

Bacteria as Analog Computers to Optimize Chemical Synthesis

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Winthrop University

12 March, 2015

Outline of Presentation

What is synthetic biology?

Original research in teaching labs using SynBio.

SynBio can improve pharmaceutical production.

Are you willing to risk failure to find success?

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.

Synthetic Biology

Genetic engineering on a new scale.

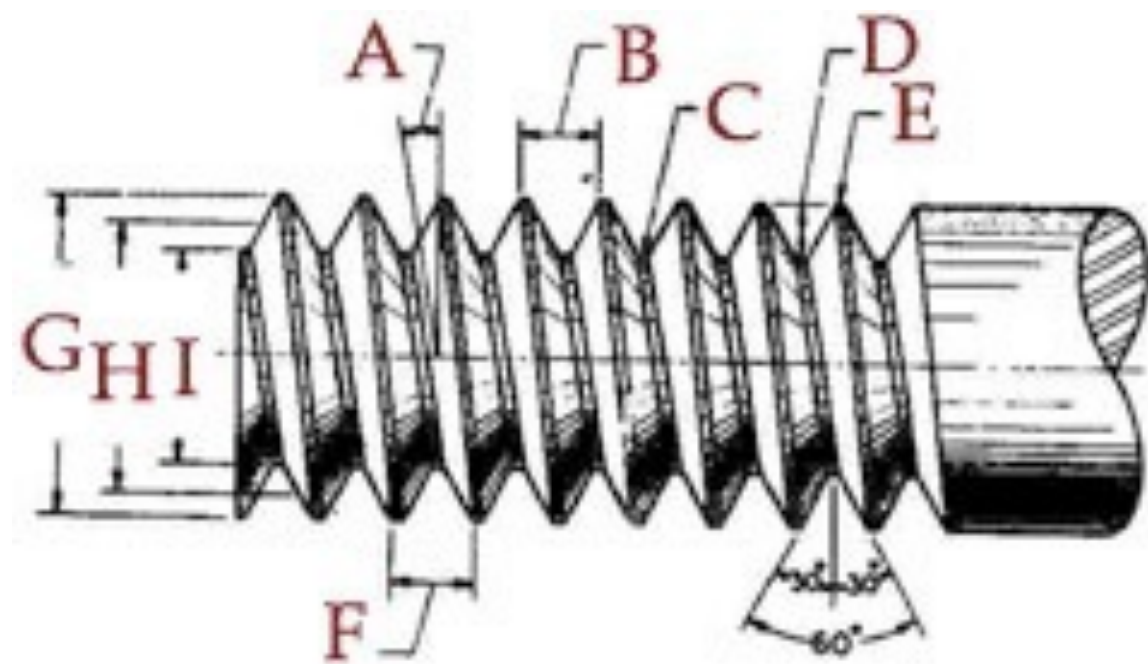
Four Characteristics:

- Standardization
- Modularity
- Abstraction
- Modeling of Designs

Standardization

On a Uniform System of Screw Thread

“In this country, no organized attempt has as of yet been made to establish any system, each manufacturer having adopted whatever his judgment may have dictated as best, or as most convenient for himself.”

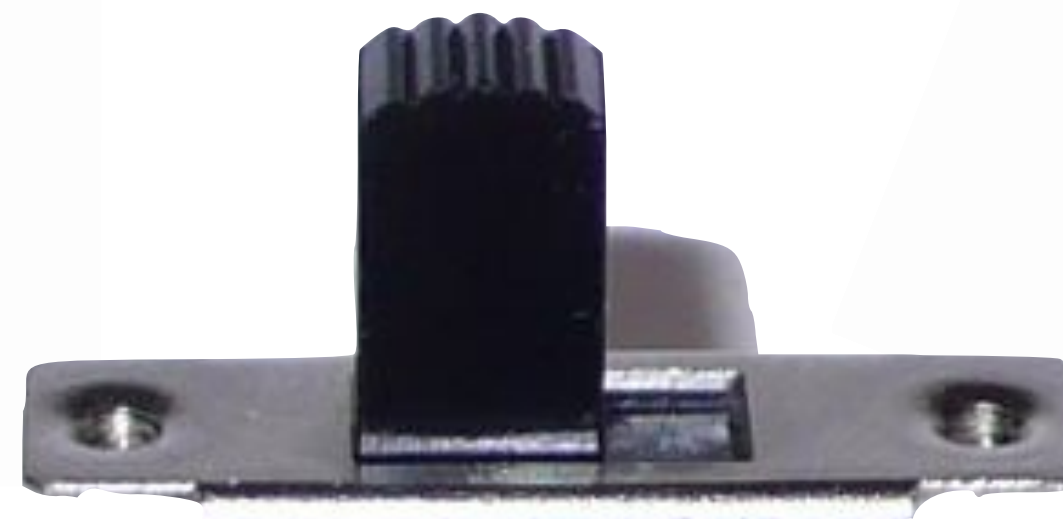
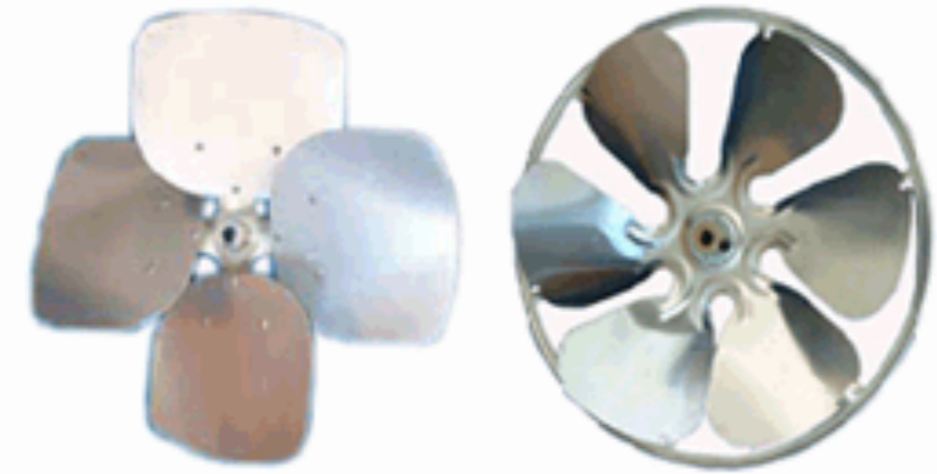
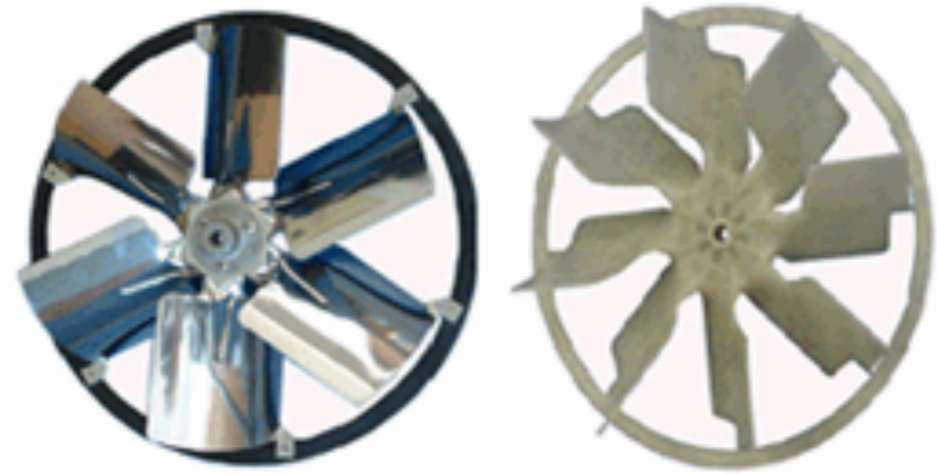


