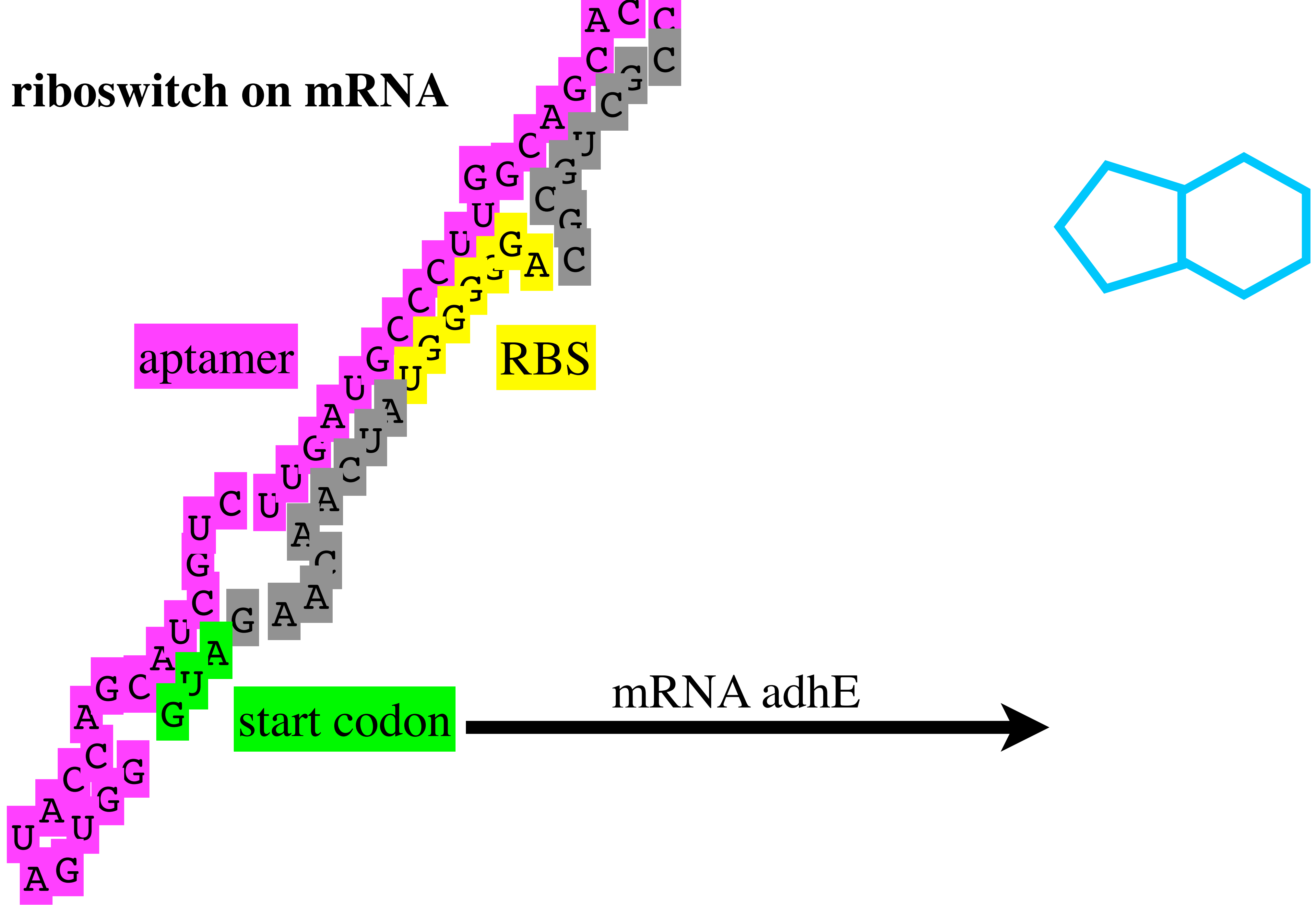
# How to Build a Fitness Module?



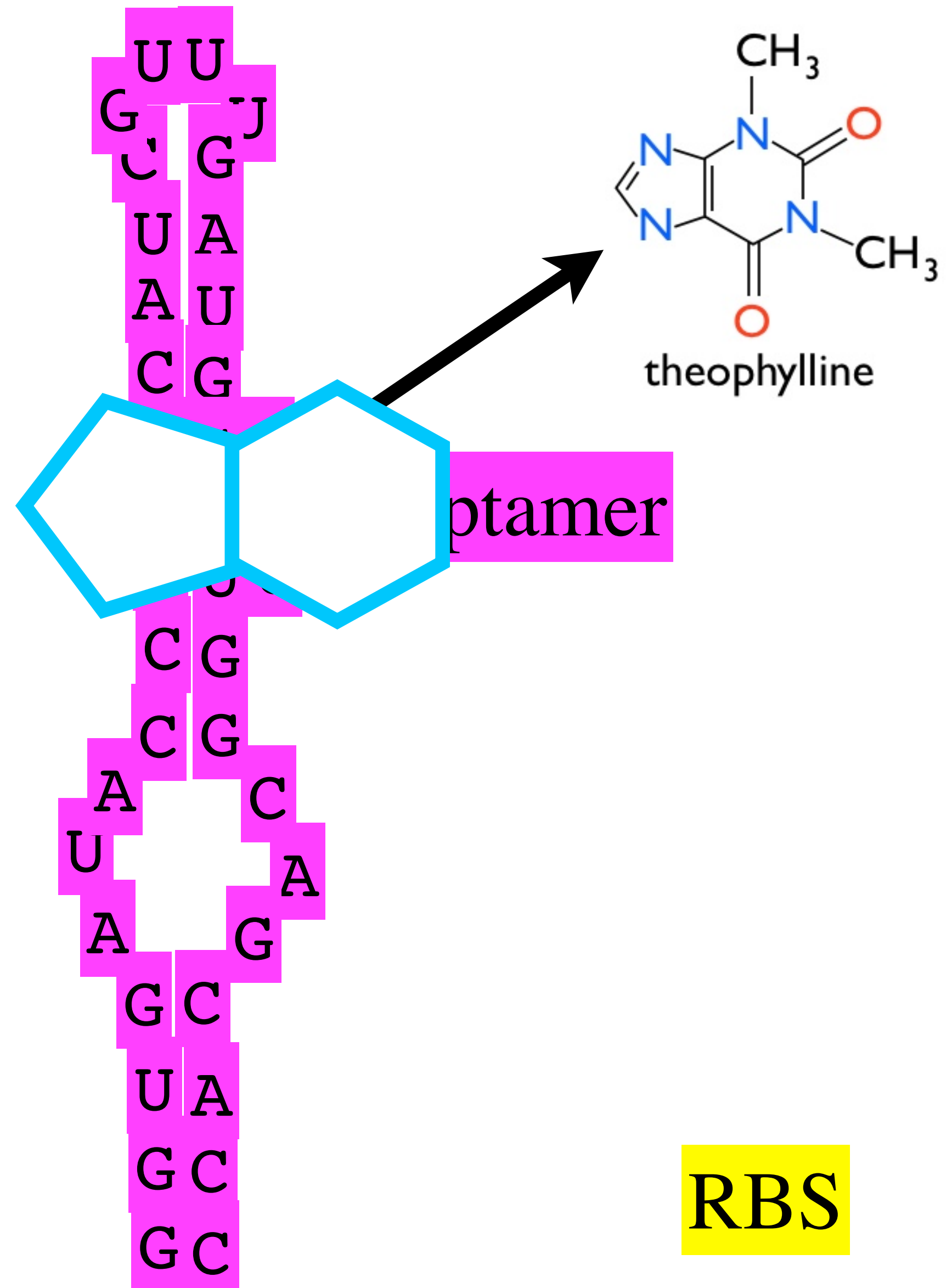
CDM  
➔



# riboswitch on mRNA







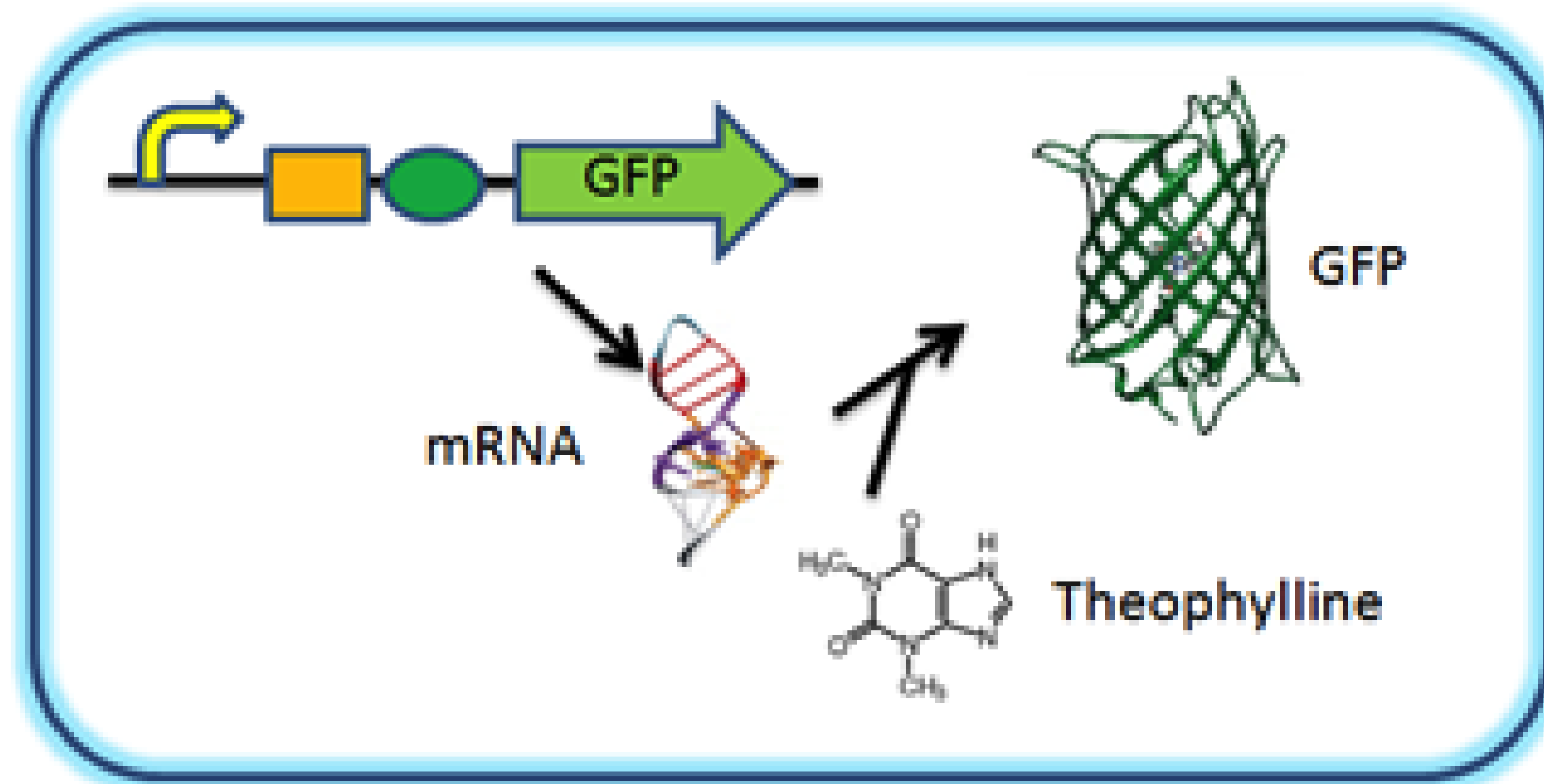
**adhE  
protein**



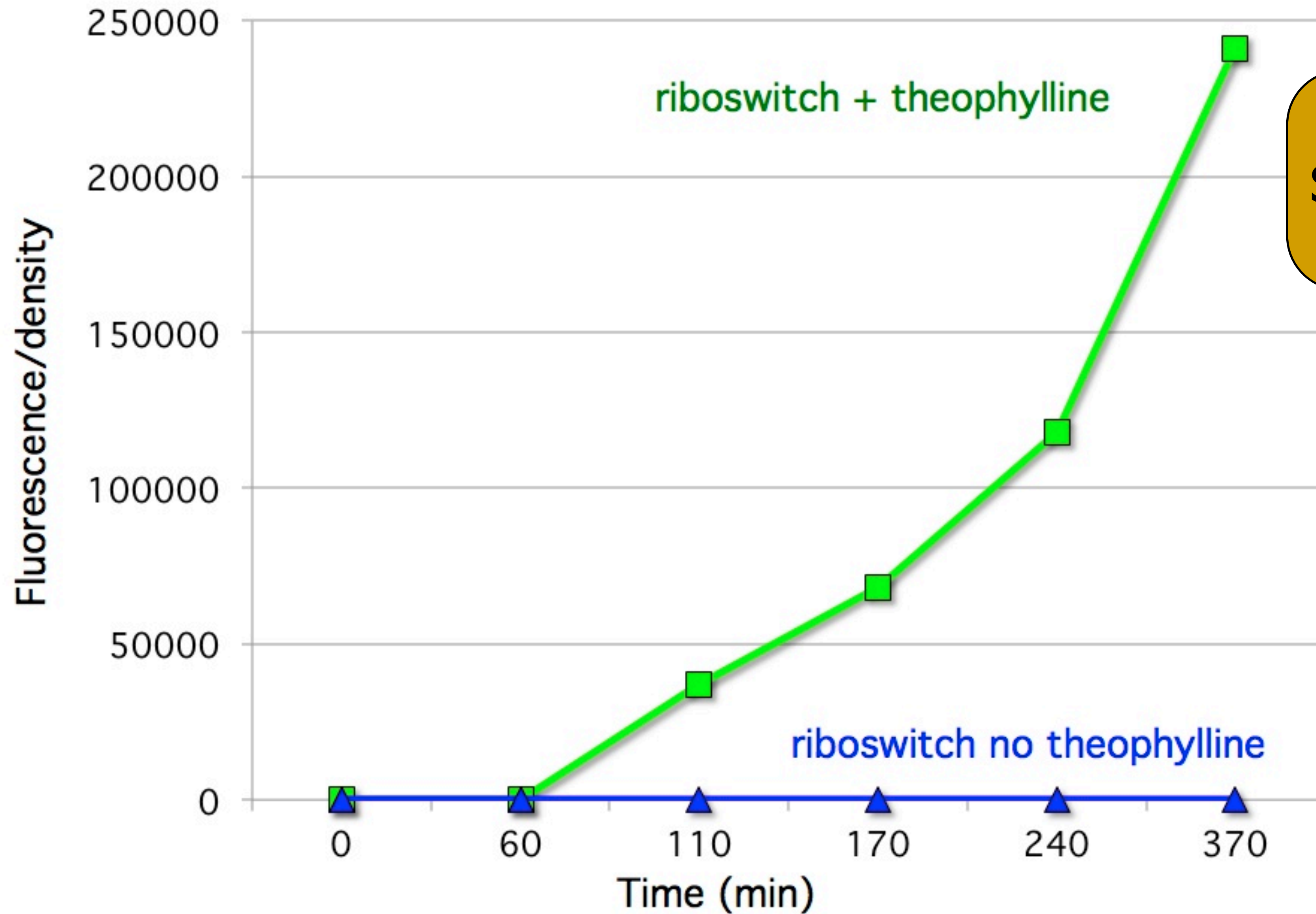
start codon

C G C U G ' G C A G G G G G U A U C A A C A A G A U G

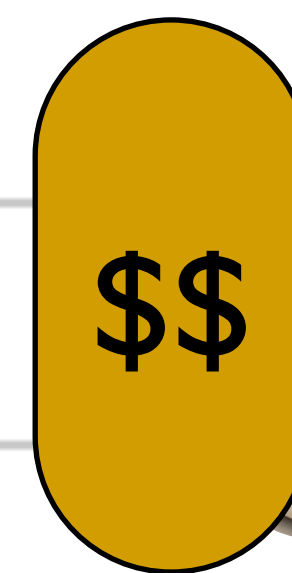
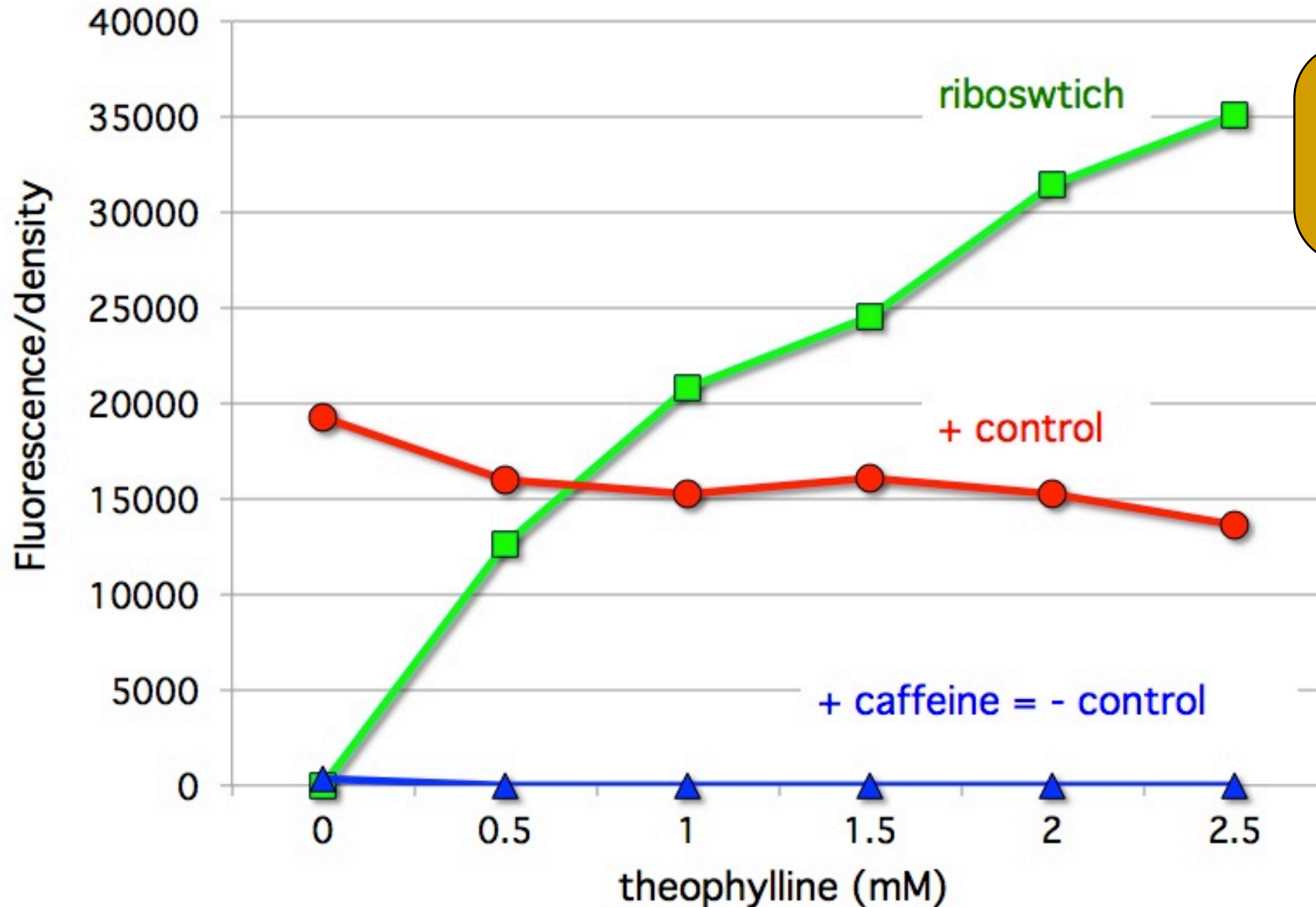
# Biosensor Module