William Sellers April 21, 1864

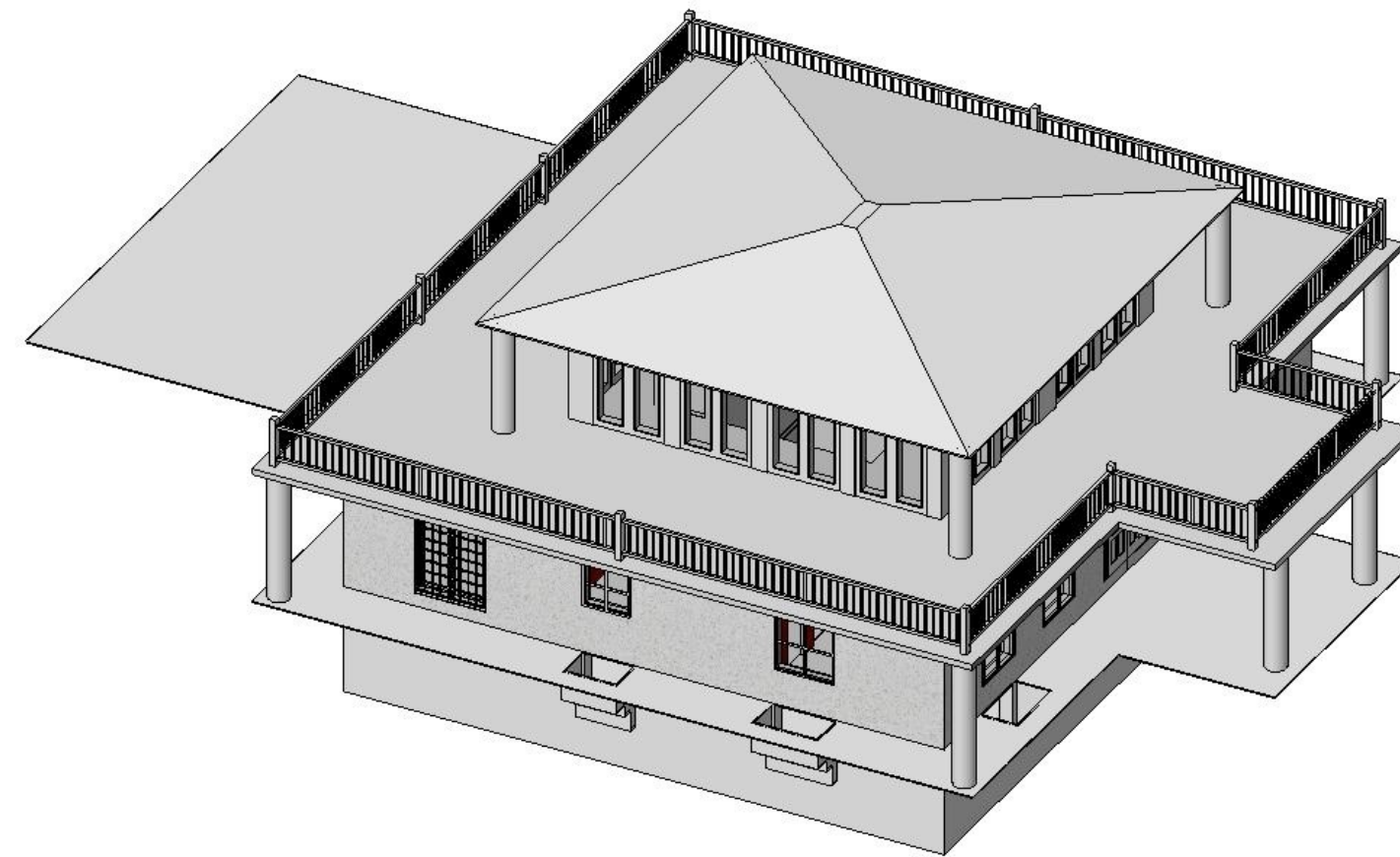
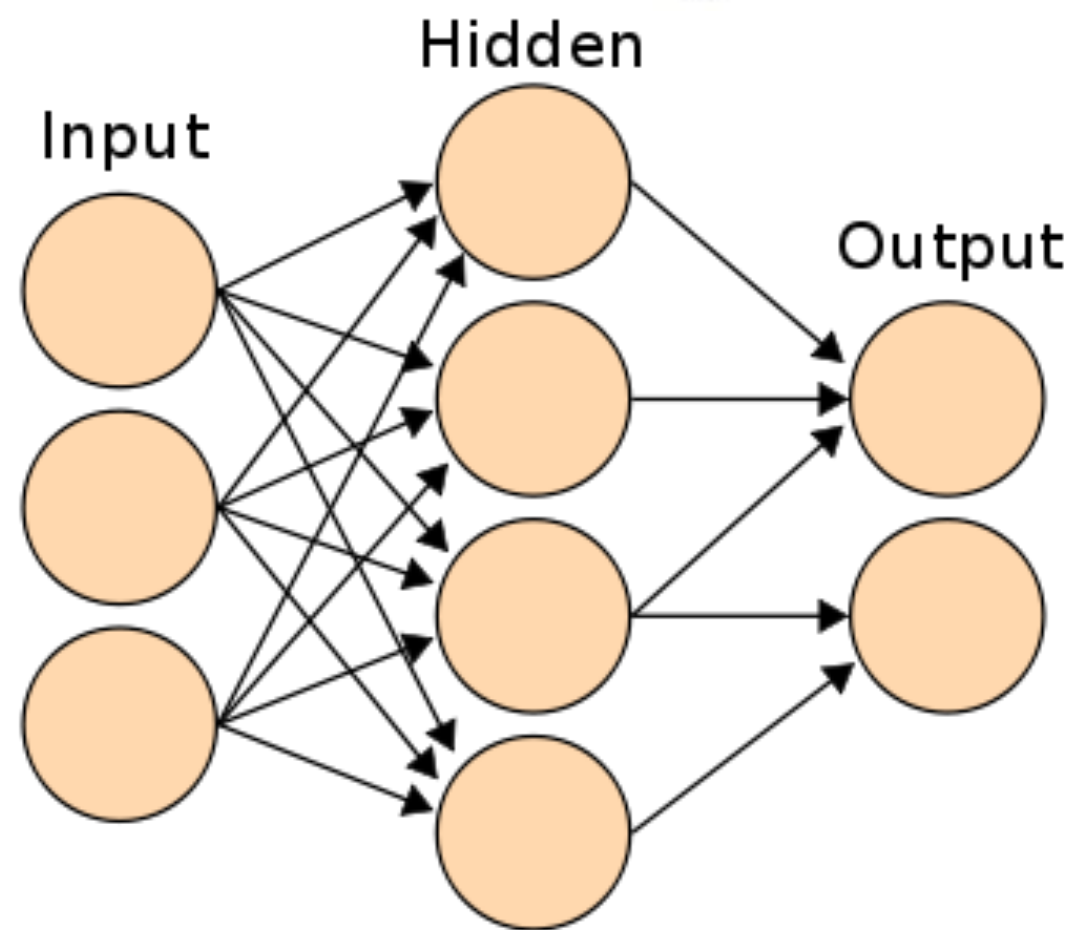
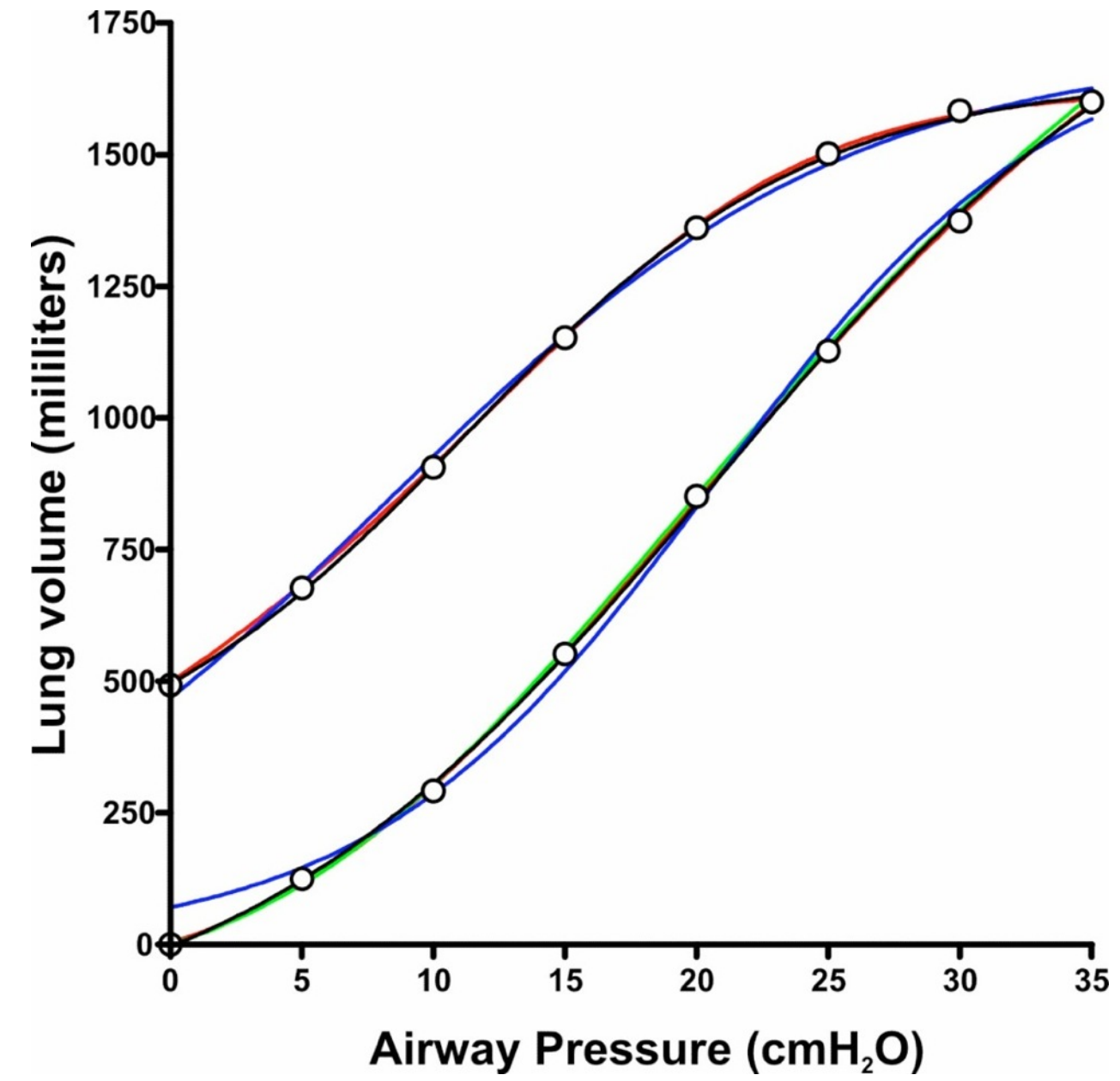
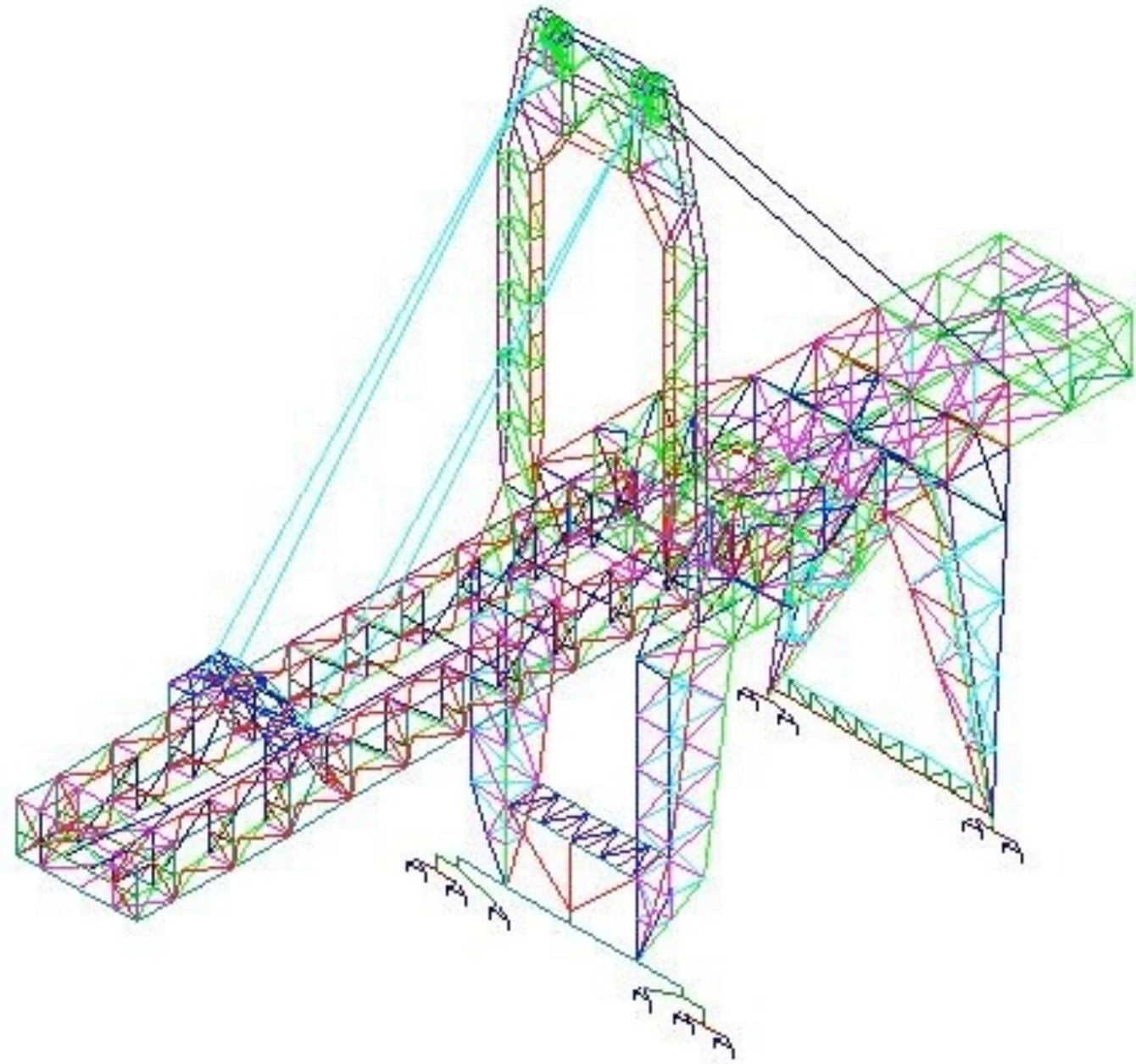
Modularity



Abstraction



Modeling of Designs



Original SynBio Research by
Undergraduates in Teaching Labs

Eco RI

GAATTC

CTTAAG

palindrome

type II

Eco RI

GAATTC
CTTAAG

palindrome

type II

Eco RI



type II

Eco RI

G

AATTC

CTTAA

G

type II

Bsa I

GAGACC

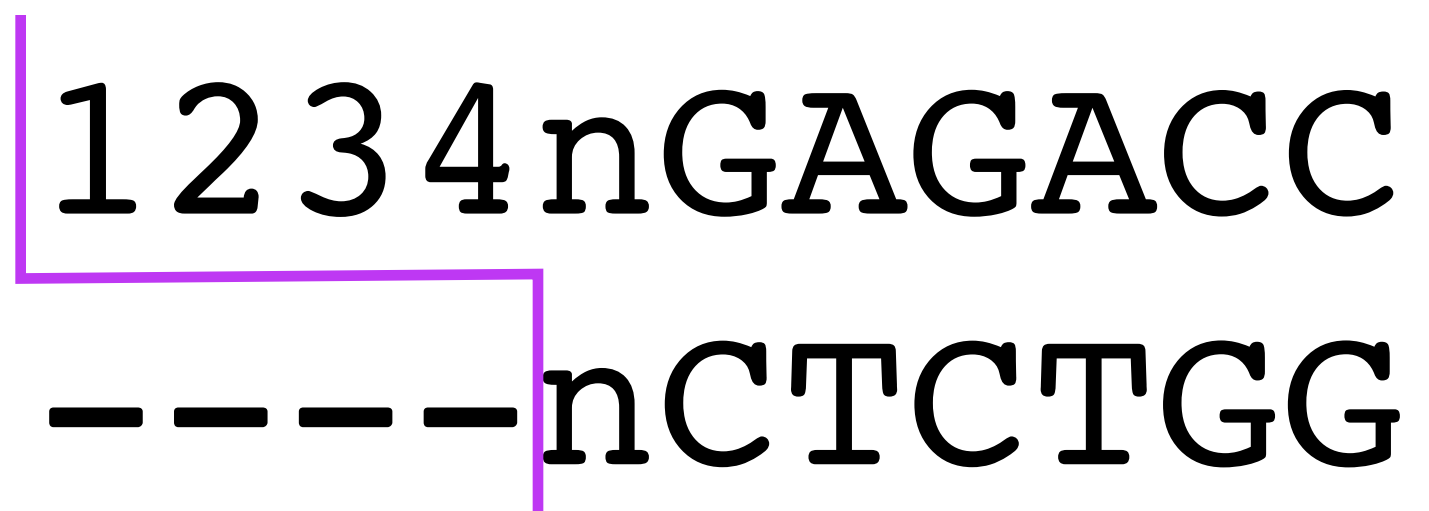
CTCTGG

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

A diagram showing the recognition sequence for the Bsa I restriction enzyme. The top strand is 5'-1 2 3 4 n G A G A C C-3' and the bottom strand is 3'-- - - - n C T C T G G-5'. A purple line highlights the recognition sequence: a vertical line at position 1, a horizontal line from position 1 to 4, and a vertical line at position 4.

type II

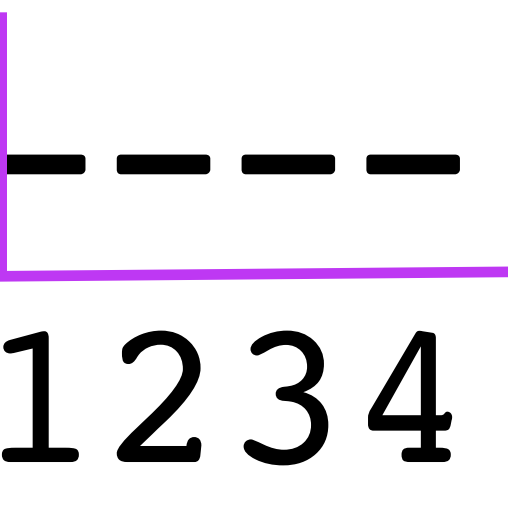
Bsa I

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

type II

Bsa I

GGTCTCn-----
CCAGAGn1234

A diagram showing the recognition sequence for Bsa I. The top strand is GGTCTCn----- and the bottom strand is CCAGAGn1234. A purple line connects the 'n' in the top strand to the '1' in the bottom strand, indicating a staggered cut site. The bottom strand has four positions labeled 1, 2, 3, and 4.

type II

Bsa I

GGTCTCn

CCAGAGn1234

type II

Bsa I

cuts
left

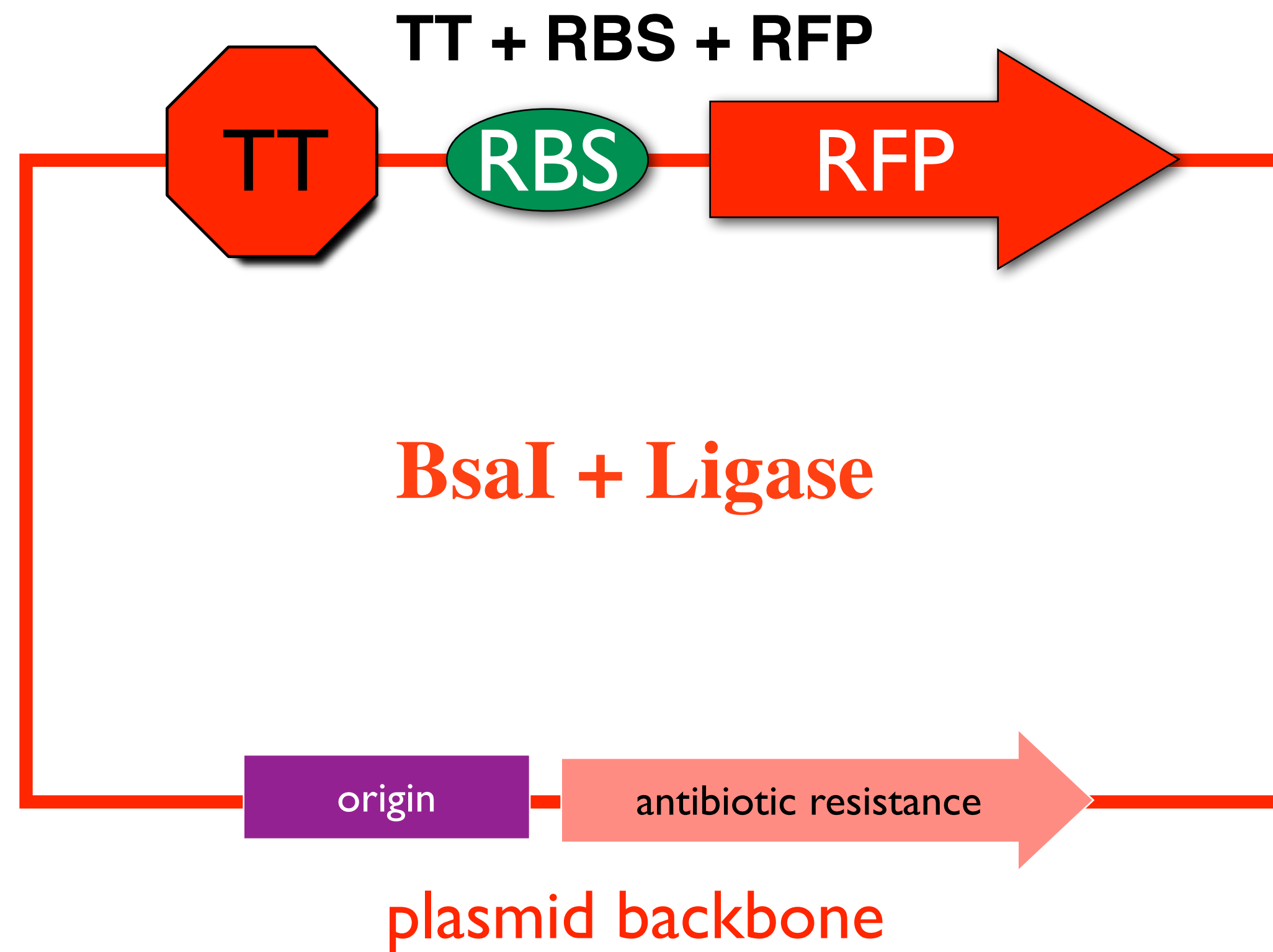
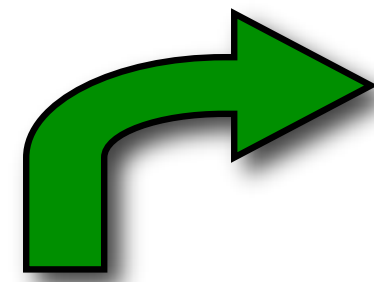
1 2 3 4 n GAGACC
-----n CTCTGG

GGTCTCn-----

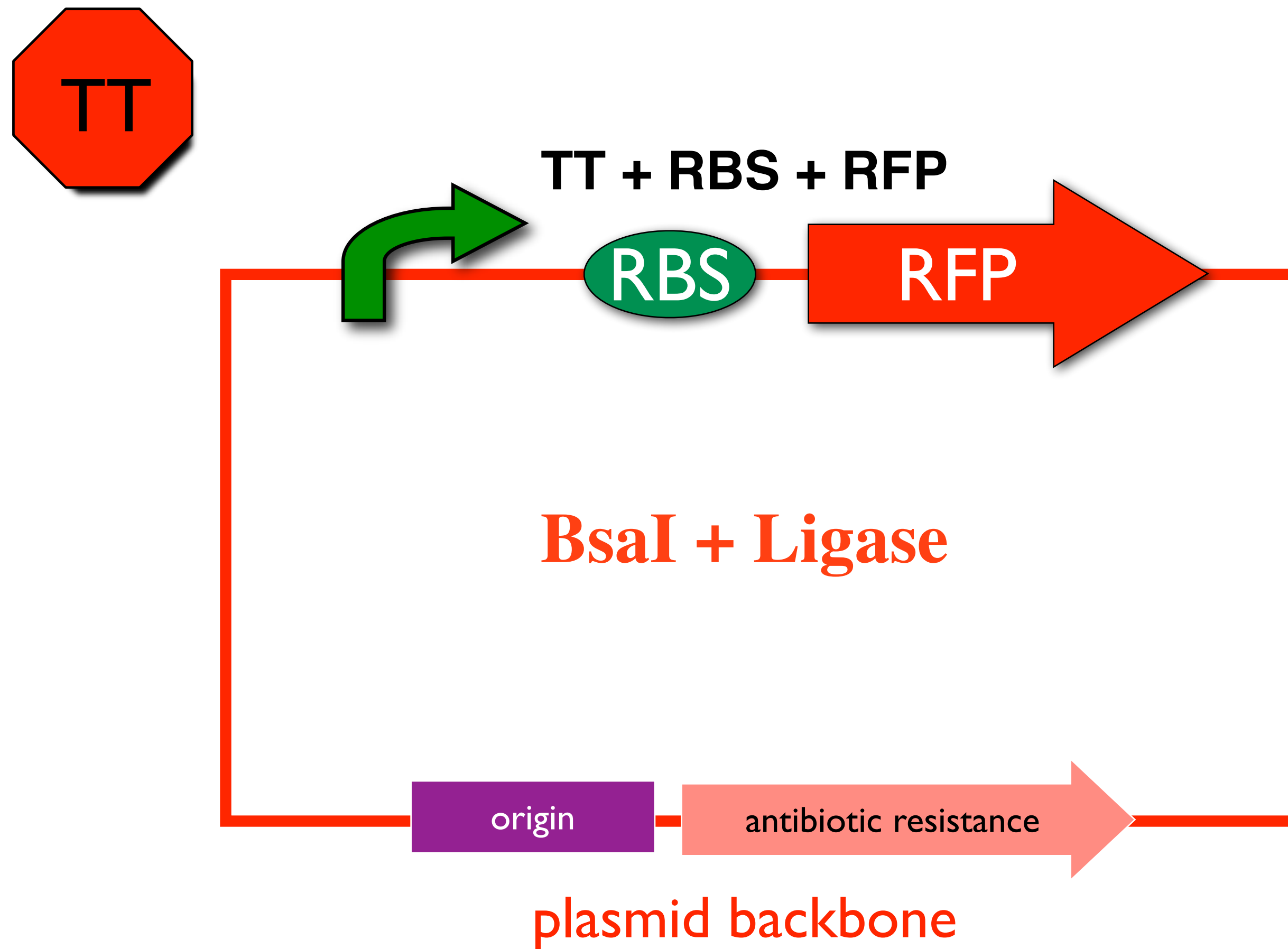
CCAGAGn 1 2 3 4

cuts
right

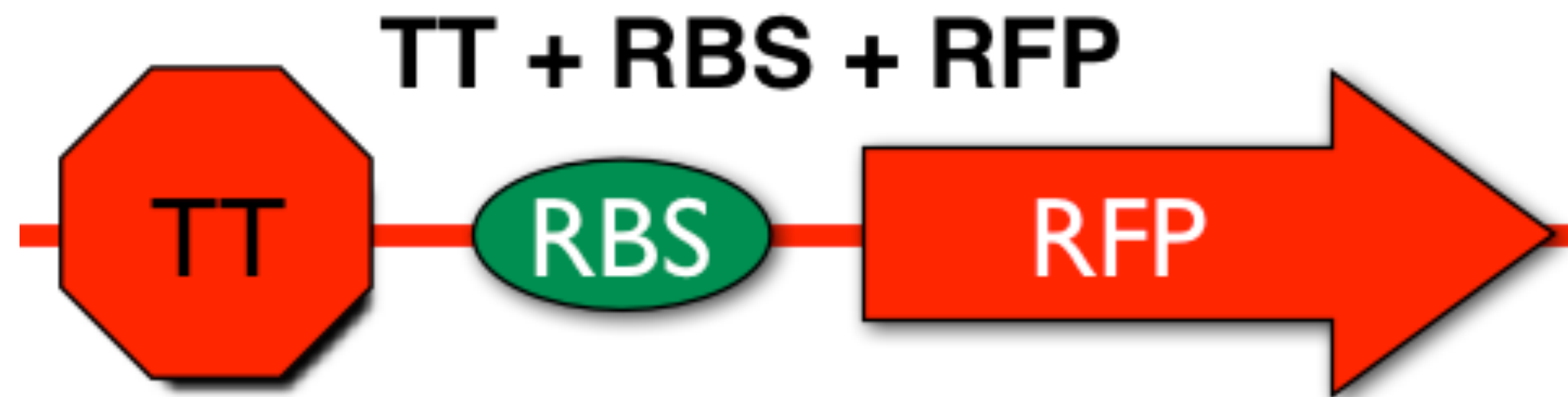
GGA Ligation Method



GGA Ligation Method

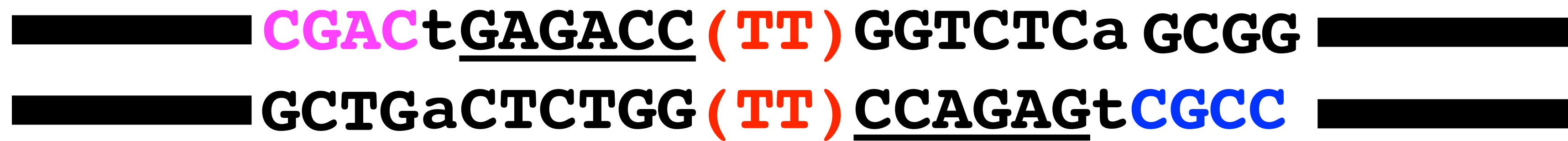


GGA Ligation Method



GGA Ligation Method

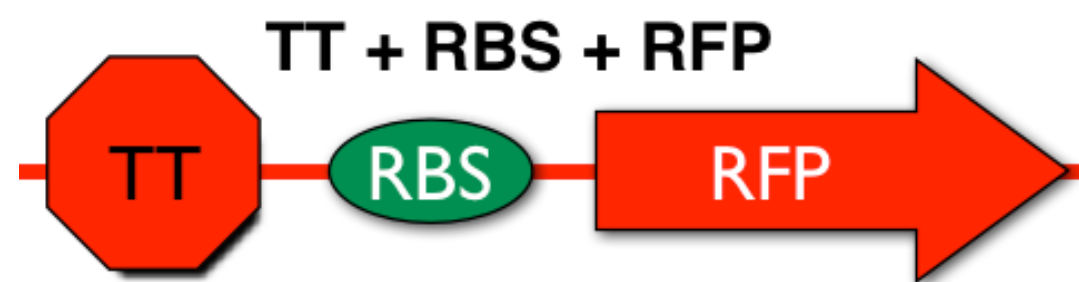
Bsa I



Bsa I

ligase

ligase



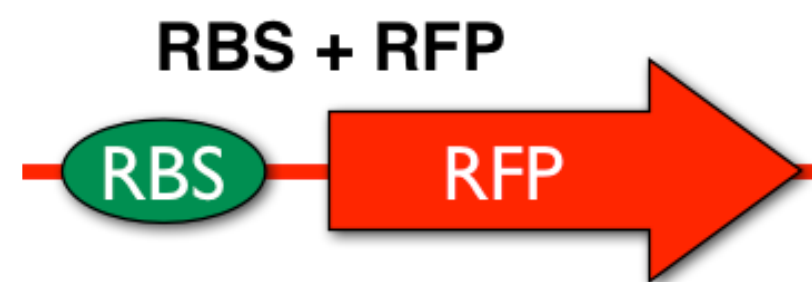
CGACtGAGACC (**TT**) GGTCTCa
aCTCTGG (**TT**) CCAGAGt**CGCC**