# Fitness Module and BioSensor



# Fitness Module and BioSensor





# *E. coli* Natural Defense Mechanism

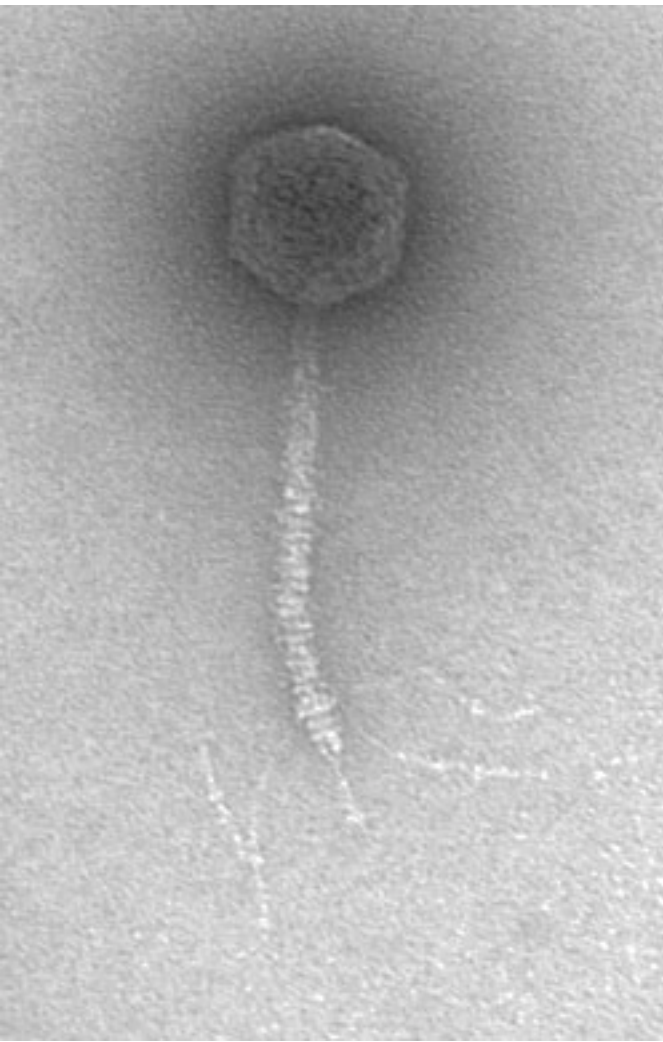


# *E. coli* Natural Defense Mechanism

CRISPR immune system



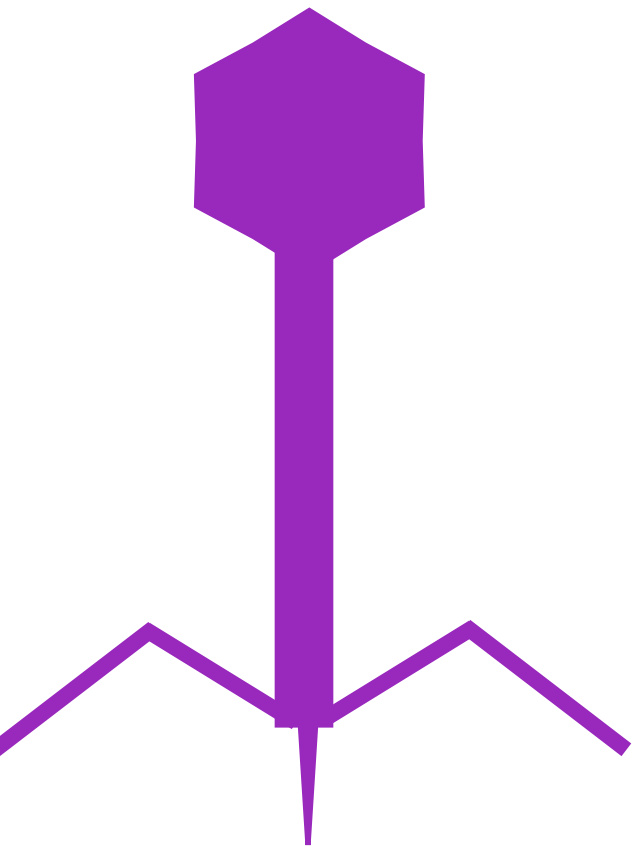
# *E. coli* Natural Defense Mechanism



CRISPR immune system



# *E. coli* Natural Defense Mechanism



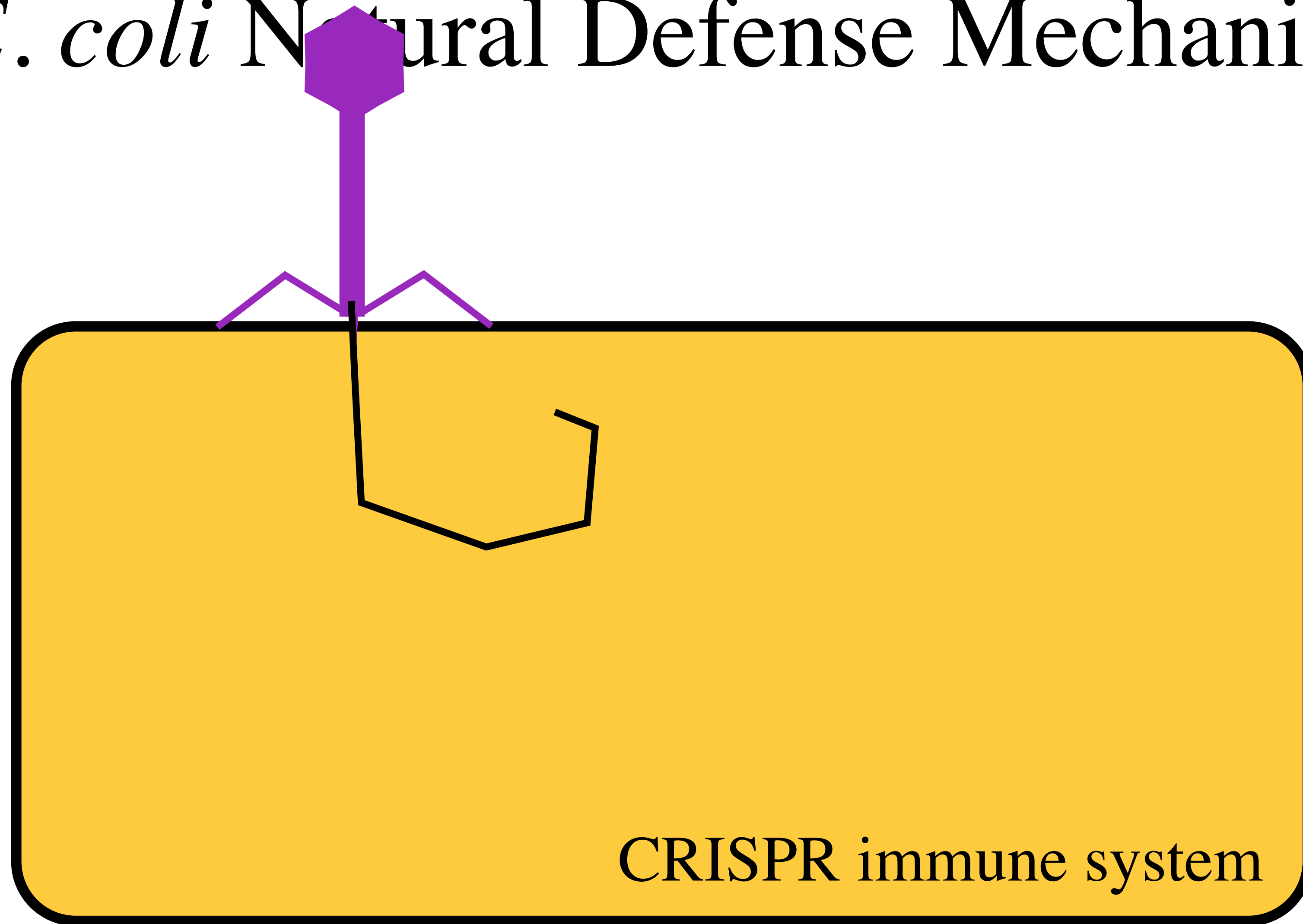
CRISPR immune system



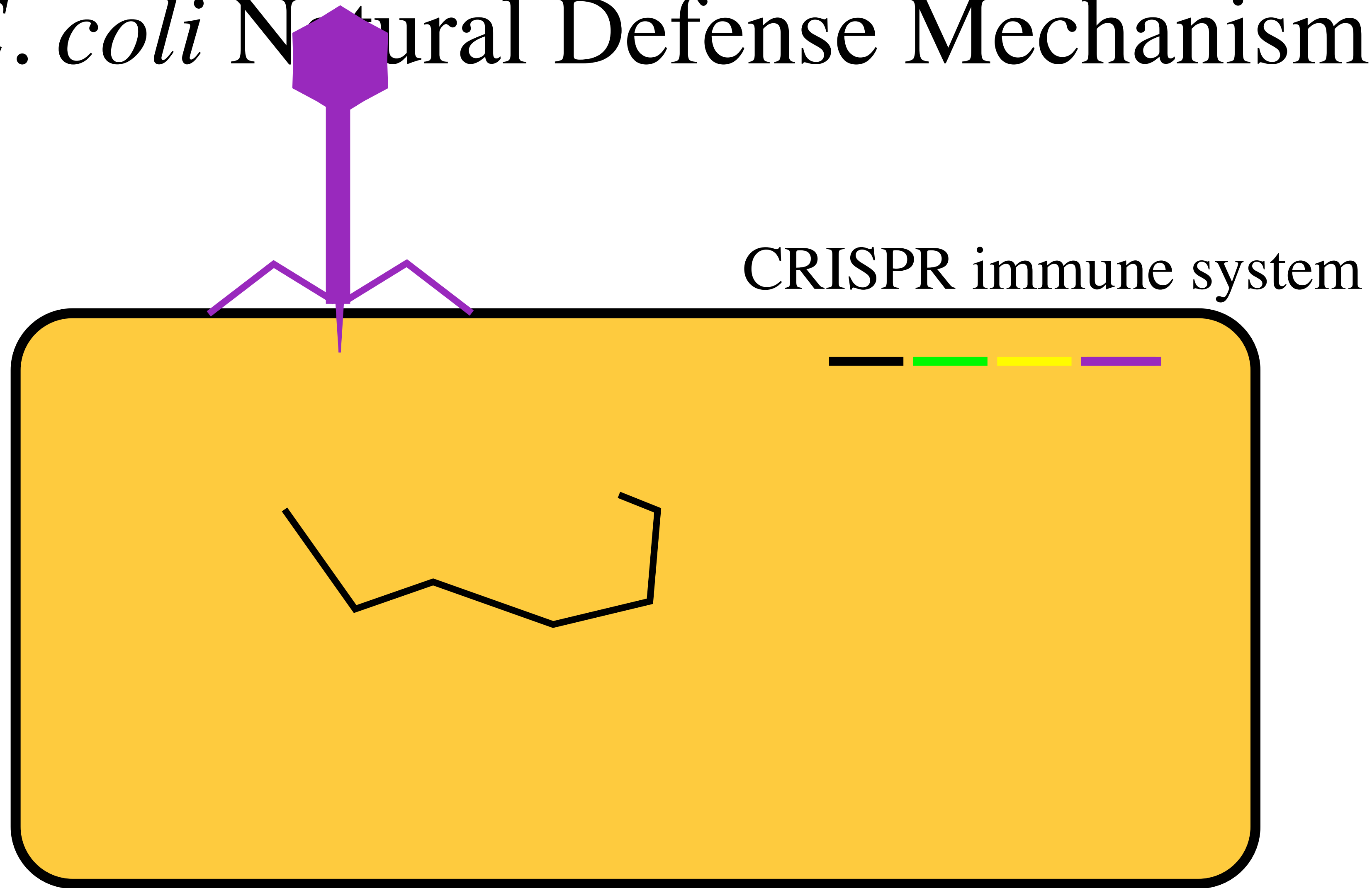
# *E. coli* Natural Defense Mechanism



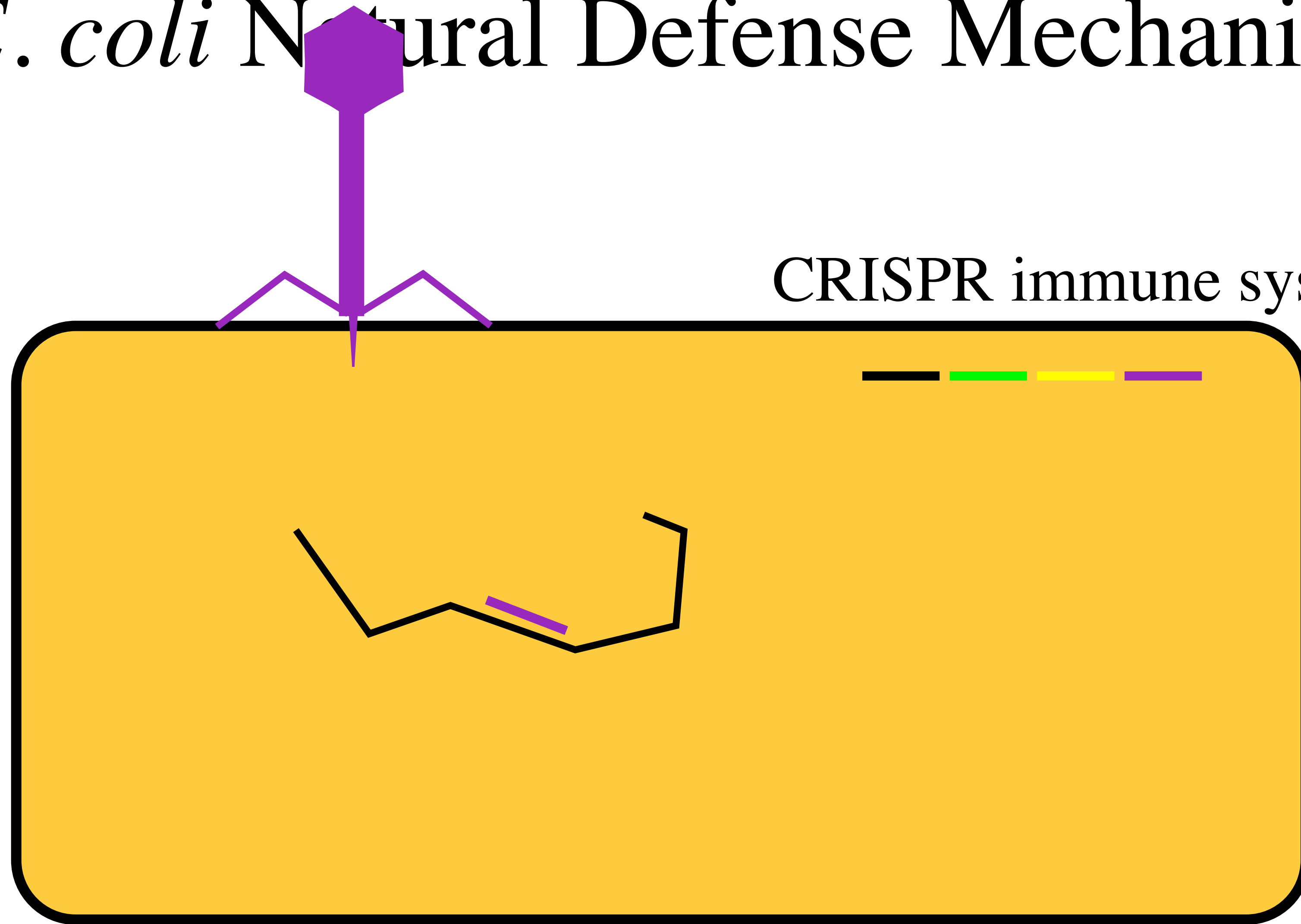