██████████
██████████ **GCTG**

ligase

GCGG ██████████
██████████

ligase



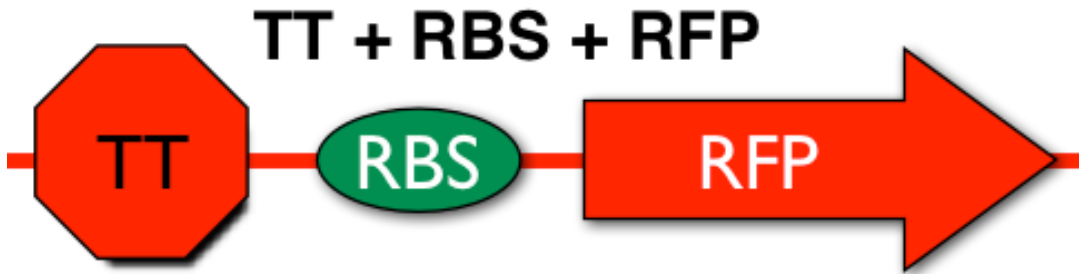
Bsa I

██████████ **CGAC** **t****GAGACC** **(TT)** **GGTCTCa** **GCGG** ██████████

██████████ **GCTGa****CTCTGG** **(TT)** **CCAGAG****t** **CGCC** ██████████

ligase

Bsa I ligase



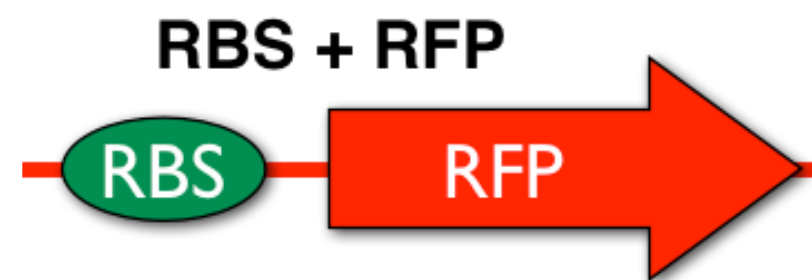
CGAC†**GAGACC** (**TT**) **GGTCTCa**
aCTCTGG (**TT**) **CCAGAG**†**CGCC**

██████████
██████████ **GCTG**

ligase

GCGG ██████████
██████████

ligase

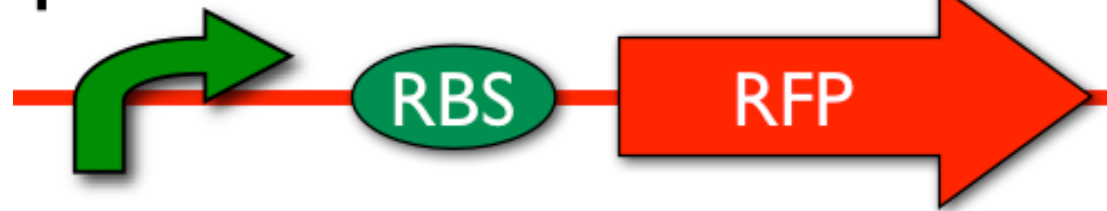


CGAC

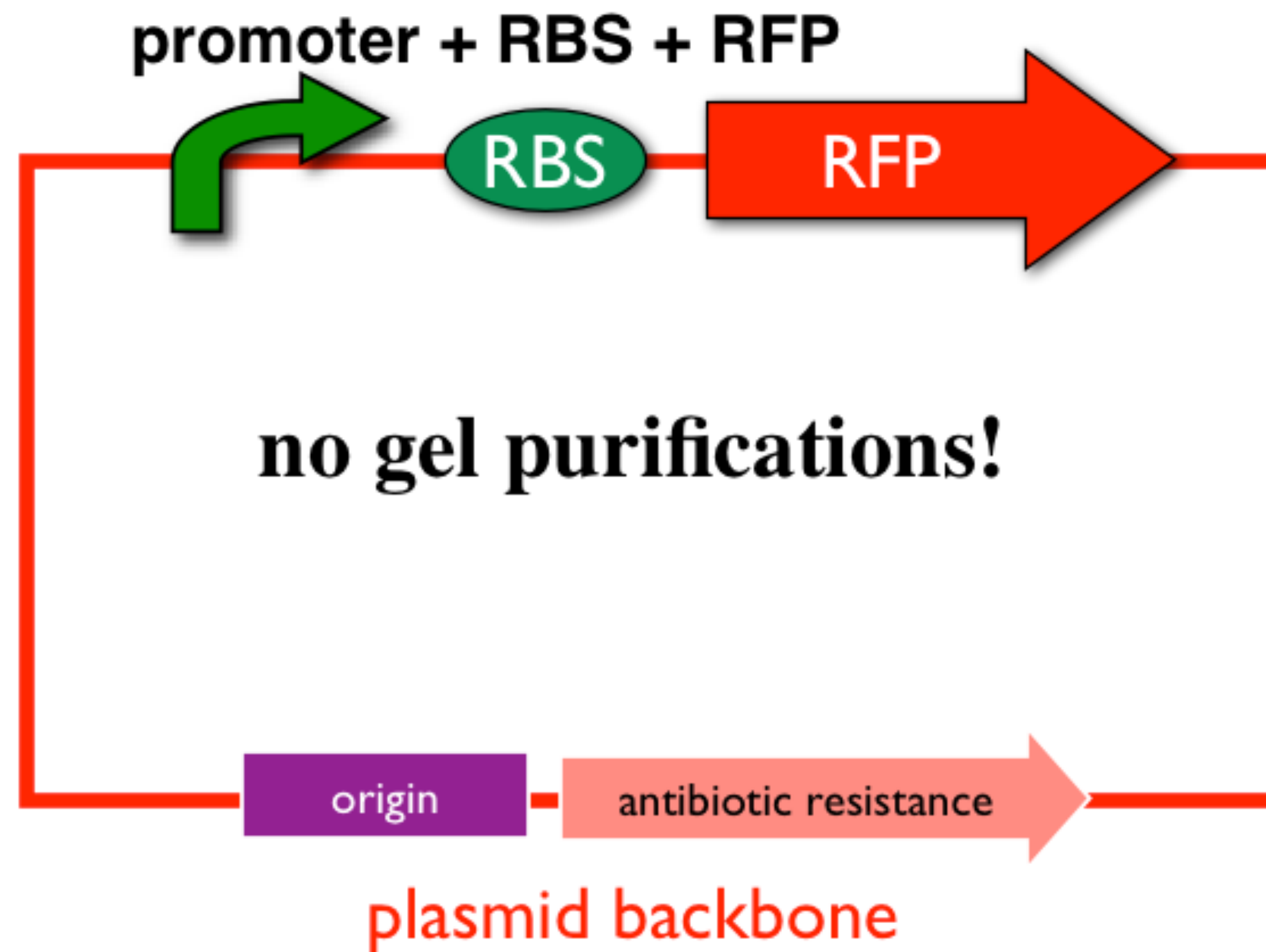
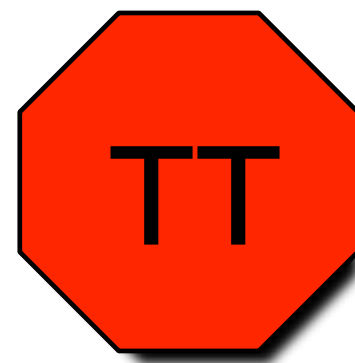
CGAC

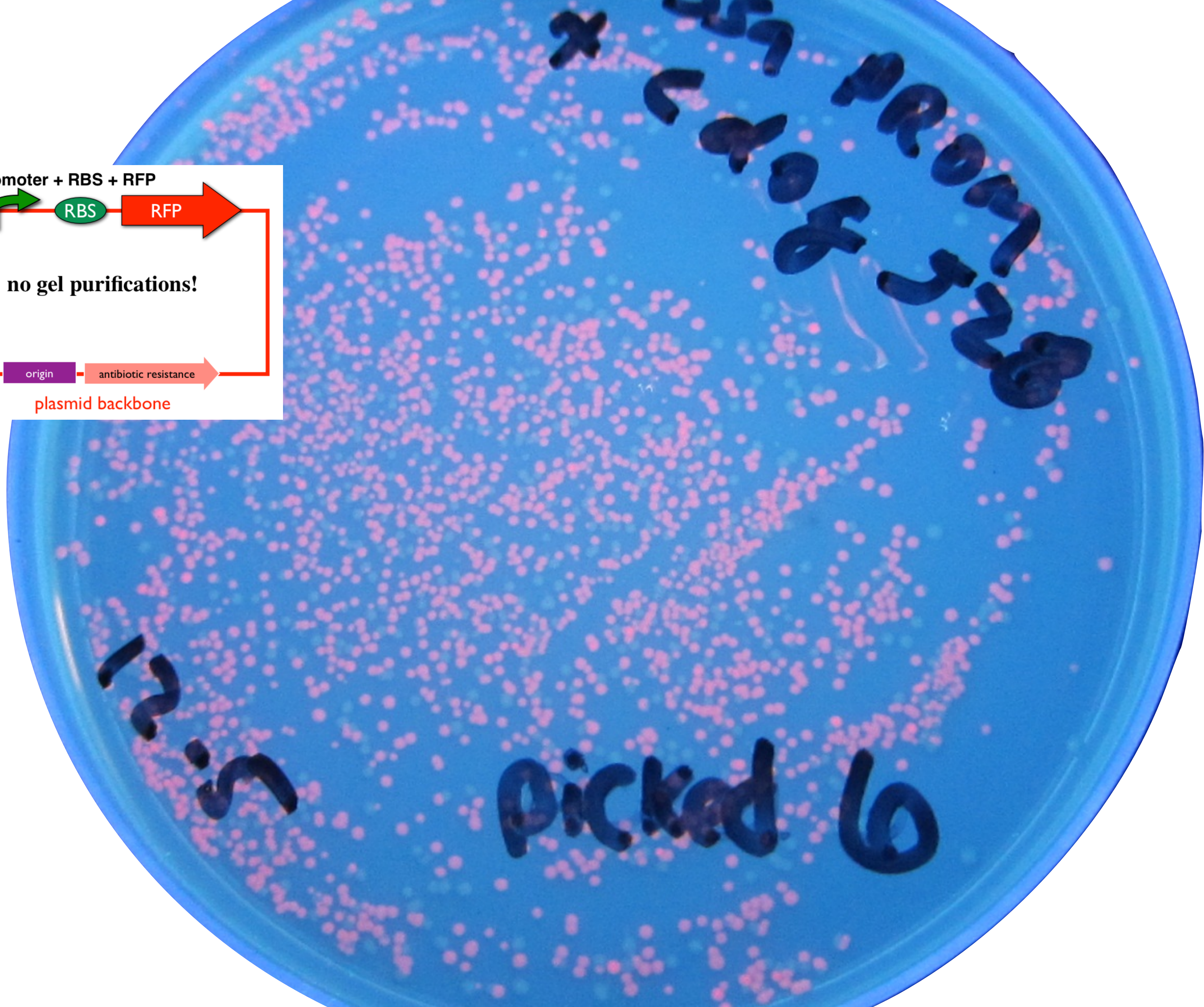
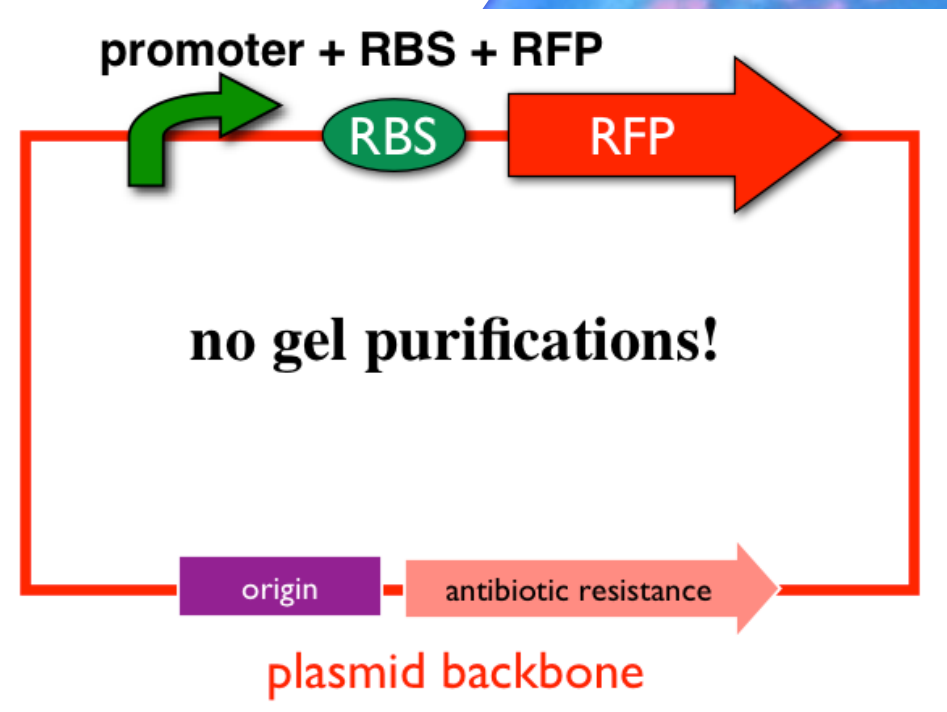