# *E. coli* Natural Defense Mechanism



# *E. coli* Natural Defense Mechanism



# *E. coli* Natural Defense Mechanism

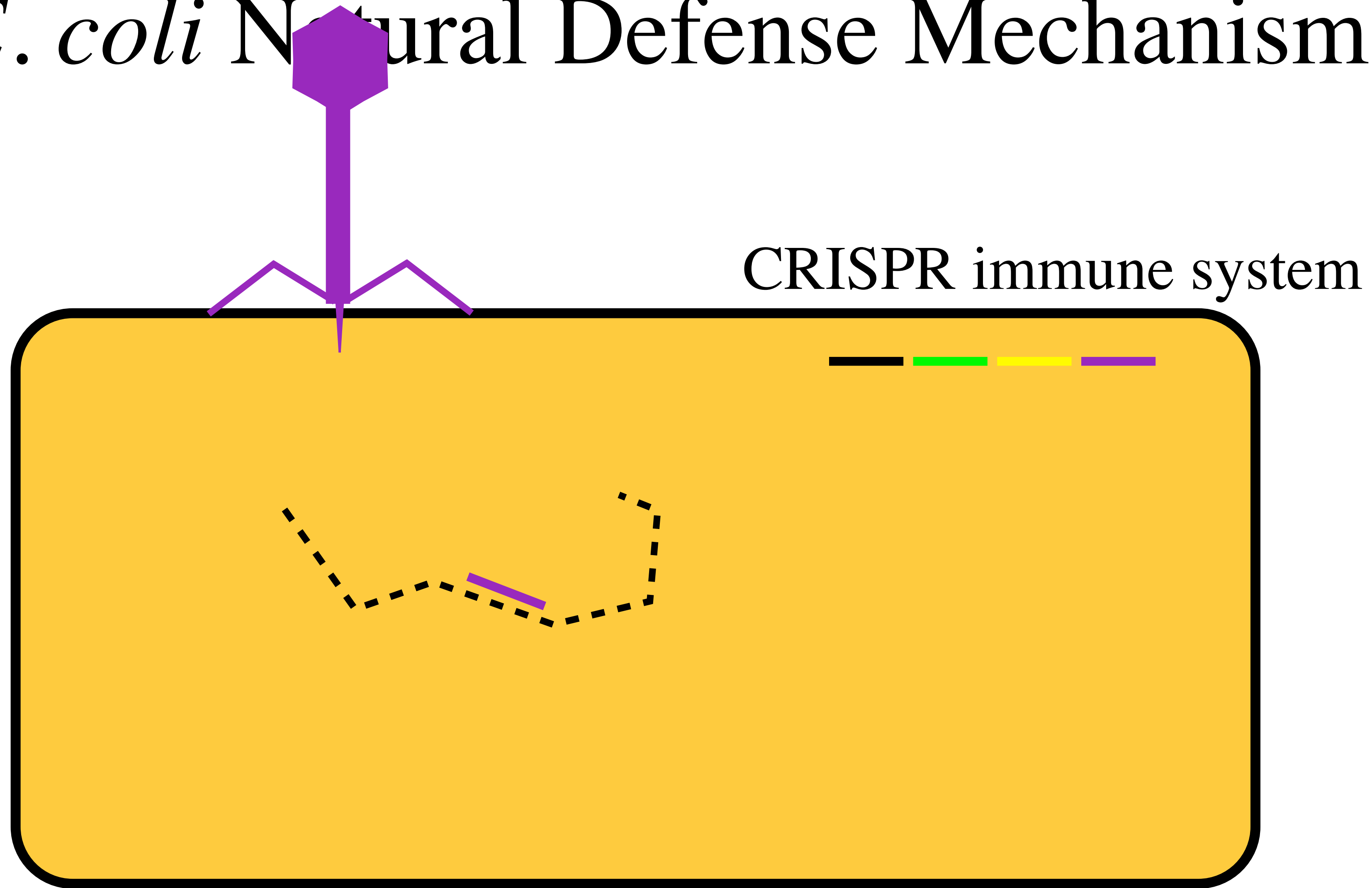


CRISPR immune system



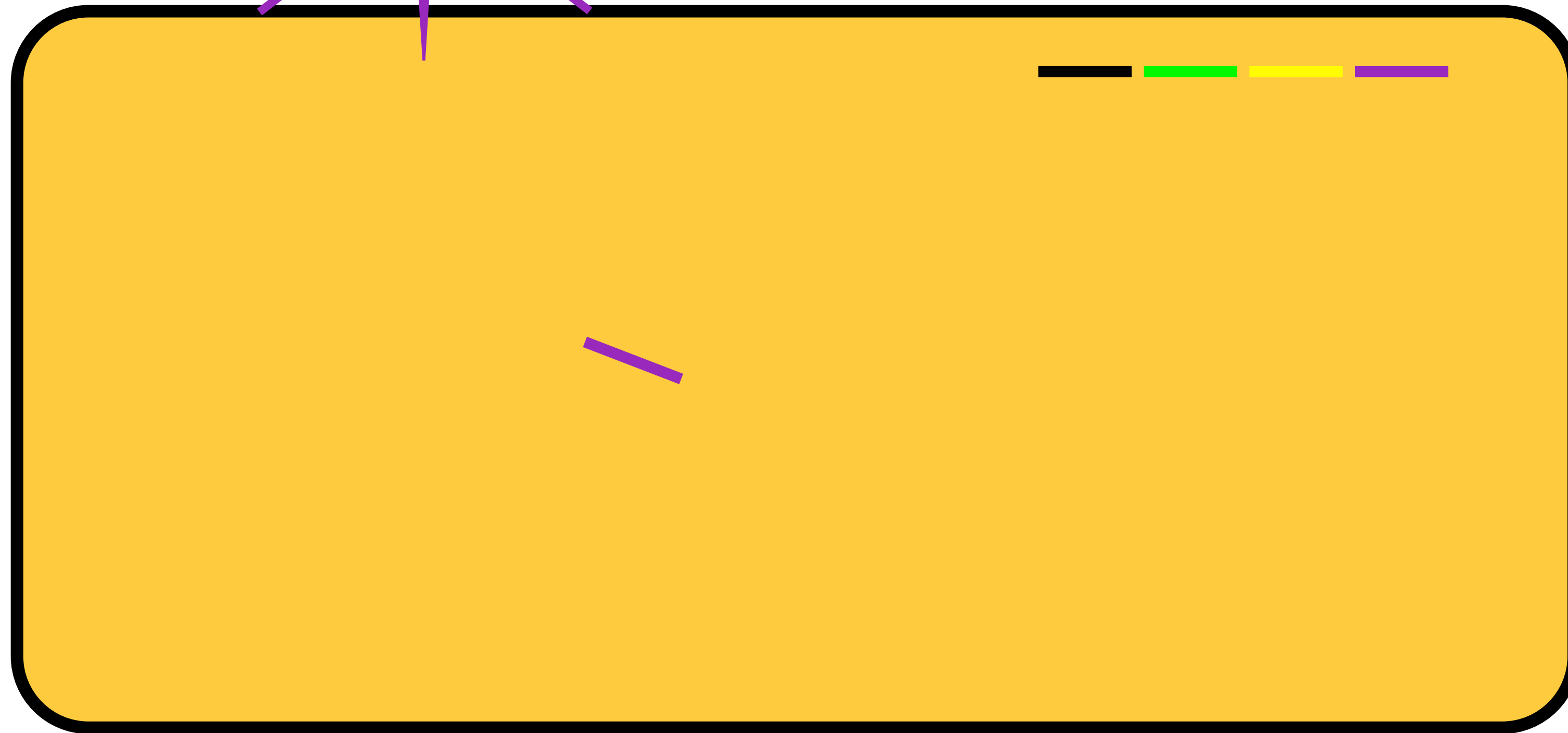


# *E. coli* Natural Defense Mechanism

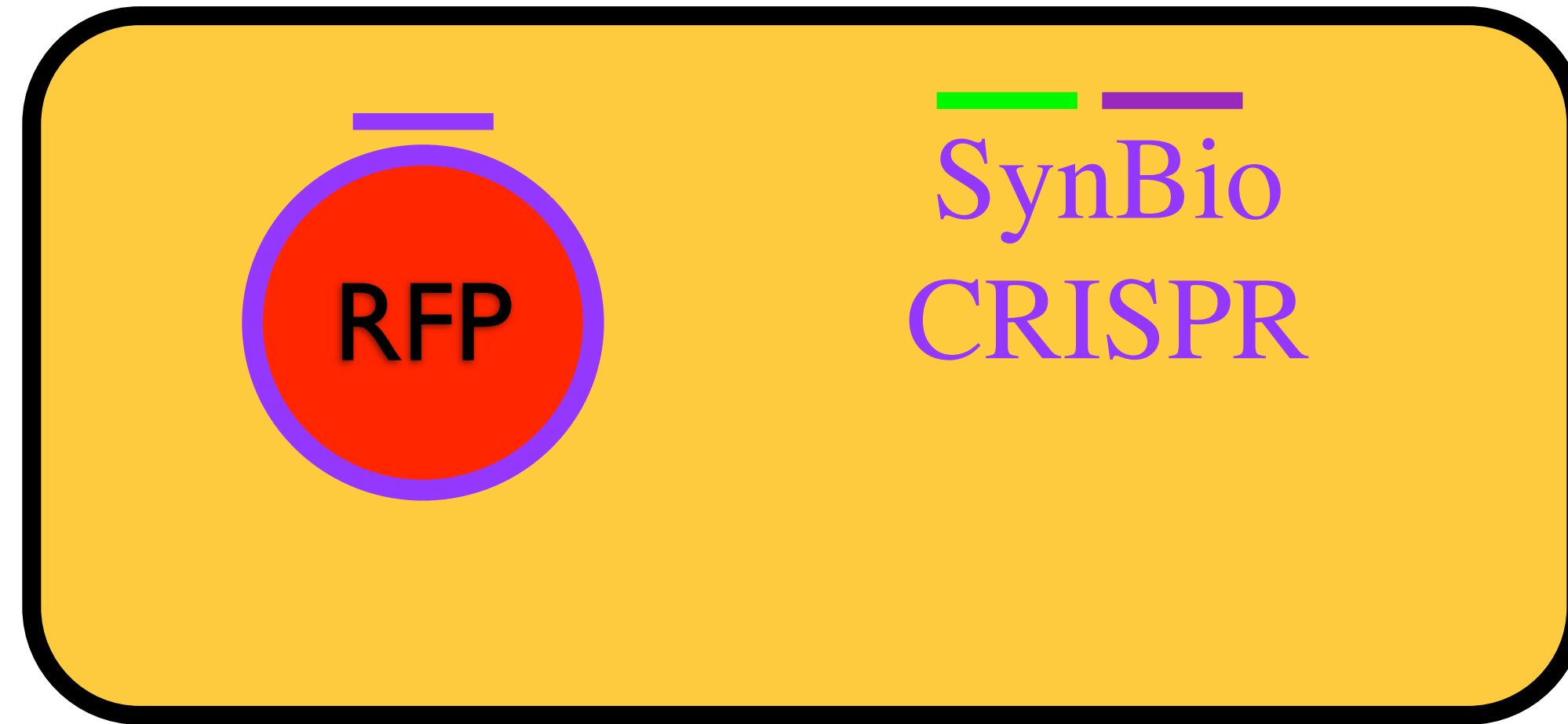


# *E. coli* Natural Defense Mechanism

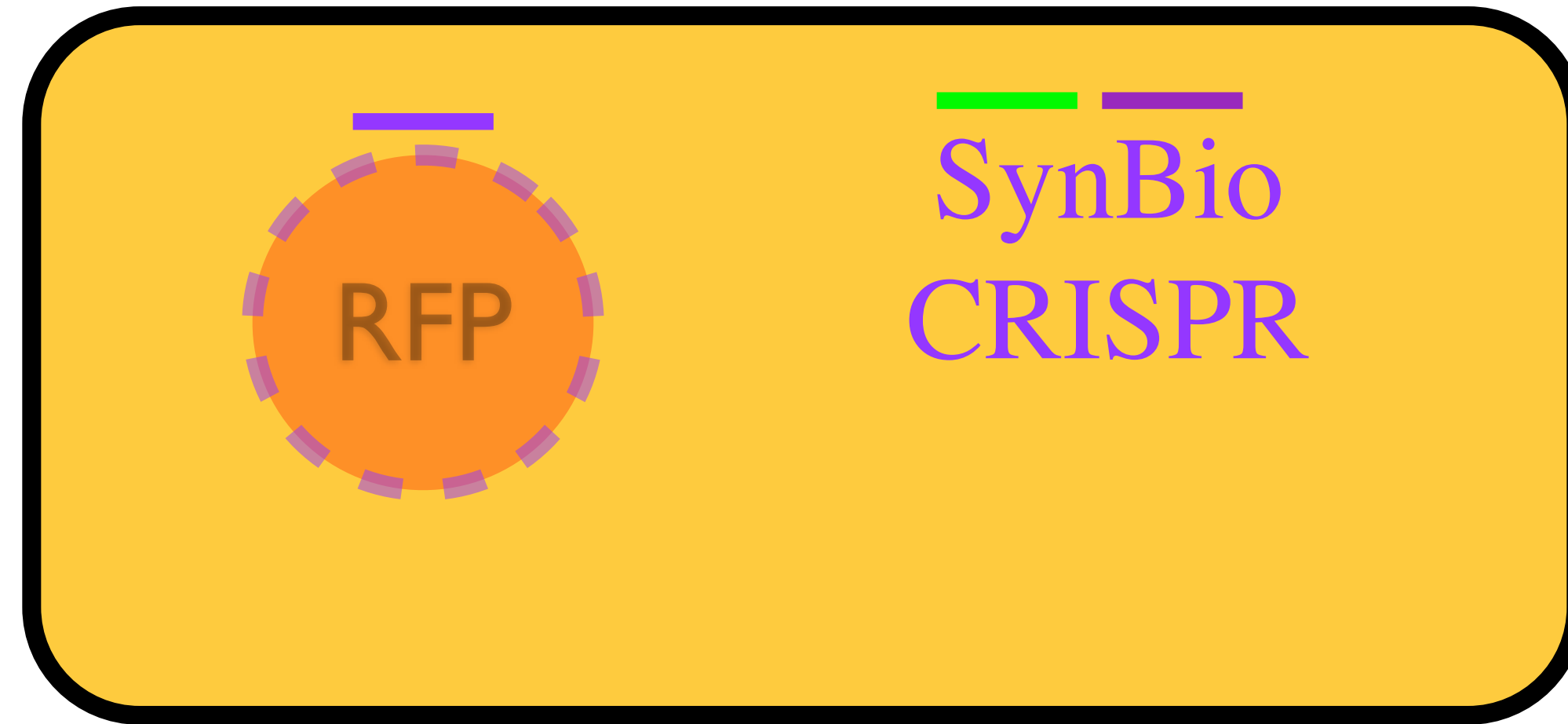
CRISPR immune system



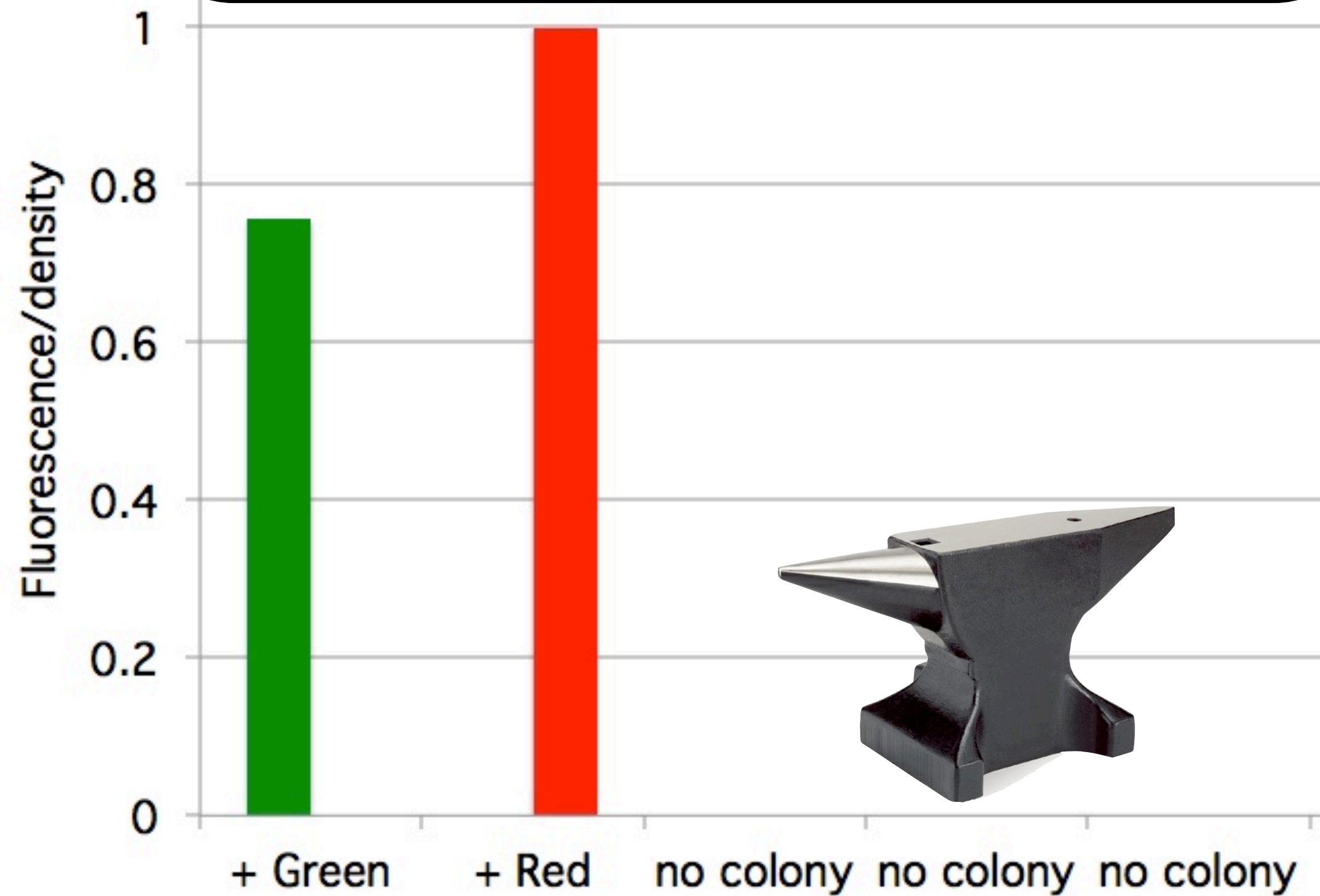
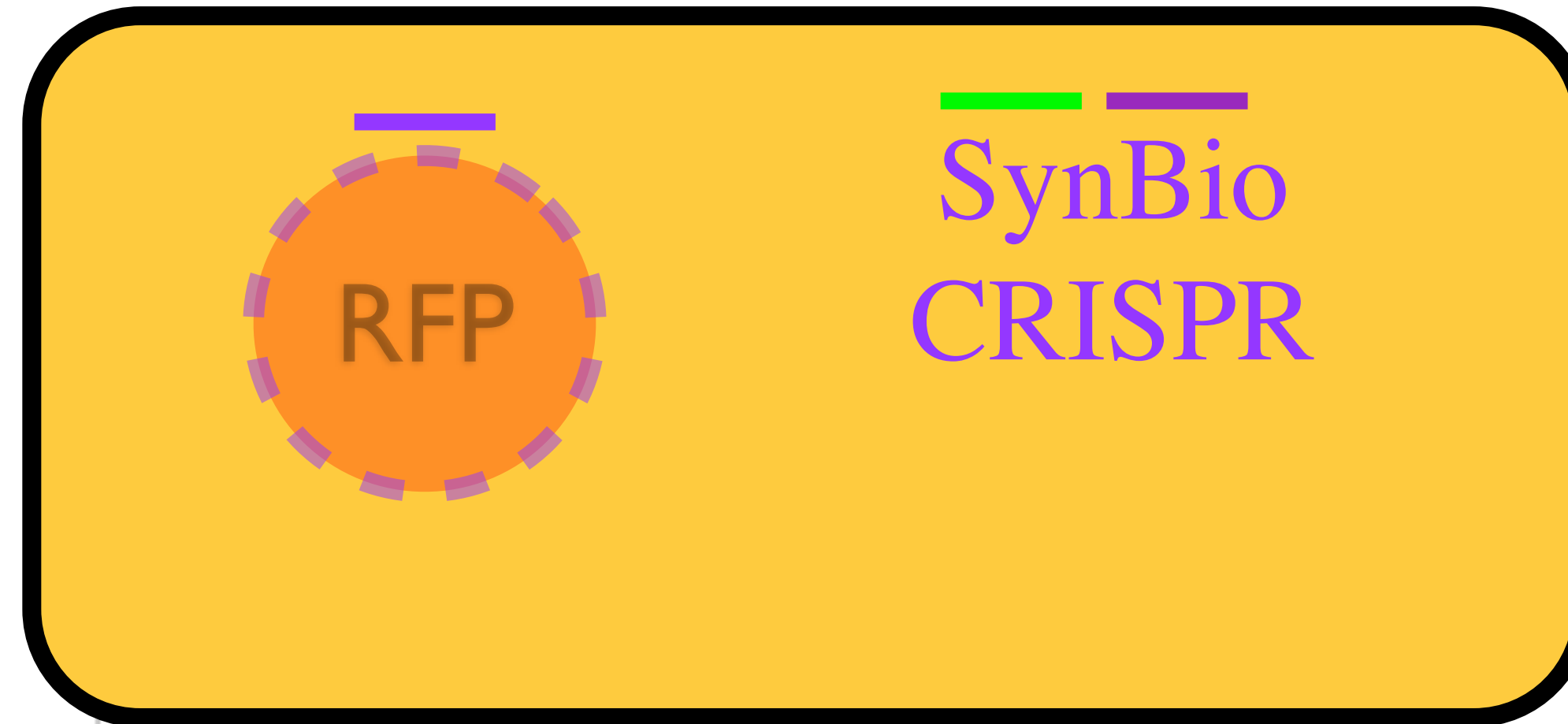
# *E. coli* Synthetic Defense Repurposed



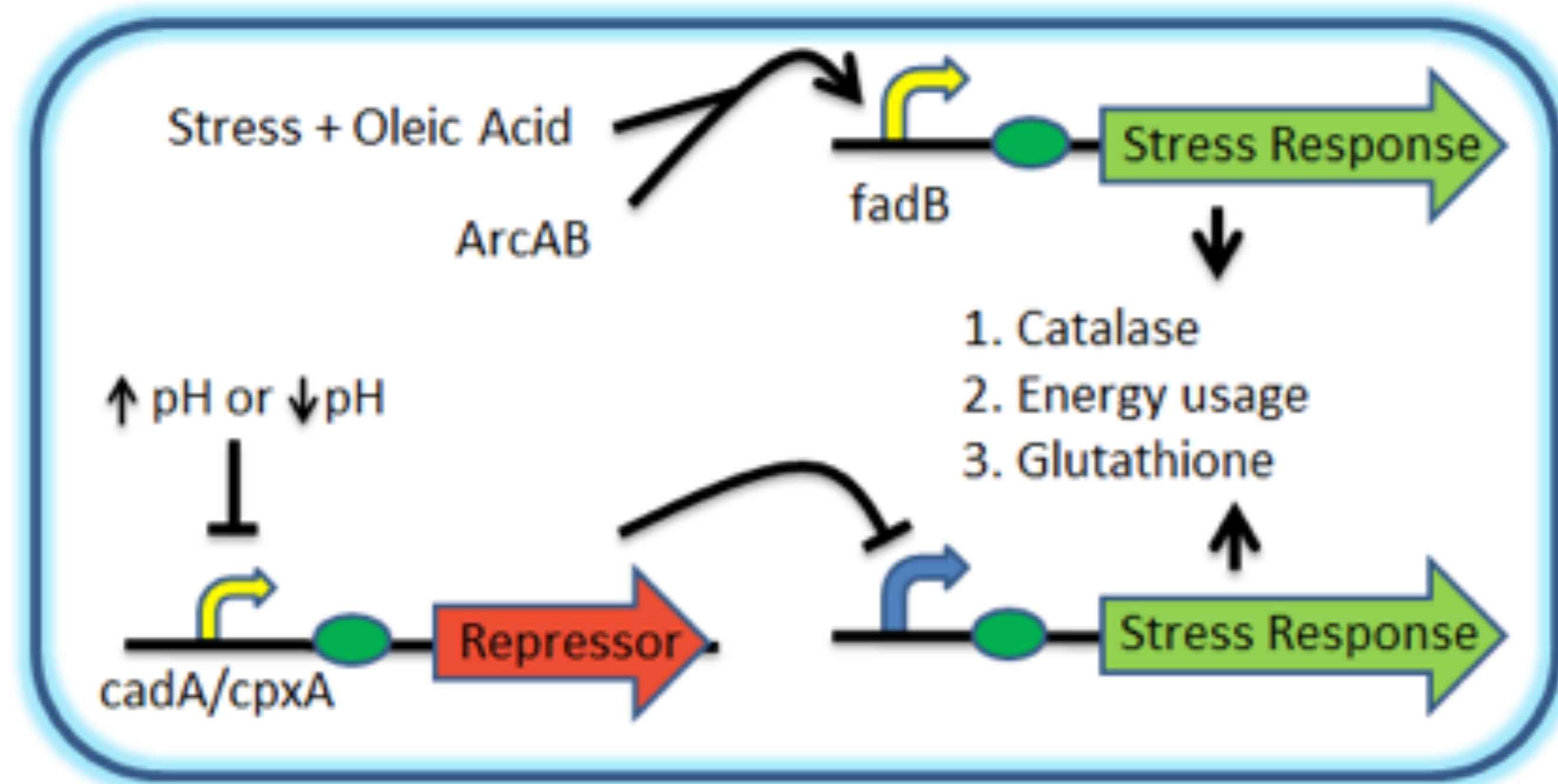
# *E. coli* Synthetic Defense Repurposed



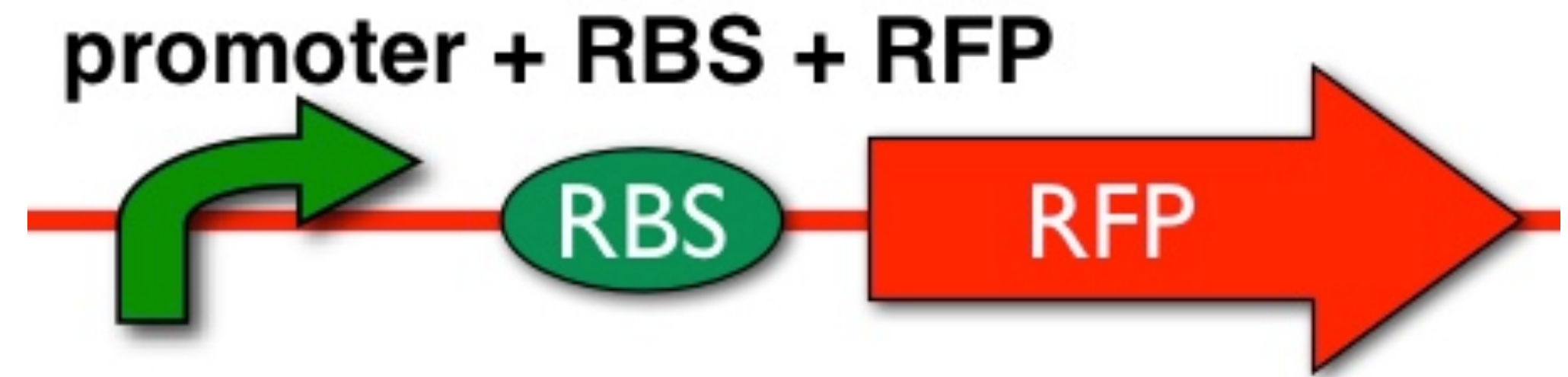
# Implementing Fitness



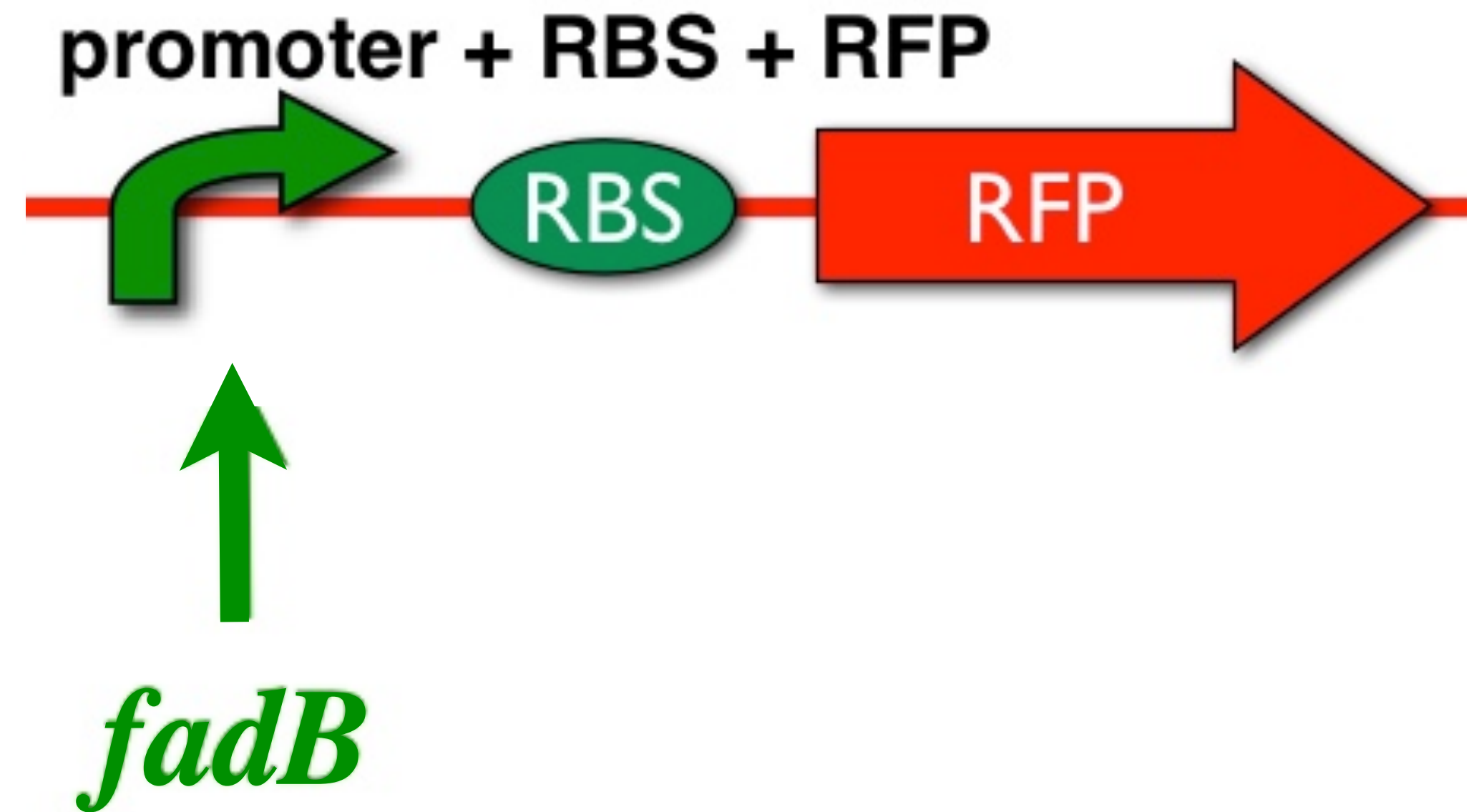
# Stress Response Module



# Engineering a Stress Module

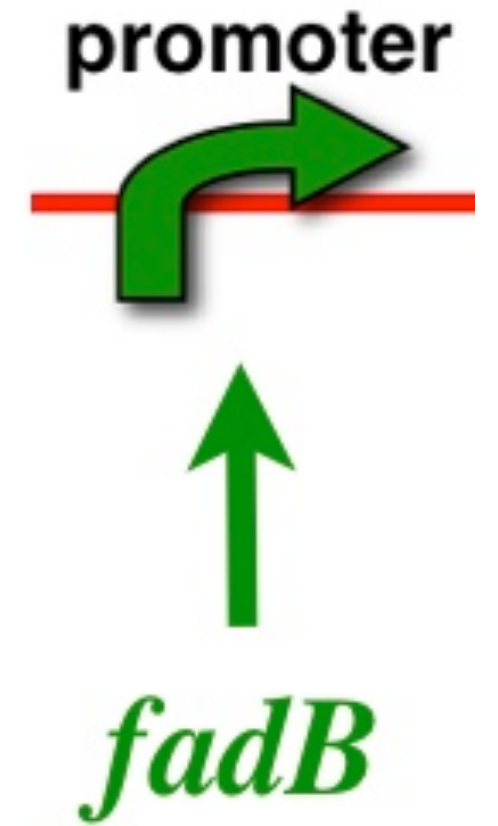


# Engineering a Stress Module





# Engineering a Stress Module



AATTCGCGGCCGCTTCTAGAGATCGGCATTTCTTTAATCTTTTGTGGCATATTTTAAACACAAAATACACACTTCGACTCATCTGGTACGACCAGATCACCTTGCTACTAGTAGCGGCCGCTGCA  
GCGCCGGCGAAGATCTCTAGCCGTAAAGAAATTAGAAAACAAACGTATAAAAATTGTGTTTTATGTGTGAAGCTGAGTAGACCATGCTGGTCTAGTGGAACGATGATCATCGCCGGCG

# Engineering a Stress Module

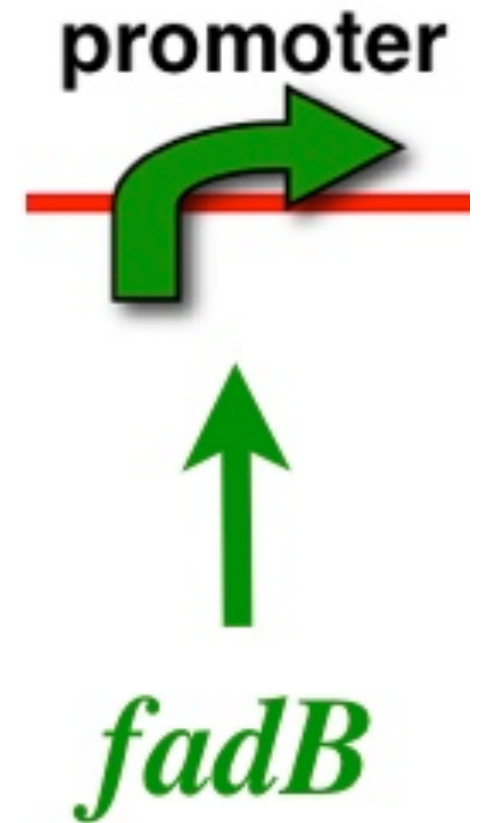
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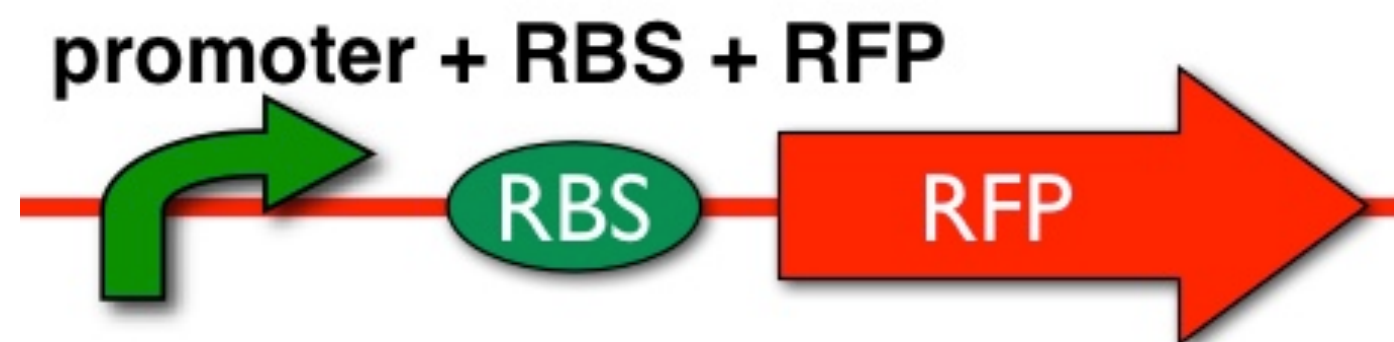
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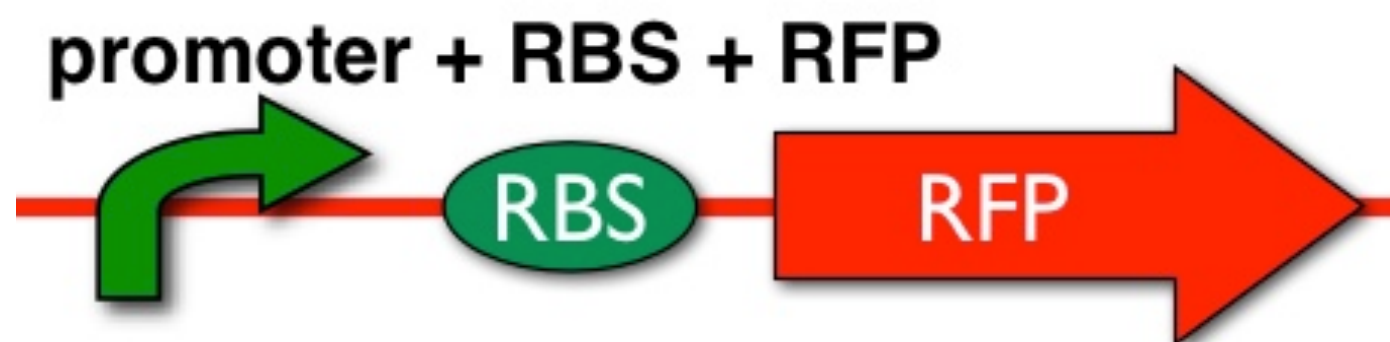
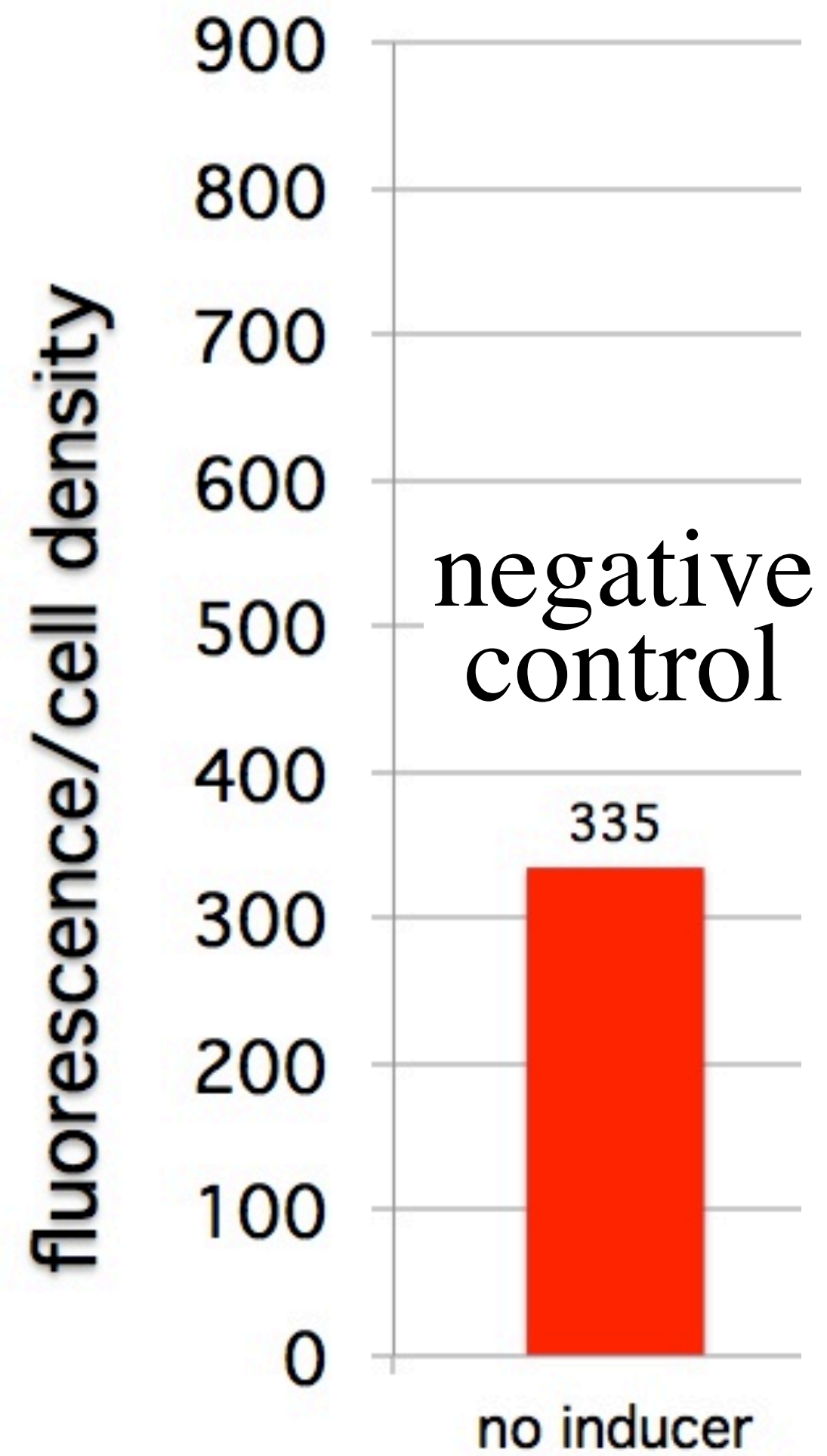


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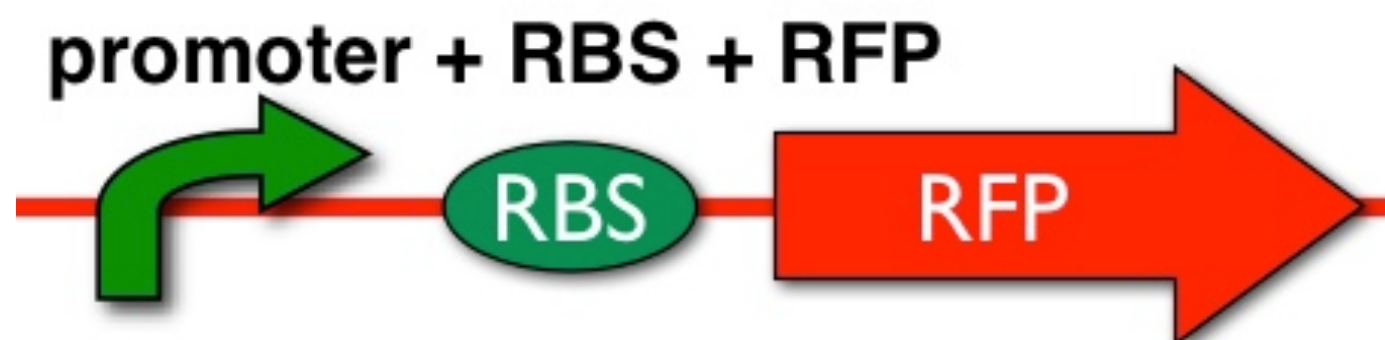
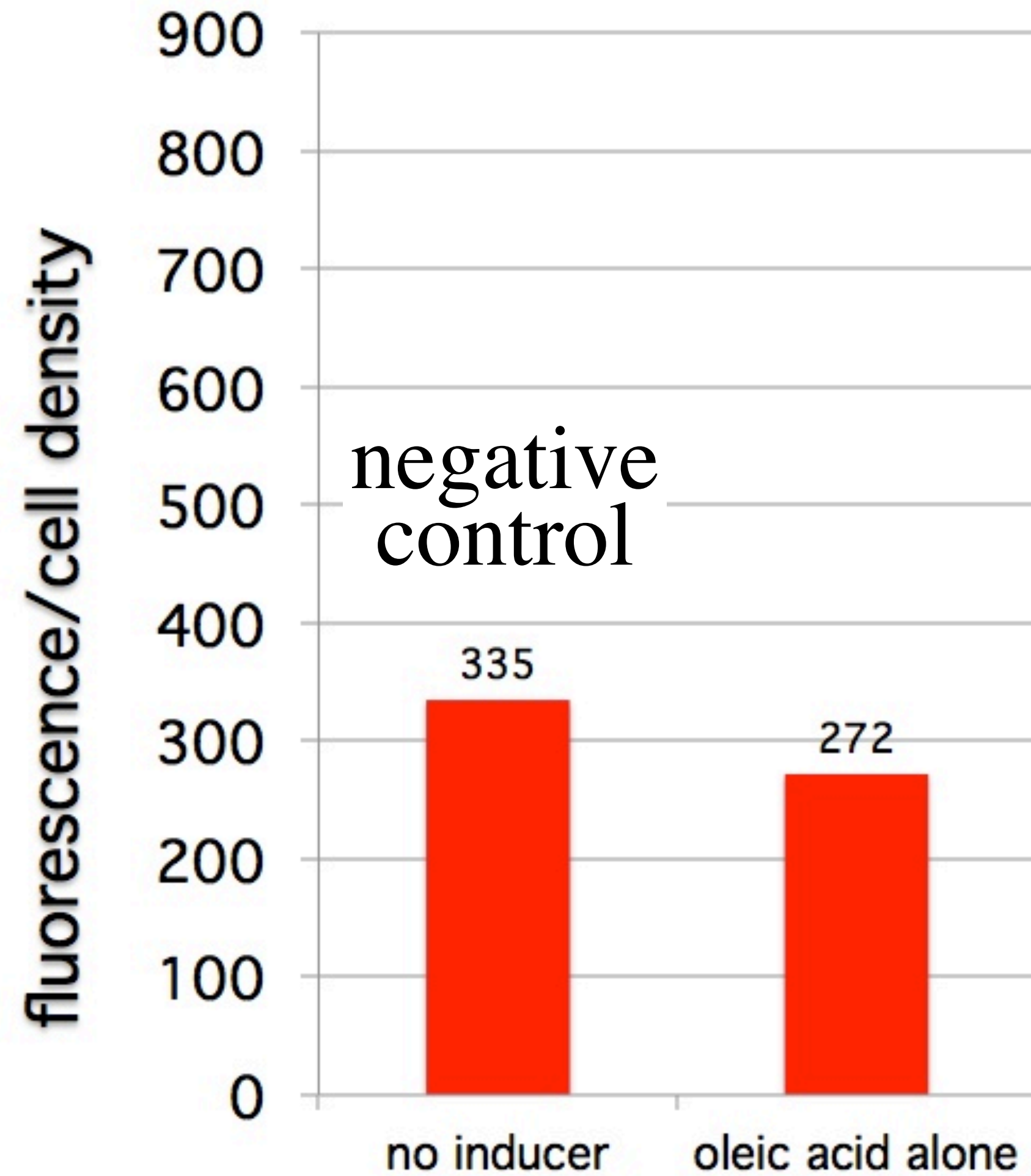
# Testing Stress Module