promoter + RBS + RFP

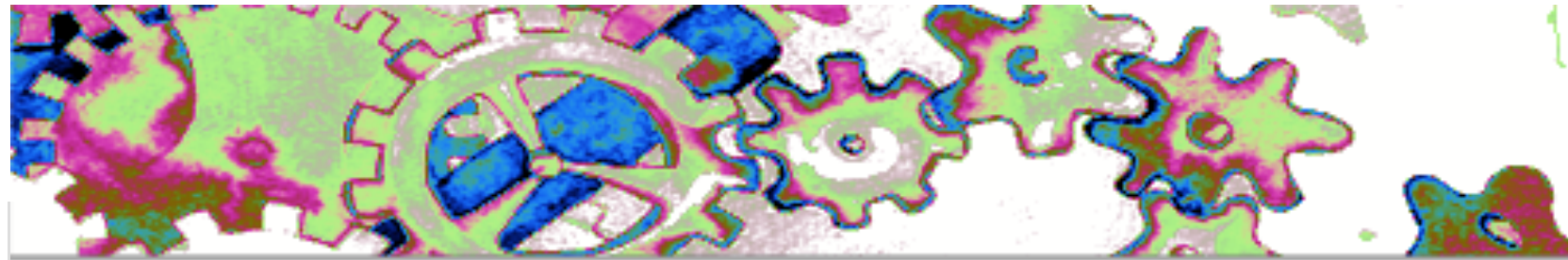


GGA Ligation Method






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	J10068: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 Niesma	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


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[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)

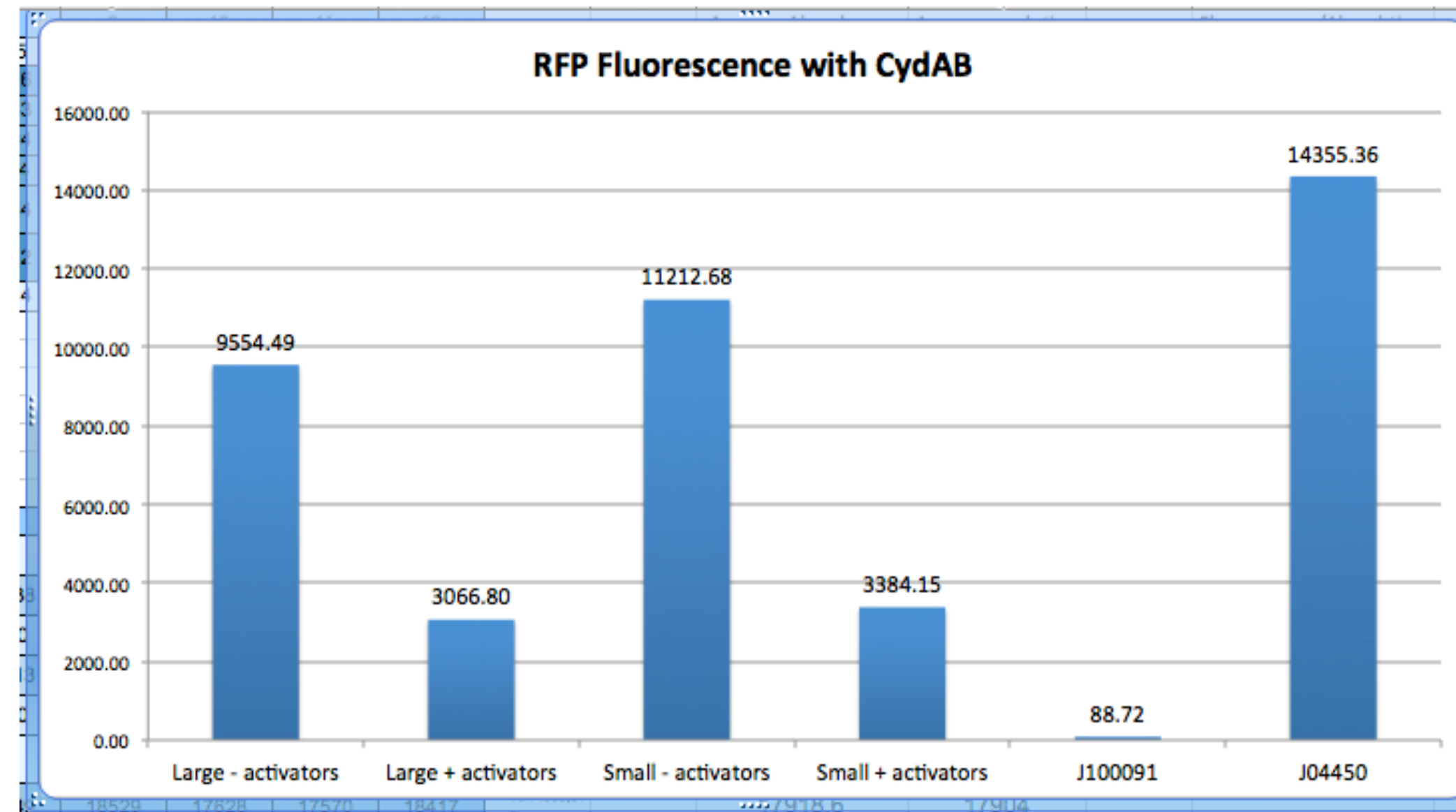


DNA Planning
Experience: Works
[Get This Part](#)

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 florescence (J04450) and a negative control with cells containing a the transcriptional terminator that does not cause red florescence (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/

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 Iffy

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	R0040	tcctatcagtgatagagattgacatccctatcagtgatagagatactgagcac	54			Regulated	Repressible	TetR			pSI
2	56 bp LacI Promoter	K091110	cgttgacaccatcgaatggcgcaaaaccttccggtatggcatgatagcgccgg	56			Constitutive					
3	200 bp LacI Promoter	R0010	caatacgcaaacgcctctccccgcgcttgccgattcattaatgcagctggcac gacaggttcccactggaaagcgggcagtgagcgaacgcaattaatgtgagtt agctcactcattaggcaccagggtttacactttatgcttccggctcgtatgtgtg ggaattgtgagcggataacaattcacaca	200			Constitutive					
4	LuxR & HSL Regulated Lux promoter	R0062	acctgtaggatcgtacaggttacgcaagaaaatggtttgatagtcgaataaa	55			Regulated	Repressible				
5	Backwards 200 LacI Promoter (right to left)	J31013	tgtgtgaattgttatccgctcacaattccacacaacatacagccggaagcataaa gtgtaaagcctggggtgcctaataatgagtgagctaactcacattaattgcgttgcgctc actgcccgttccagtcggaaacctgtcgtgccagctgcattaatgaatcgcca acgcgccccggagaggcggtttgcgtattg	200			Regulated	Repressible				
6	OmpC Promoter	K199017	tttacatttgaacatctatagcgataaatgaacatcttaaaagttttagtatcatattc gtgttgattattctgcattttgggagaatggact	99			Constitutive					
7	23K series very strong constitutive Promoter	J23100	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

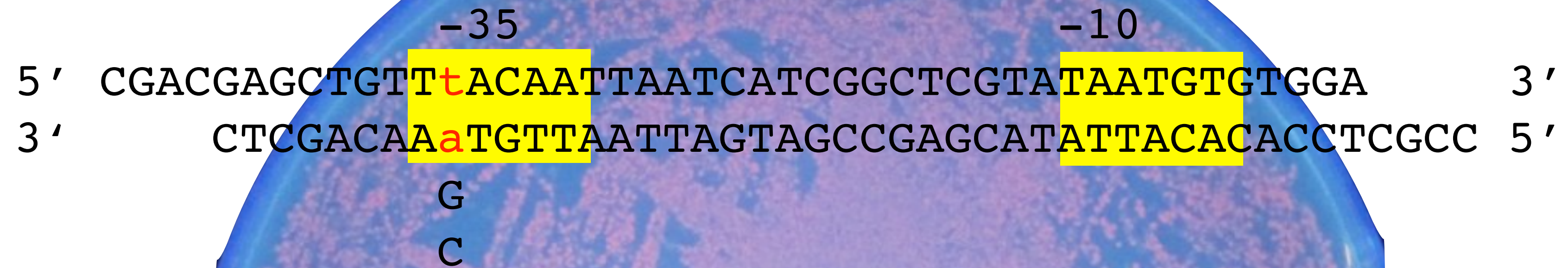
A petri dish containing a bacterial culture on a blue agar surface. The surface shows a central zone of dense growth and several smaller, more diffuse growth spots. Handwritten in blue ink on the rim of the dish are the words "EB amp oligos Ptac" at the top, "20 cyes" on the right, and "P100" on the left. The DNA sequence below is overlaid on the dish image.

-35 -10

5' CGACGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 3'

3' CTCGACA ACTGTTAATTAGTAGCCGAGCATATTACACACCTCGCC 5'

Student Sample, November 2012



Student Sample, November 2012

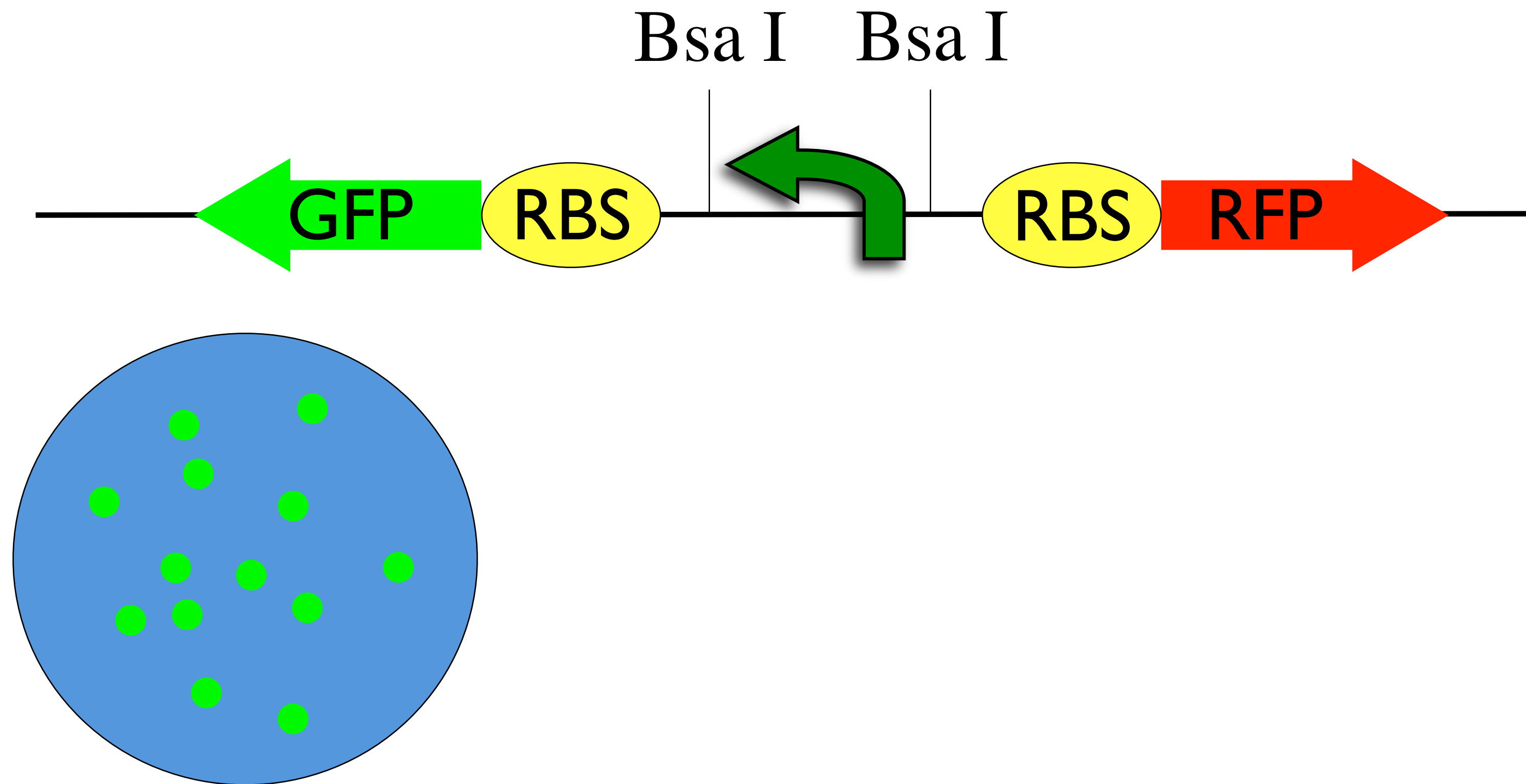
TBA

-35 ATAA (deleted) -10

5' CGACGAGCTGTTGACA-----ATCATCGGCTCGTATAATGTGTGGA 3'
3' CTCGACA ACTGT-----TAGTAGCCGAGCATATTACACACCTCGCC 5'