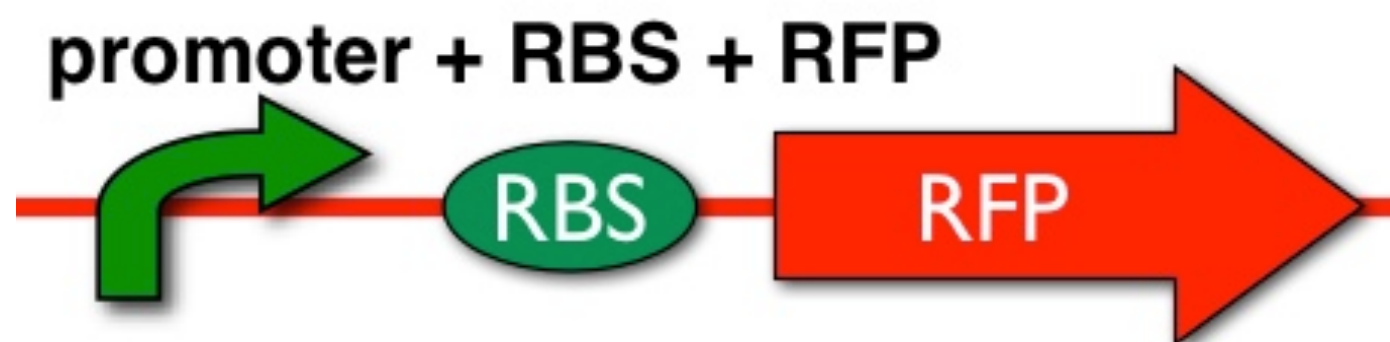
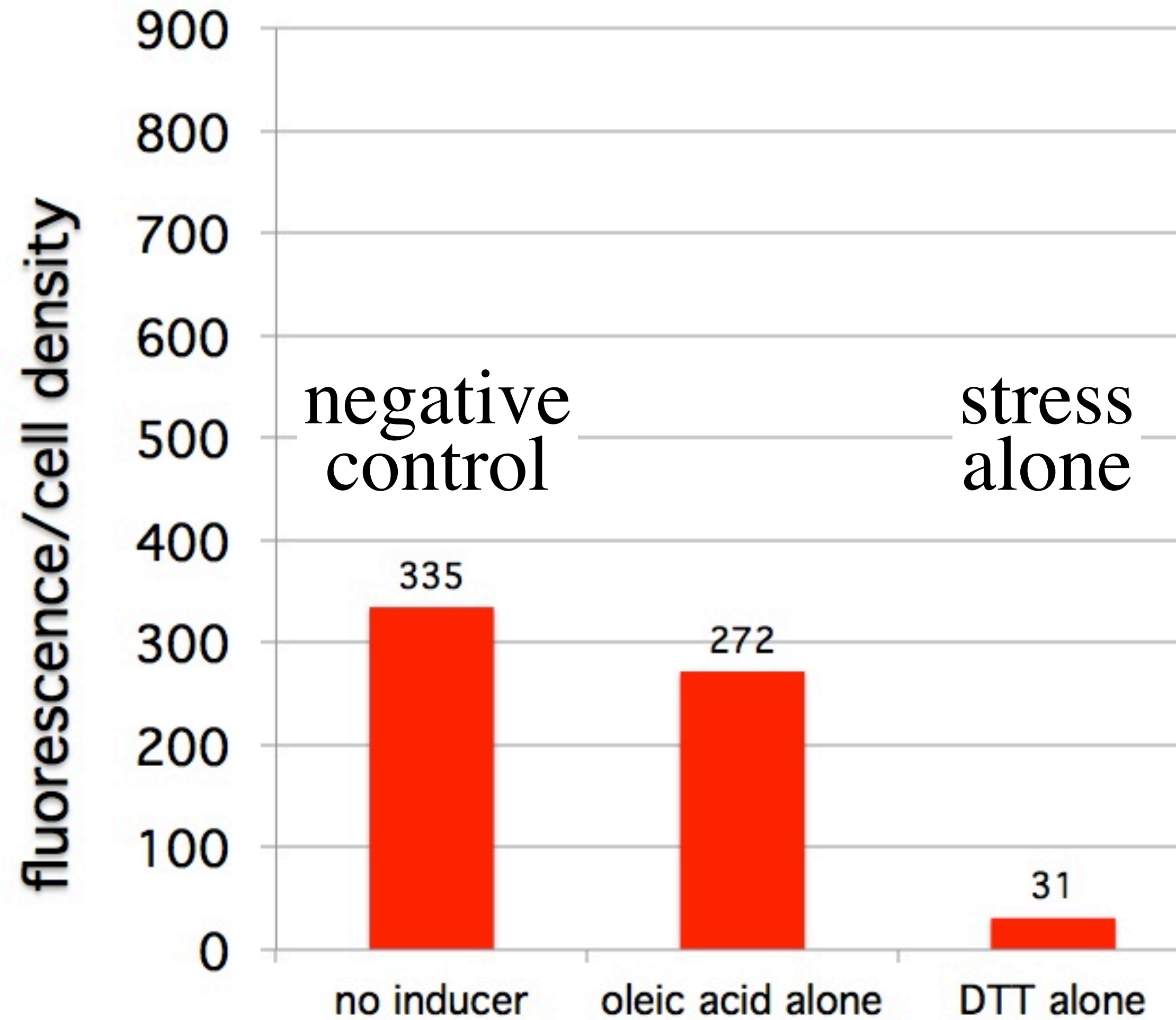
# Testing Stress Module



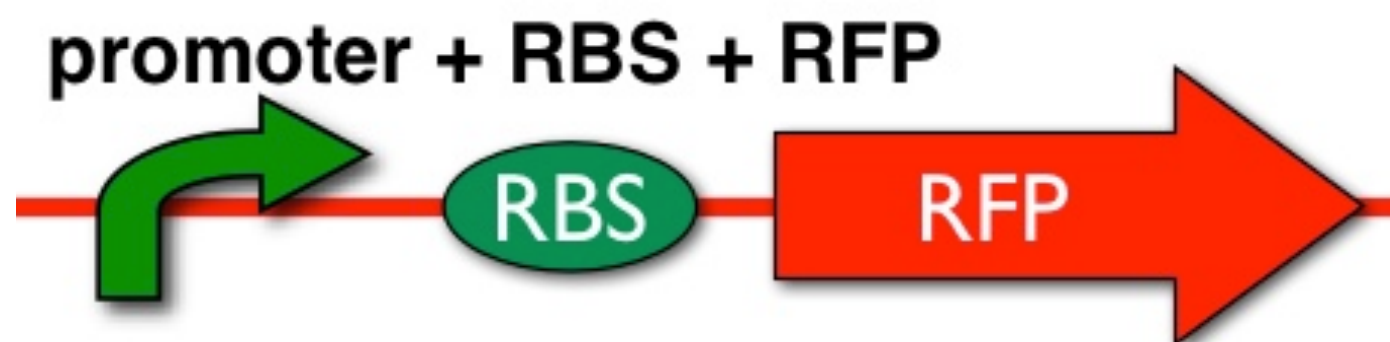
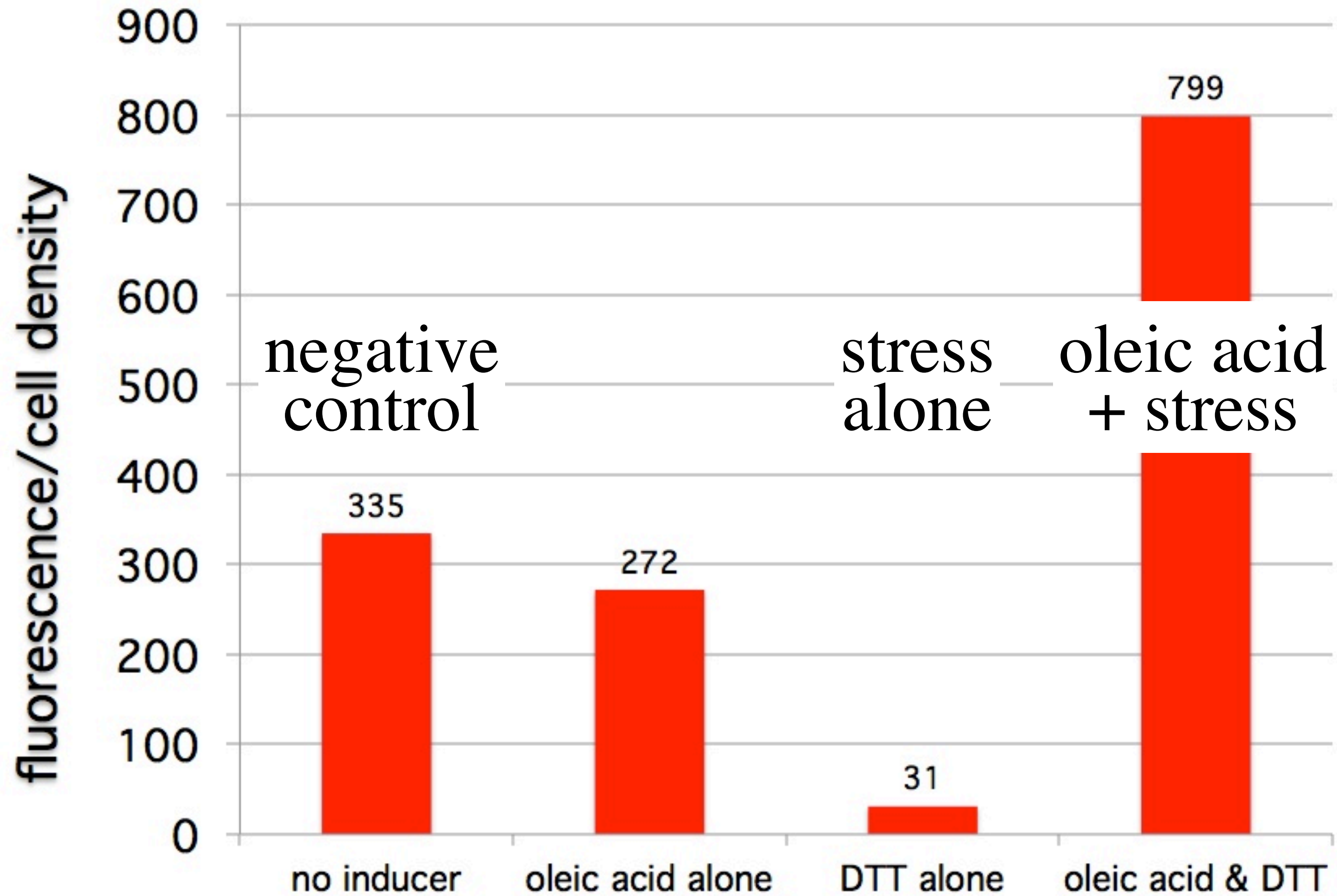
# Testing Stress Module



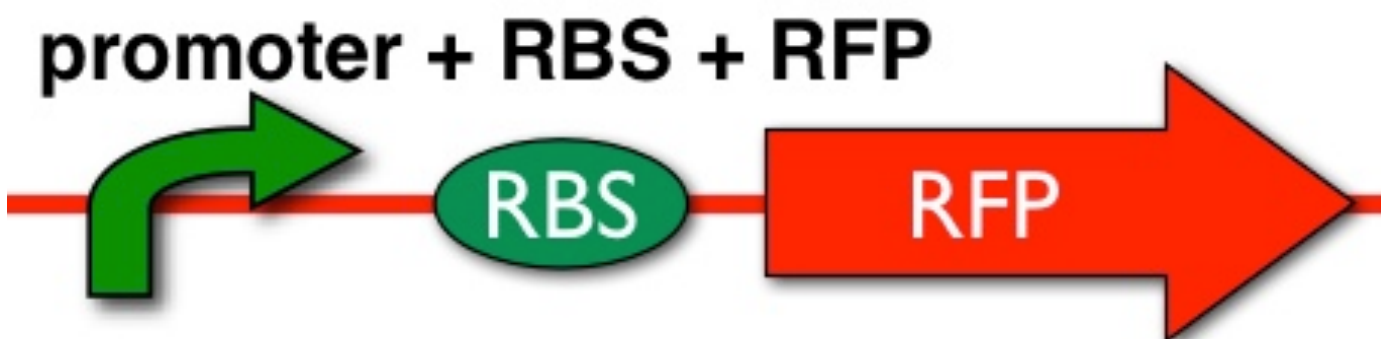
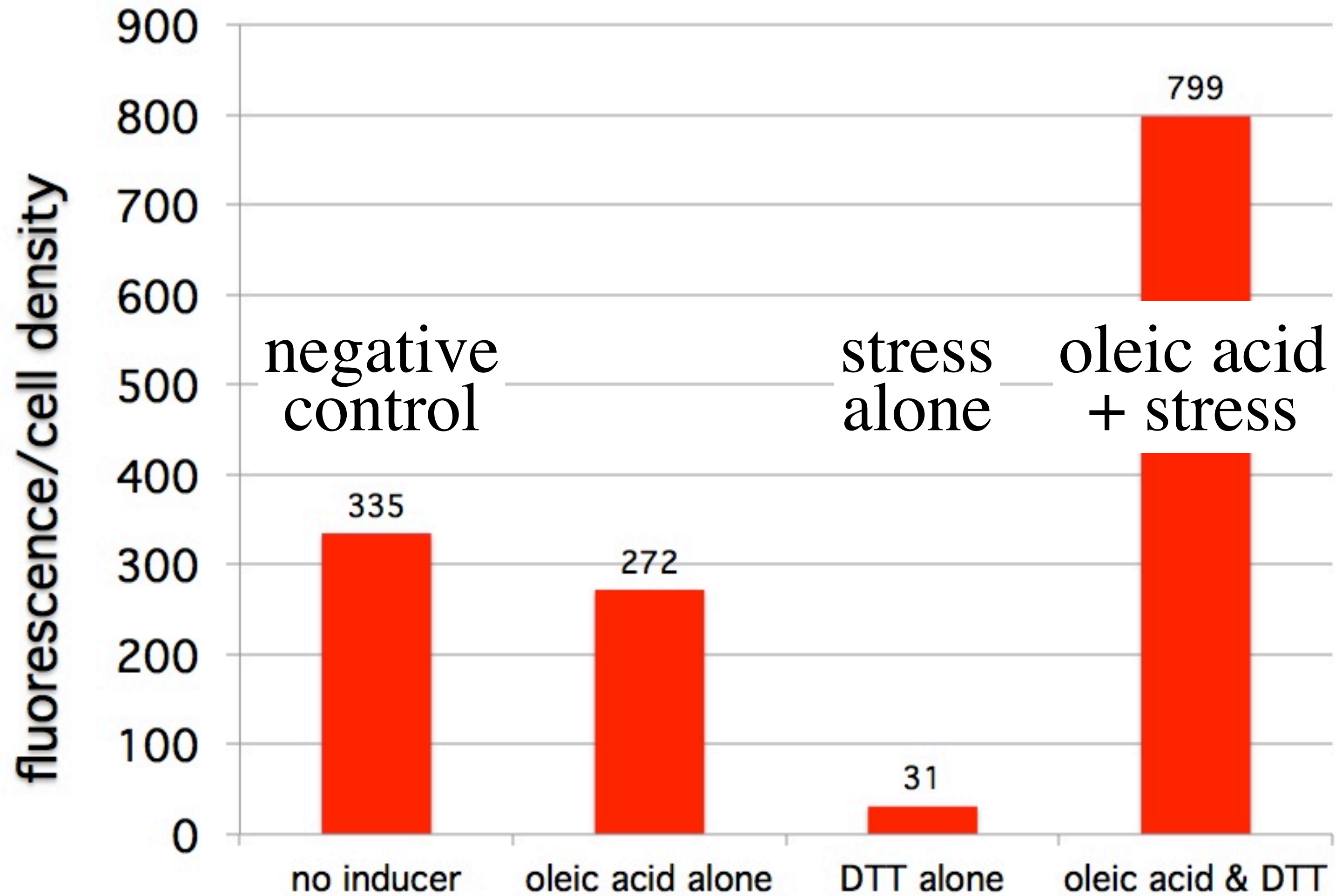
# Testing Stress Module