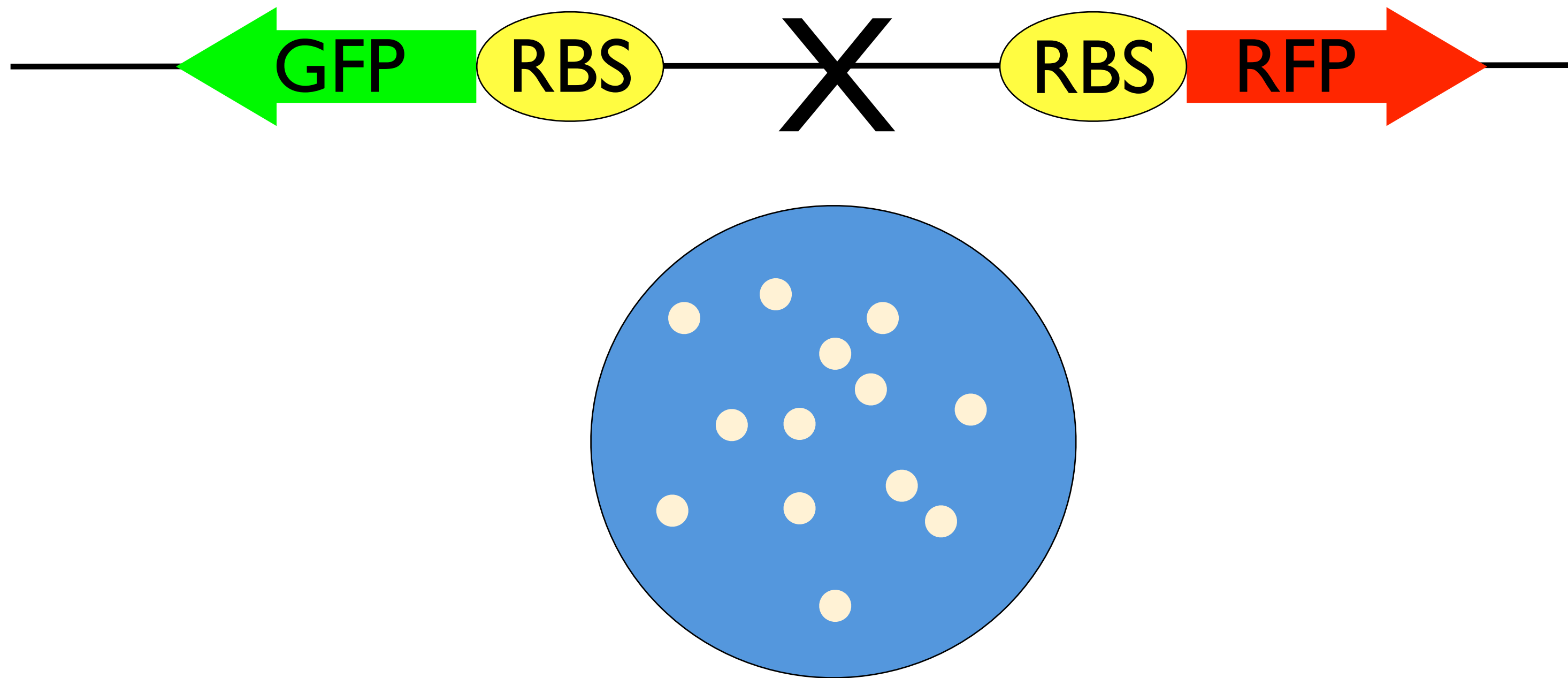
11-7-12

pClone Red J119137



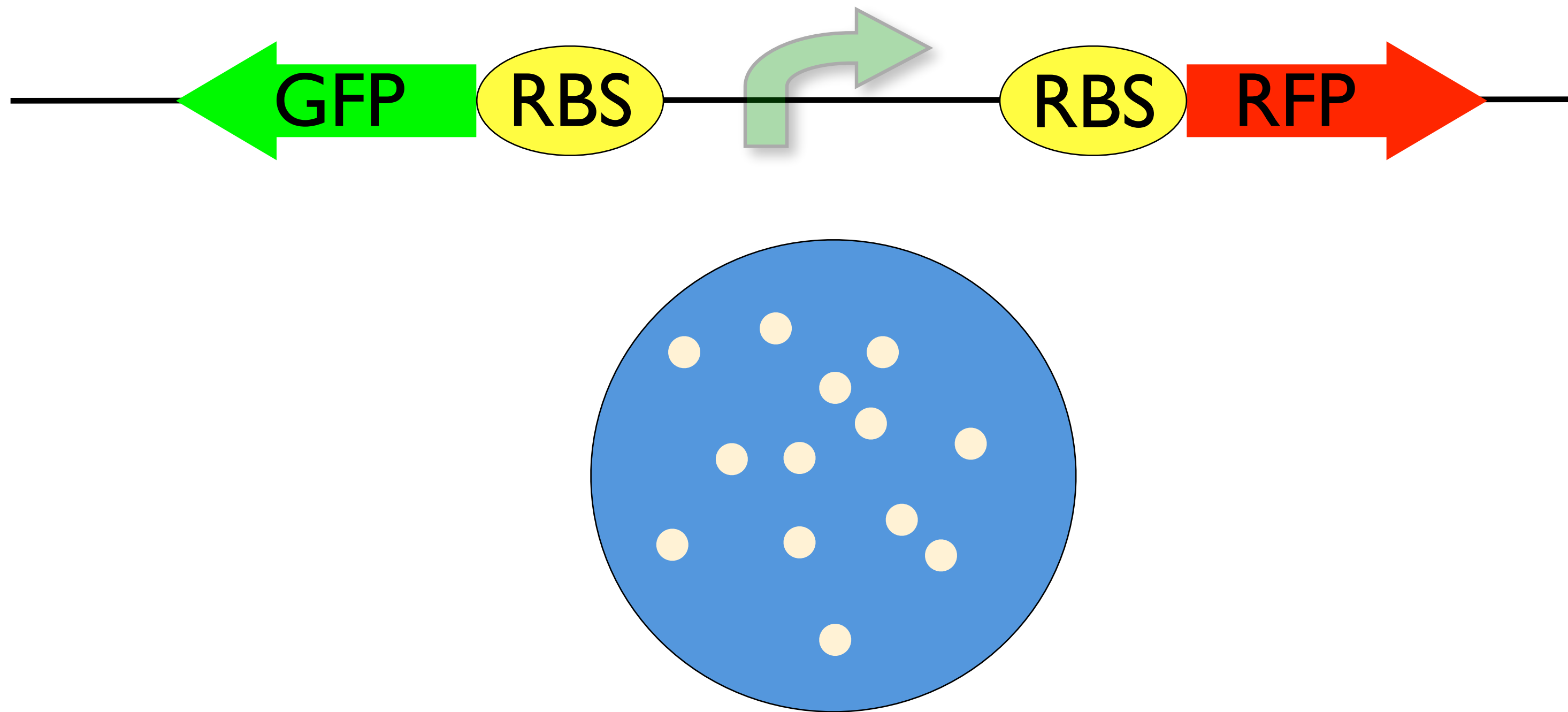
Remove Initial Promoter

J119137



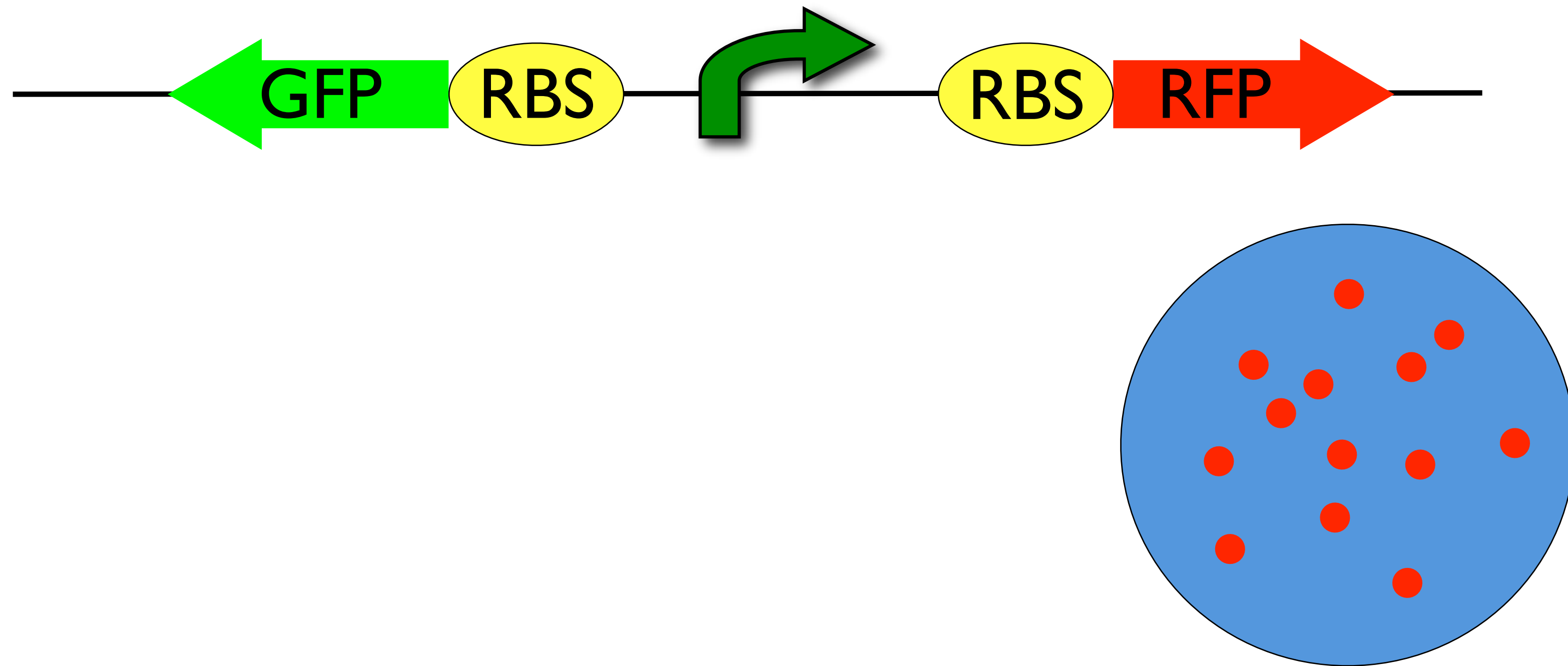
Insert Non-functional Promoter

J119137

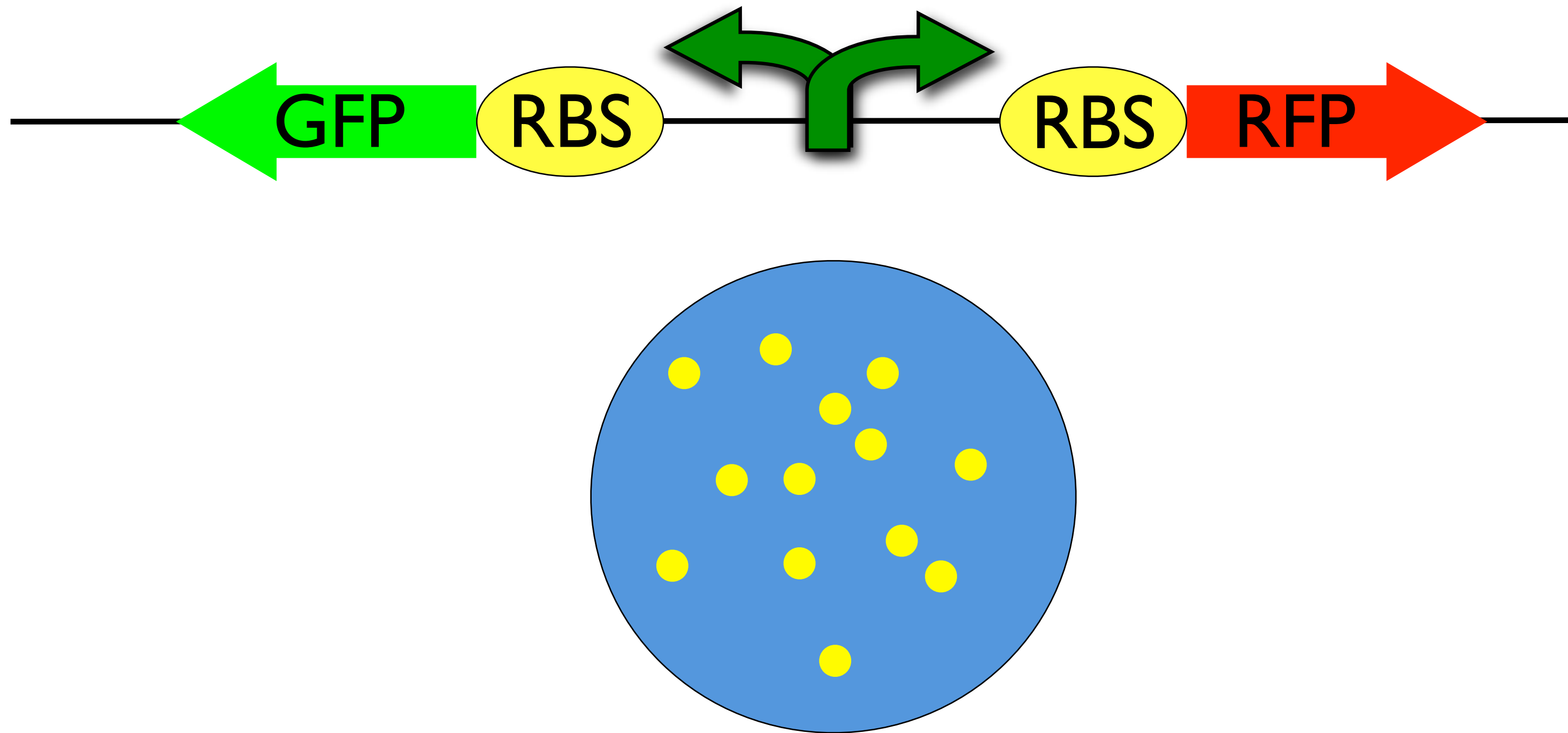


Insert Forward Promoter

J119137



Insert Bi-directional Promoter J119137



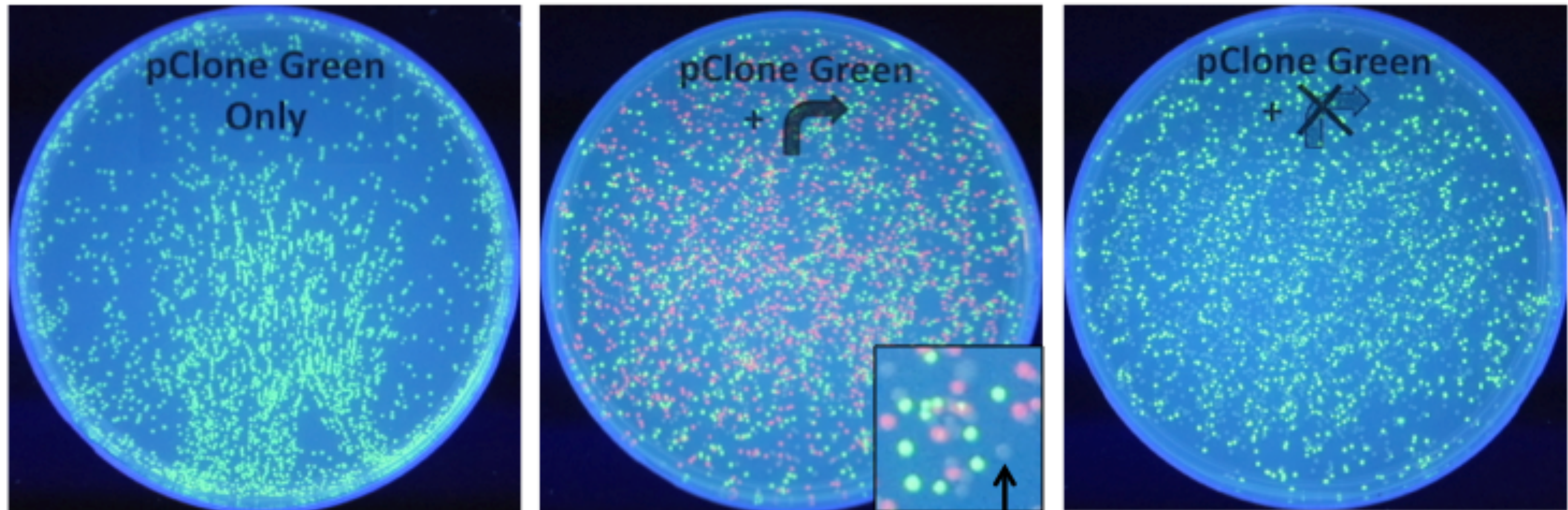
pClone Red J119137

A

pClone Red

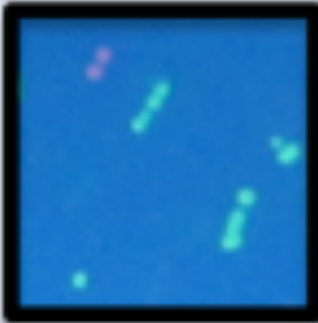