# Testing Stress Module



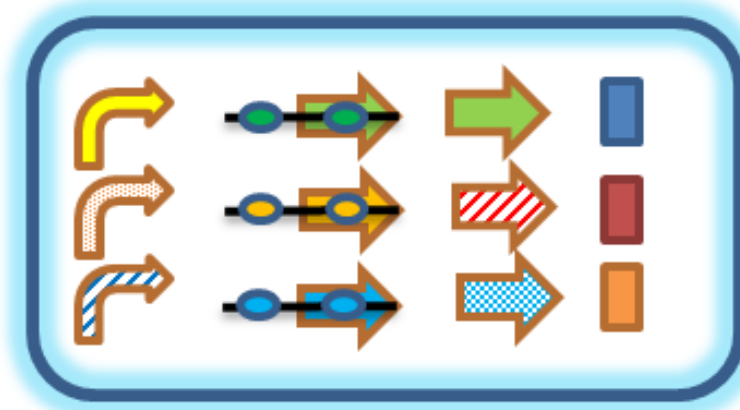
# Testing Stress Module



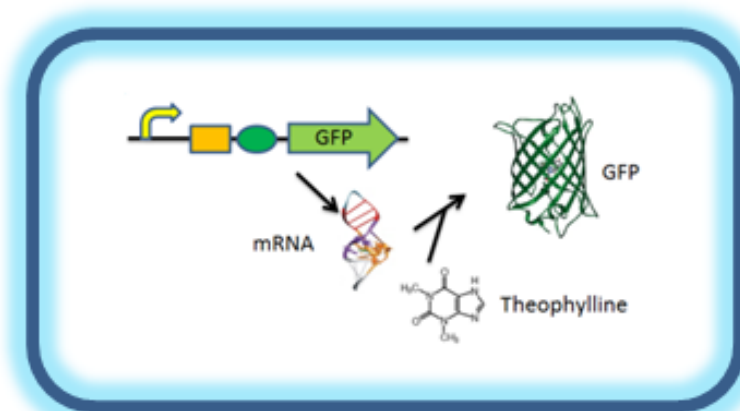
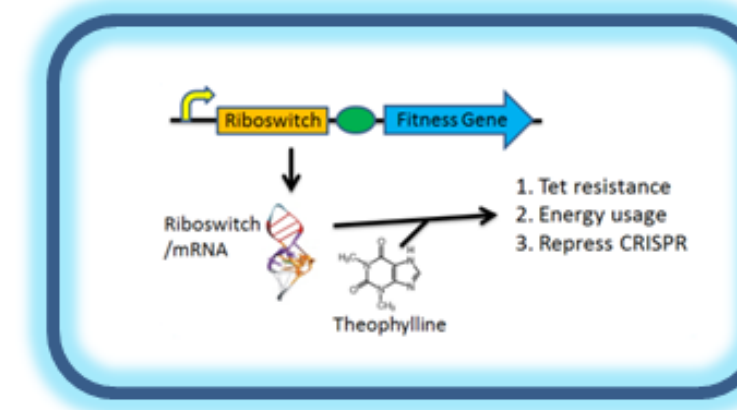


# Programmed Evolution

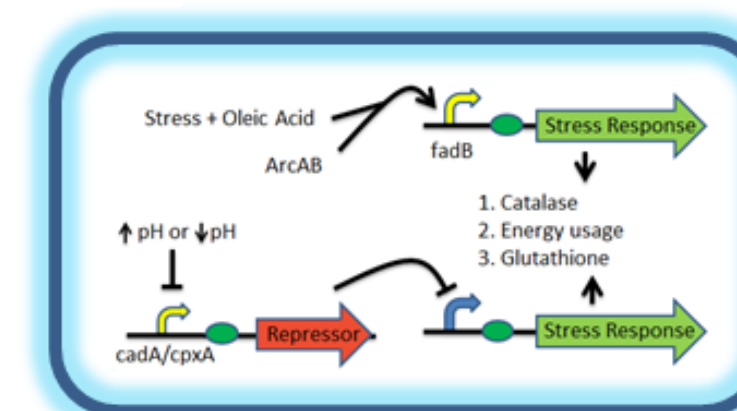
Combinatorics Module



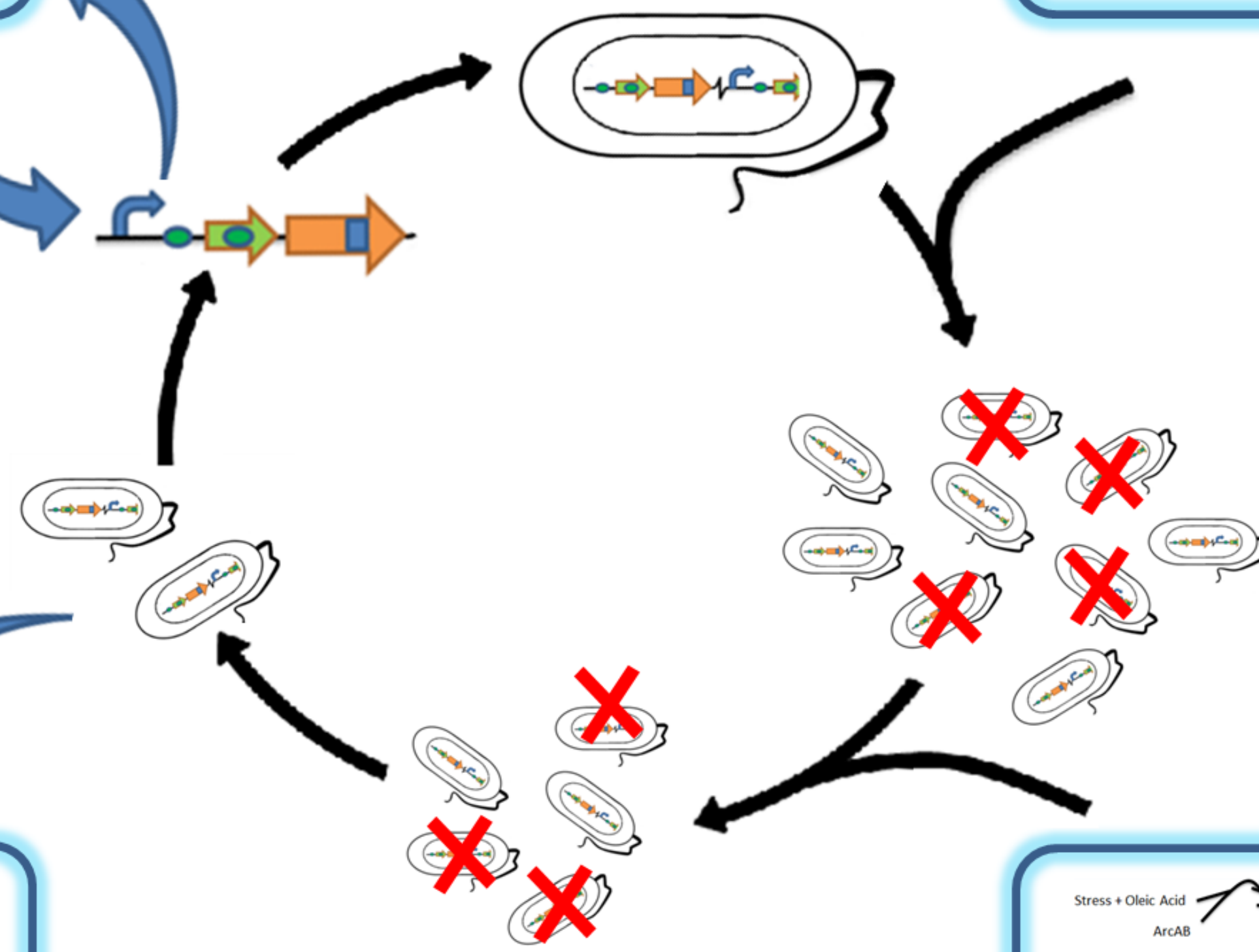
Fitness Module



Biosensor Module



Stress Response Module



No one *gives* you an education.

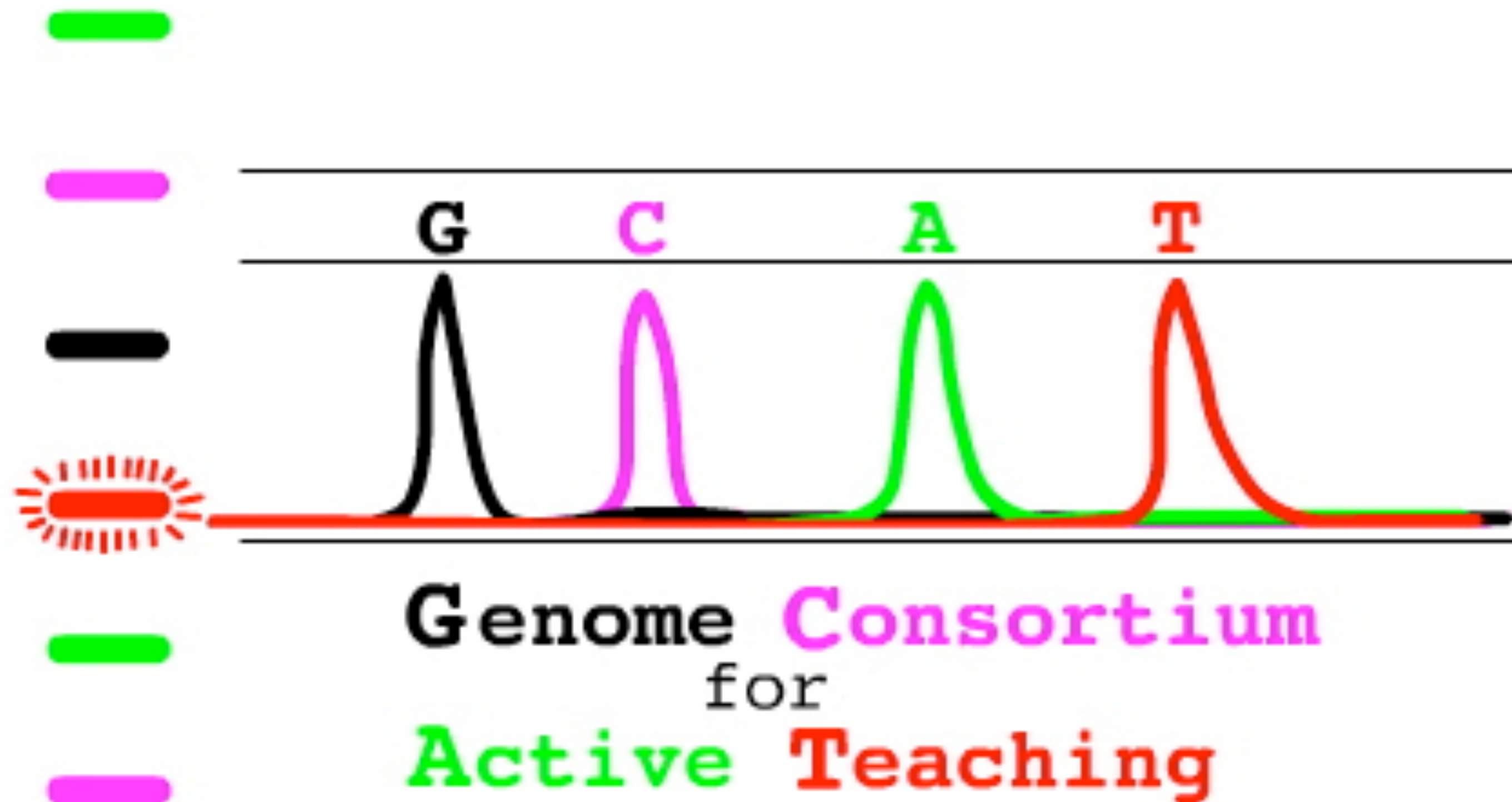


If you want one, you have to take it.

John Taylor Gotto

**Is there a community of  
PUI faculty researchers?**

# 13 Year Collaboration Three Countries



[www.bio.davidson.edu/GCAT](http://www.bio.davidson.edu/GCAT)

# GCAT

## Faculty Development



**NSF funded**

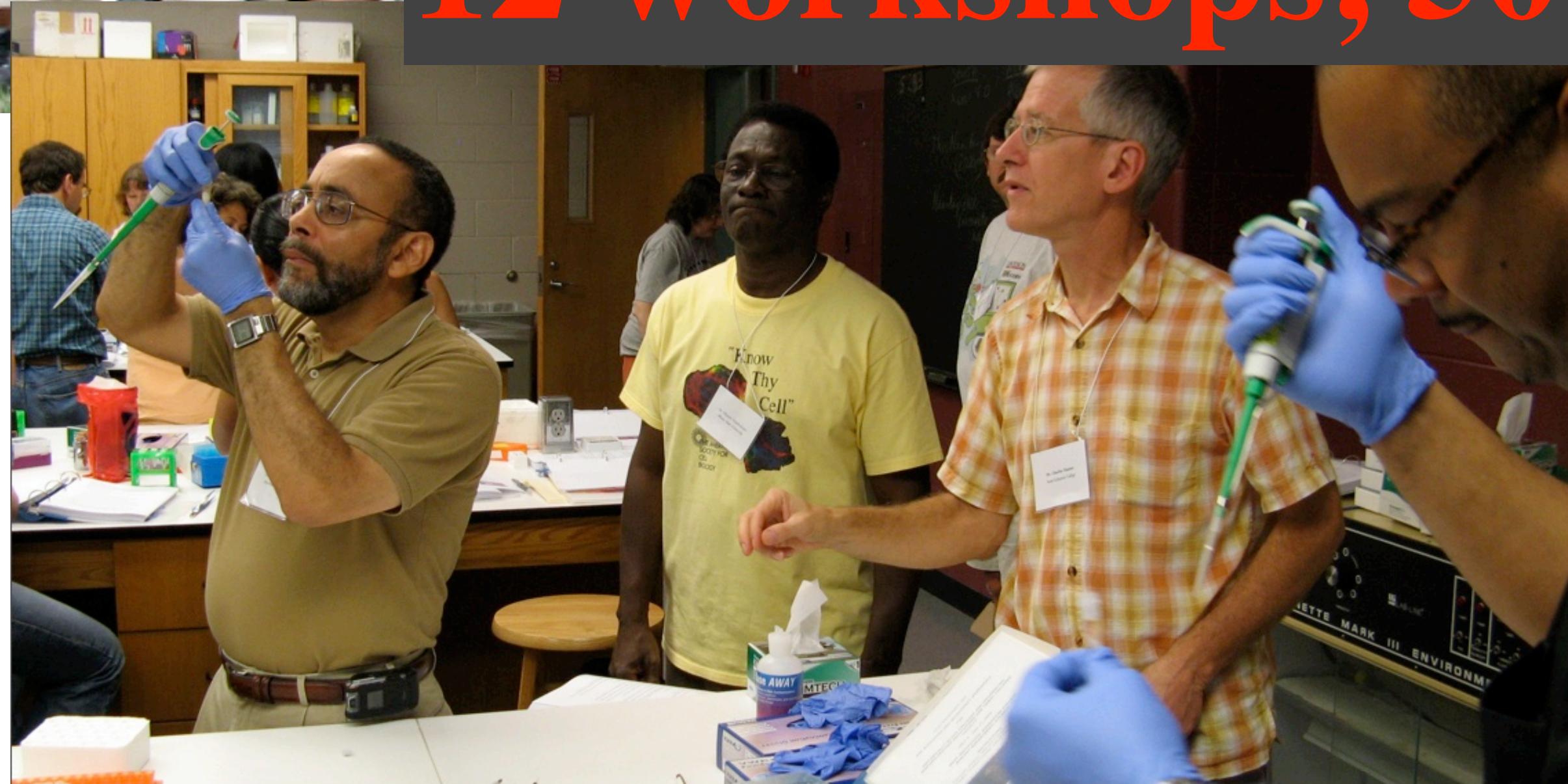


# GCAT

## Faculty Development



**12 workshops, 500 faculty**



# GCAT

## Faculty Development

500 faculty  
X 100 students each  
50,000 students/year



# Faculty Appreciate **GCAT** Resources

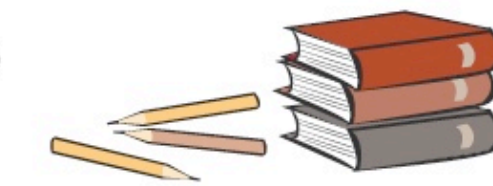
	Mean	SD
Use microarray technology without <b>GCAT</b>	1.5	0.75
Online <b>GCAT</b> protocols useful	4.4	0.69
The <b>GCAT</b> -Listserv helpful	4.2	1.0
<b>GCAT</b> network significant factor	4.2	0.79
Positive experience using <b>GCAT</b>	4.6	0.60
I would use <b>GCAT</b> again in the future	4.7	0.63