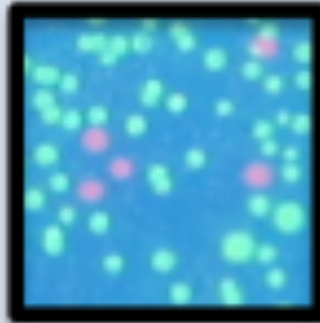
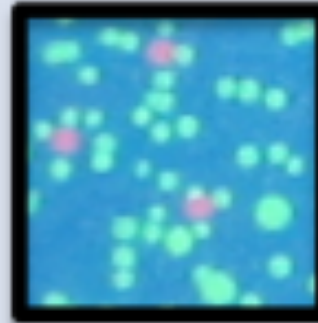
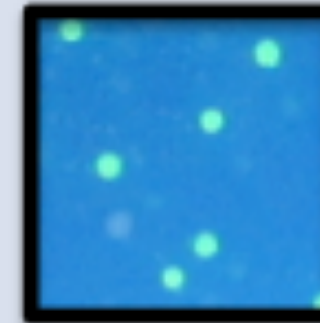
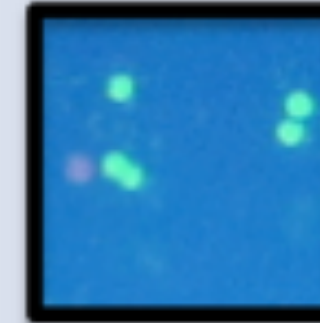
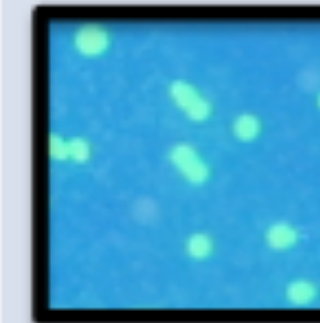

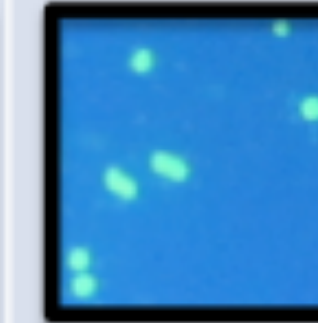










B



Quantify with Phone and ImageJ

J119137

Mutant	J119319	J119320	J119321	J119322	J119323	J119324	J119325	J119326
pClone Green plate								
Isolated clones								
Expression Ratio	4.09	3.94	3.84	2.04	1.54	1.34	3.52	1.00