1 = strongly disagree

5 = strongly agree



# GCAT



## All Species Microarrays



nature medicine  
**SCIENCE ON A SHOESTRING**

### Teachers' group brings genomics revolution to minority colleges

When the human genome sequence was released in 1999, it meant two things to Edison Fowlks, a biology professor at Hampton University in Virginia. First, genomics technologies were about to revolutionize science. And second, students and faculty of so-called minority-serving institutions such as Hampton, a historically black college, needed to be part of the revolution. But where were such institutions going to come up with the funds to train faculty in the new technologies—much less buy microarrays and the scanners needed to read them? In 2004, Fowlks found an answer when he met fellow biologist A. Malcolm Campbell, who since 2000 had been organizing a program called Genome Consortium for Active Teaching (GCAT) for faculty at small undergraduate institutions. Campbell is himself a researcher at

and genomics without all the powerful equipment that major universities have. Fowlks joined forces with Campbell to expand GCAT's reach. The pair wrote a grant, awarded by the US National Science Foundation, to support a GCAT workshop at Morehouse College in Atlanta in 2005. The agency has committed to funding yearly workshops through 2009; the most recent of these held



Bring on the revolution: Using donated microarrays and a single scanner...

Biological research has been transformed in recent years by substantial advances in efficient data accumulation. The transcription output for every gene in a genome now can be measured in an afternoon; before it might have taken years. However, the recent advances in technology have yet to be incorporated into many biology classrooms (1). Most undergraduates are taught the same way their instructors were taught, which seldom reflects leading-edge research practices. Training faculty in the latest research methods is not well supported on most campuses (2). Worse yet, when students with outdated undergraduate science experiences become primary and secondary school teachers, they condemn future generations to inadequate preparation for college. Today's teachers may also neglect the more quantitative aspects and increased interdisciplinary involvement of modern biology (3-5). Educational options that reflect quantitative, interdisciplinary, and technological trends would provide students with experiences that mirror today's scholarship. We have developed the Genome Consortium for Active Teaching (GCAT) (6) to engage undergraduates in genomics experimental design and data analysis. GCAT faculty use DNA microarrays to bring the excitement of interdisciplinary research to students. Students

discover the importance of quantitative data analysis, and the faculty are reinvigorated by the opportunity to learn new technology. **Origins of GCAT** GCAT was formed in 1999 with the intent of bringing genomics into undergraduate curricula, primarily through student research (7, 8). Leading scientists donated materials and equipment. Undergraduates designed and performed experiments (see photograph above), mailed their microarrays for scanning, and then downloaded and analyzed their data (9). Two limiting factors, long-term scanner access and a growing appetite for microarrays, were addressed by grant support and further donations from scientists (10-12). GCAT thus grew in size and expertise. GCAT supports free access to information and results through its Web site (6) and a listserv of more than 200 subscribers. GCAT projects replaced student laboratory methods less prevalent in today's research, such as cloning and sequencing a gene and Northern blotting. **Rapid Growth** GCAT is committed to enabling any institution to adopt the use of microarrays in its undergraduate curriculum at affordable prices. To date, about 5000 undergraduates from 120

schools have used about 3400 microarrays. For the 2005-2006 academic year, GCAT provided more than 750 microarrays of nine plant, animal, and microbial species to students on 64 different campuses (6, 9). Tested protocols and teaching aids are available from GCAT. Continued grant support (11) covers the cost of microarrays. Schools pay a nominal fee to GCAT for microarrays and scanning. Students produce and hybridize their own probes. Other than the scanners, only standard molecular biology equipment is required; the software is free. The summer workshop costs, which are currently covered by grant support, are about \$2300 per participant. The number of interested faculty continues to grow. Although this enthusiasm is more a measure of the importance of the microarray method in molecular biology today than of GCAT itself, it also serves as a testament to GCAT's user-friendly format. GCAT faculty use the microarrays in various ways. Some analyze existing data sets, such as the yeast diauxic shift data (13) that shows how yeast switch from one metabolic route to another. Other faculty members offer courses in which students collect their own microarray data. Students have studied the effects of environmental conditions on growth, aging in yeast, chromatin structure, and the cellular side effects of chemotherapy (6). Microarrays offer a view of the connections between different pathways in a cell in ways that are hidden by many other methods. For example, one student project looked for expression changes in DNA replication mutants and found cell wall assembly changes, thus linking cytokinesis to mitosis. **Dissemination Through Faculty Development** GCAT has sponsored data generation (wet lab) and data analysis (dry lab) workshops in various settings (14). Wet and dry lab sessions work best when they run 2 and 3 days, respectively. Participants learn data analysis using MAGIC Tool freeware (15). MAGIC Tool works on any computer platform and is designed to enhance student understanding of

GCAT: Genome Consortium for Active Teaching

**JMBE**  
 Journal of Microbiology & Biology Education

**NSF Current**  
 Monthly Highlights of Research and Education Sponsored by the National Science Foundation

Research grants funded  
 Published basic research

May 2007 Volume 8  
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 Introductory Biology Discussion Group Evaluation  
 Marcy Peteroy-Kelly  
 Online Versus Onsite Bioinformatics Instruction  
 Kristina Obom and Patrick Cummings  
 Microbial Mats as Educational Tools  
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In This Issue: Latest Plant Genome Awards • Teachers Jockey Genes  
 RNA Plays Novel Role • New Nanotechnology Centers • NSF's 2005 Facility Plan

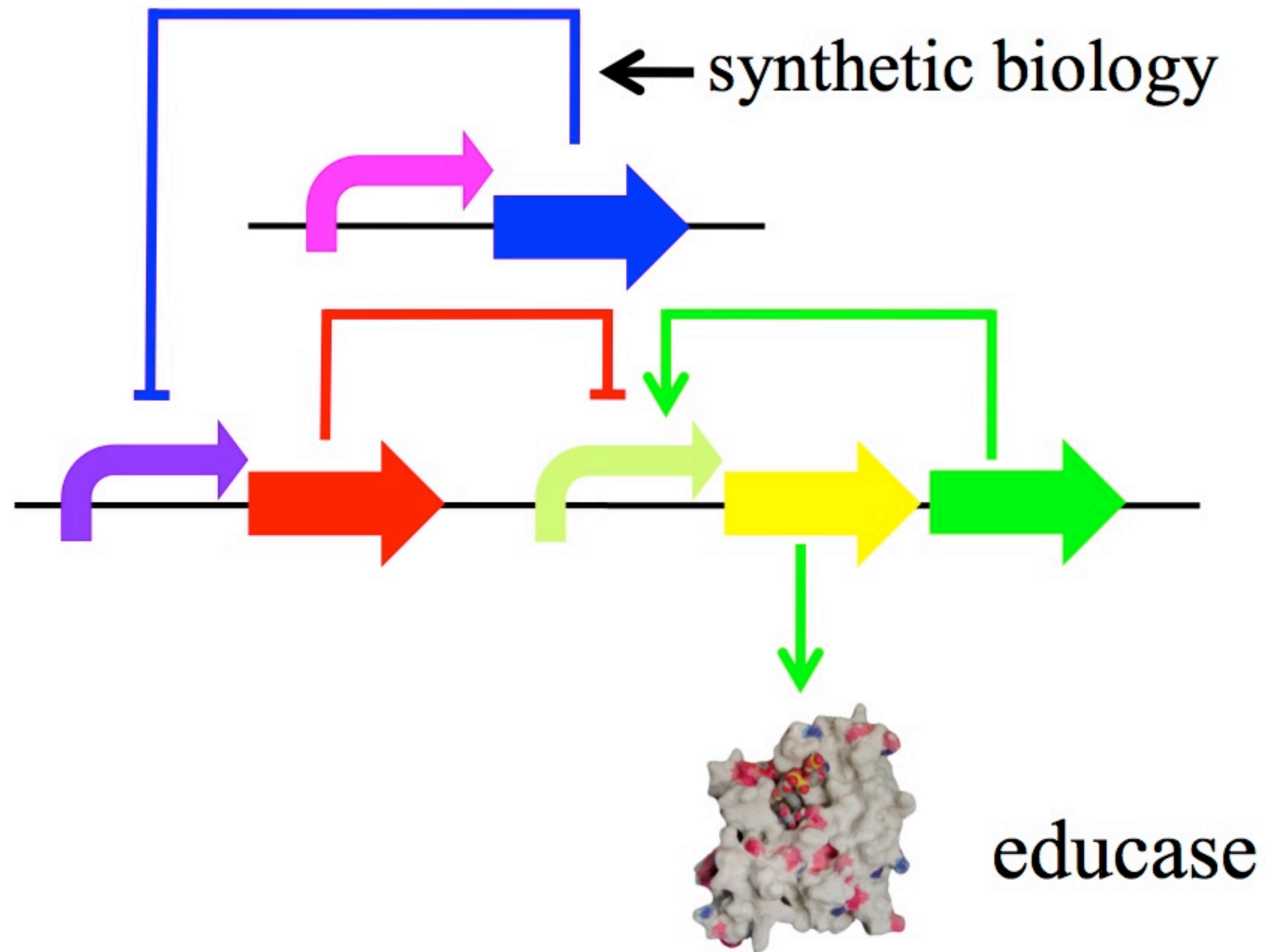
October 2005  
**Awards 19 New Plant Genome Research Projects**  
 genomes of economically important plants are often large and complex, but through in-depth studies scientists uncover information that can be translated into new and improved agricultural products and uses. National Science Foundation (NSF) made 19 new awards totaling \$7 million in the eighth year of its Plant Genome Research Program (PGRP). The two- to five- year awards, ranging from \$622,000 to \$7.7 million, fund research and tools to reveal information in the genomes of economically important crop plants, such as wheat and soybean, as well as increase understanding of the genetics underlying plant processes including disease resistance, flavor development, seed growth and wood formation. NSF's [press release](#) and the [list of 2005 PGRP awards](#) for more information.

NSF made 19 new awards in the eighth year of its Plant Genome Research Program. The awards will support genomics research in major crop plants such as soybean and also in trees including the loblolly pine and poplar. Credit: N. Rager Fuller, NSF.

**Faculty from Minority-Serving Institutions Learn to Teach Microarray Technology**  
 Microarray technology, one of the hottest techniques in biological research, simultaneously measures the expression levels of tens of thousands of genes. Performing DNA microarray experiments and analyzing the mounds of resulting data are generally thought to be beyond the reach of all but a small number of undergraduates working in top research labs. However, the [Genome Consortium for Active Teaching](#) (GCAT), composed of faculty from over 120 primarily undergraduate institutions, has allowed over 4,000 undergraduates to conduct research using DNA microarrays.

Published pedagogy  
 Teaching awards

# G**C**A**T** SynBio



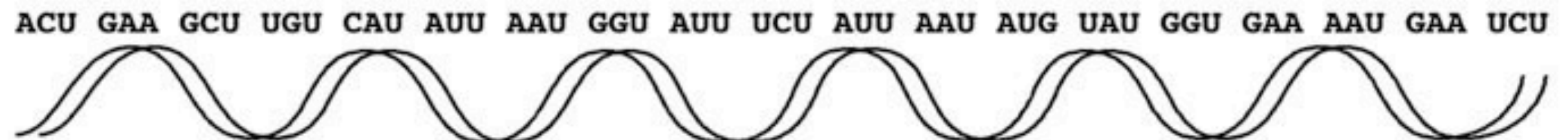
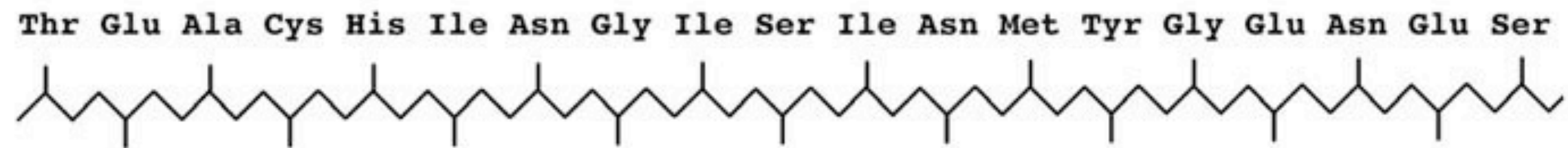
# G**C**A**T** SynBio Faculty Workshops

15 pairs of faculty

1 Bio + 1 Other

Summers 2010-2014

## TEACHING IS IN MY GENES



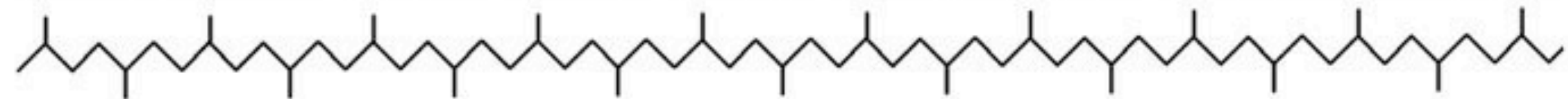
# GCAT SynBio Faculty Workshops

30 faculty X 5 years X 100 students each

**45,000 undergraduates over 5 years**

## TEACHING IS IN MY GENES

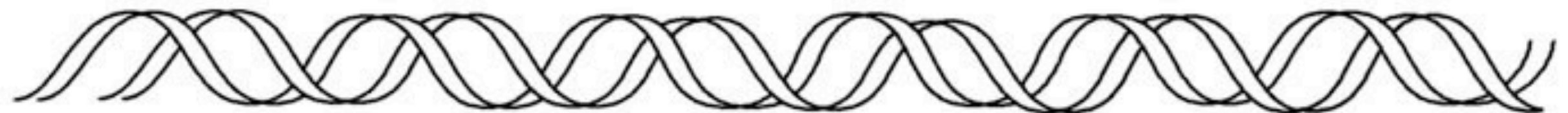
Thr Glu Ala Cys His Ile Asn Gly Ile Ser Ile Asn Met Tyr Gly Glu Asn Glu Ser



ACU GAA GCU UGU CAU AUU AAU GGU AUU UCU AUU AAU AUG UAU GGU GAA AAU GAA UCU



TGA CTT CGA ACA GTA TAA TTA CCA TAA AGA TAA TTA TAC ATA CCA CTT TTA CTT AGA  
ACT GAA GCT TGT CAT ATT AAT GGT ATT TCT ATT AAT ATG TAT GGT GAA AAT GAA TCT



**The scenery only changes for the lead dog.**



# The scenery only changes for the lead dog.



# Acknowledgements

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Genome Consortium for Active Teaching (GCAT)

Davidson College James G. Martin Genomics Program

MWSU SGA, Foundation & Summer Research Institute