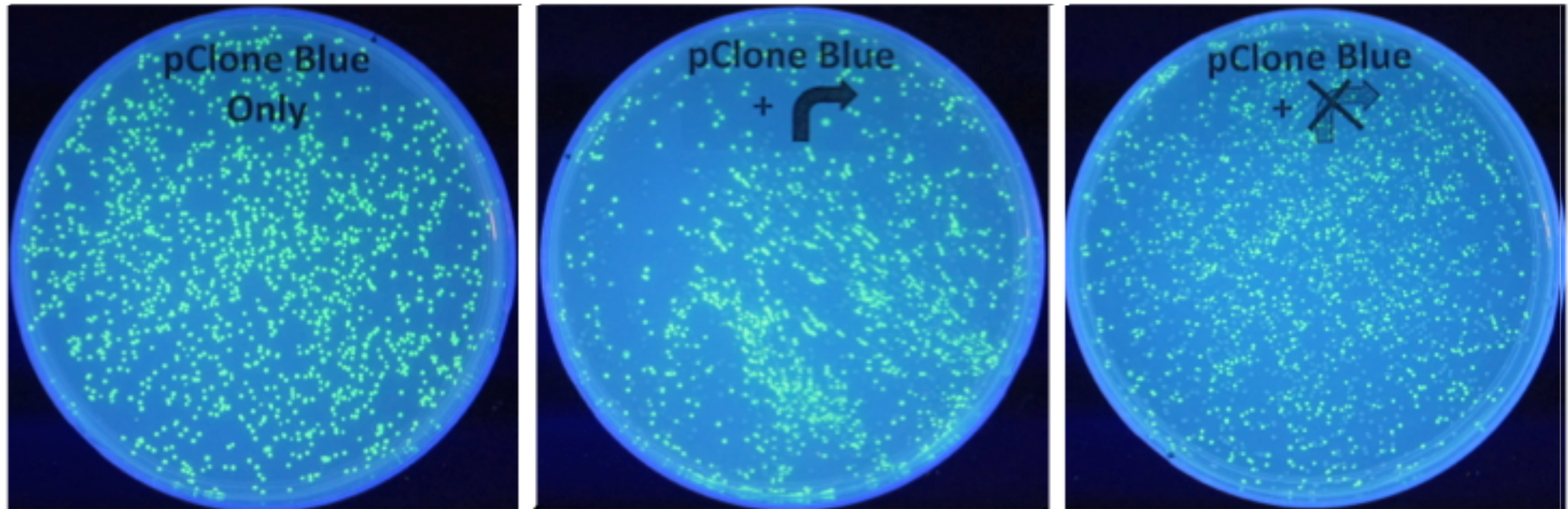
pClone Blue J119313

A

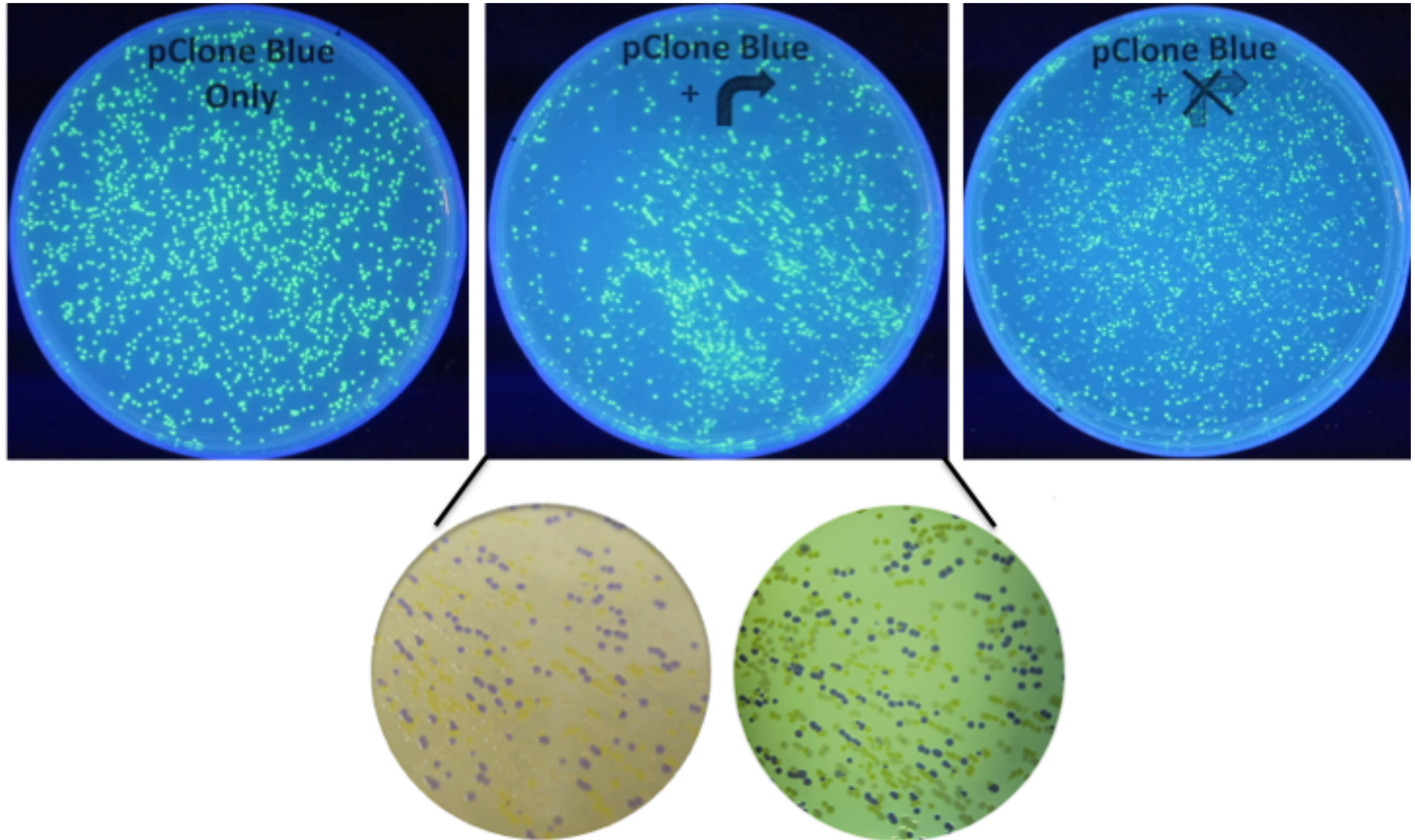
pClone Blue



B



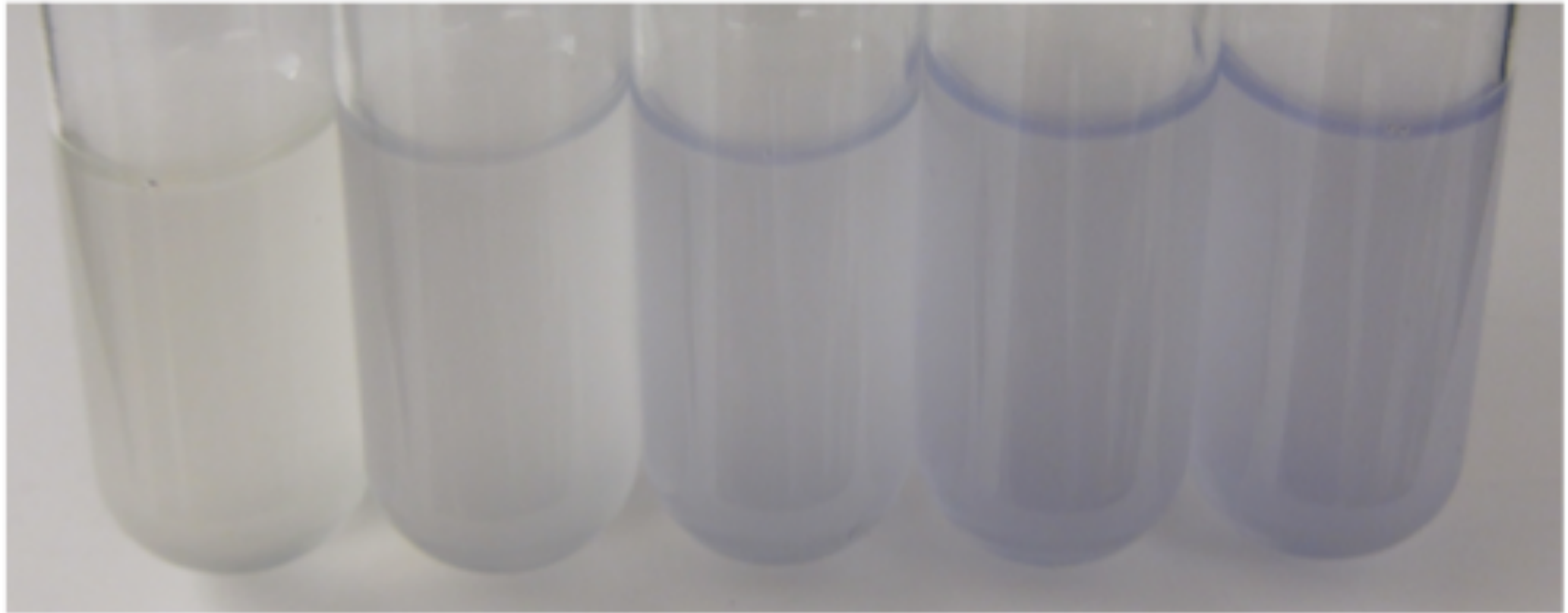
pClone Blue



Measure Promoter Qualitatively

J119313

A



0% Blue

40% Blue

70% Blue

90% Blue

100% Blue

Assessment Davidson Intro Bio

	Learning objective	Pretest experimental	Posttest experimental	Comparison course	$F(2,88)$	Effect size (η^2)	Conclusion
1	Function of promoter	43%	87% ^a	48%	8.008, $p = 0.001$	0.154	Large effect
2	Repressor diagram	23%	53% ^a	13%	7.206, $p = 0.001$	0.141	Large effect
3	Activator diagram	0%	41% ^a	0%	7.250, $p = 0.001$	0.167	Large effect
4	Experiment overview	0%	13% ^a	0%	4.538, $p = 0.013$	0.103	Moderate effect
5	Transformation method	0%	20% ^a	0%	7.374, $p = 0.001$	0.143	Large effect
6	Verify promoter cloned	50%	40%	48%	0.34, $p = 0.713$	0.008	No effect
7	Test promoter strength	43%	60%	39%	1.525, $p = 0.223$	0.034	No effect
8	Type IIs restriction enzymes	7%	50%	6%	1.873, $p = 0.16$	0.041	No effect
9	GGA method	10%	63% ^a	0%	31.929, $p < 0.001$	0.421	Large effect

^aSignificant improvement between pre- and posttest.

Assessment MWSU Genetics (soph)

	Learning objective	Pretest experimental	Posttest experimental	Control course (ecology)	$F(2252)$	Effect size (η^2)	Conclusion
1	Function of promoter	36%	59% ^a	20%	13.527, $p < 0.001$	0.097	Moderate effect
2	-10 and -35 sites	3%	70% ^a	0%	145.374, $p < 0.001$	0.536	Large effect
3	Mutational analysis	30%	75% ^a	33%	28.773, $p < 0.001$	0.186	Large effect
4	Student-designed mutation	0%	0%	0%	0, $p > 0.05$	0.000	No effect
5	Transformation method	11%	51% ^a	12%	30.731, $p < 0.001$	0.196	Large effect
6	Verify promoter cloned	19%	44% ^a	18%	10.264, $p < 0.001$	0.075	Moderate effect
7	Test promoter strength	17%	33% ^a	18%	4.421, $p = 0.013$	0.034	Moderate effect
8	Type IIs restriction enzymes	2%	29% ^a	4%	21.661, $p < 0.001$	0.147	Large effect
9	GGA method	14%	22%	14%	1.56, $p = 0.212$	0.012	No effect

^aSignificant improvement between pre- and posttest.

Assessment Davidson Intro Bio

	Learning objective	Pretest experimental	Posttest experimental	Comparison course	$F(2,88)$	Effect size (η^2)	Conclusion
1	Function of promoter	43%	87% ^a	48%	8.008, $p = 0.001$	0.154	Large effect
2	Repressor diagram	23%	53% ^a	13%	7.206, $p = 0.001$	0.141	Large effect
3	Activator diagram	0%	41% ^a	0%	7.250, $p = 0.001$	0.167	Large effect
4	Experiment overview	0%	13% ^a	0%	4.538, $p = 0.013$	0.103	Moderate effect
5	Transformation method	0%	20% ^a	0%	7.374, $p = 0.001$	0.143	Large effect
6	Verify promoter cloned	50%	40%	48%	0.34, $p = 0.713$	0.008	No effect
7	Test promoter strength	43%	60%	39%	1.525, $p = 0.223$	0.034	No effect
8	Type IIs restriction enzymes	7%	50%	6%	1.873, $p = 0.16$	0.041	No effect
9	GGA method	10%	63% ^a	0%	31.929, $p < 0.001$	0.421	Large effect

^aSignificant improvement between pre- and posttest.

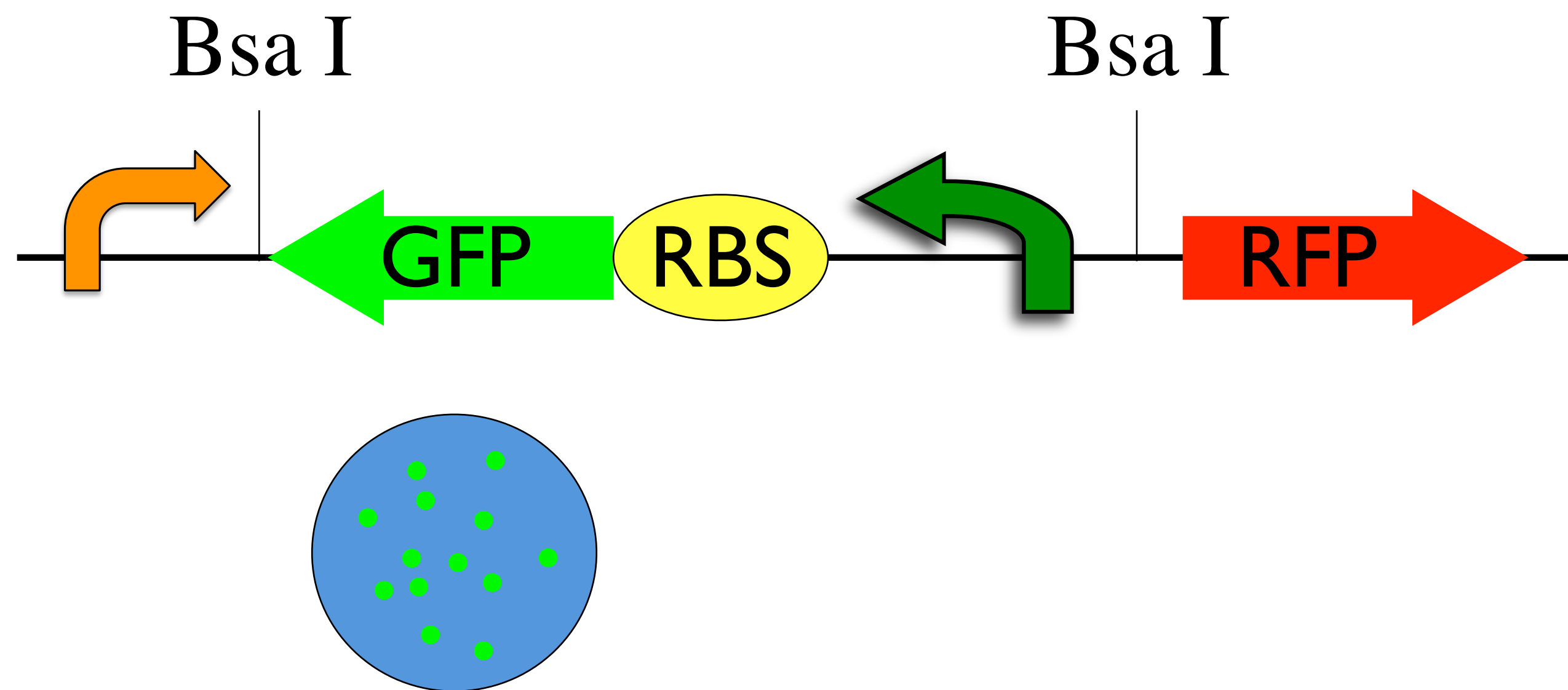
Assessment MWSU Genetics (soph)

	Learning objective	Pretest experimental	Posttest experimental	Control course (ecology)	$F(2,252)$	Effect size (η^2)	Conclusion
1	Function of promoter	36%	59% ^a	20%	13.527, $p < 0.001$	0.097	Moderate effect
2	-10 and -35 sites	3%	70% ^a	0%	145.374, $p < 0.001$	0.536	Large effect
3	Mutational analysis	30%	75% ^a	33%	28.773, $p < 0.001$	0.186	Large effect
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^aSignificant improvement between pre- and posttest.

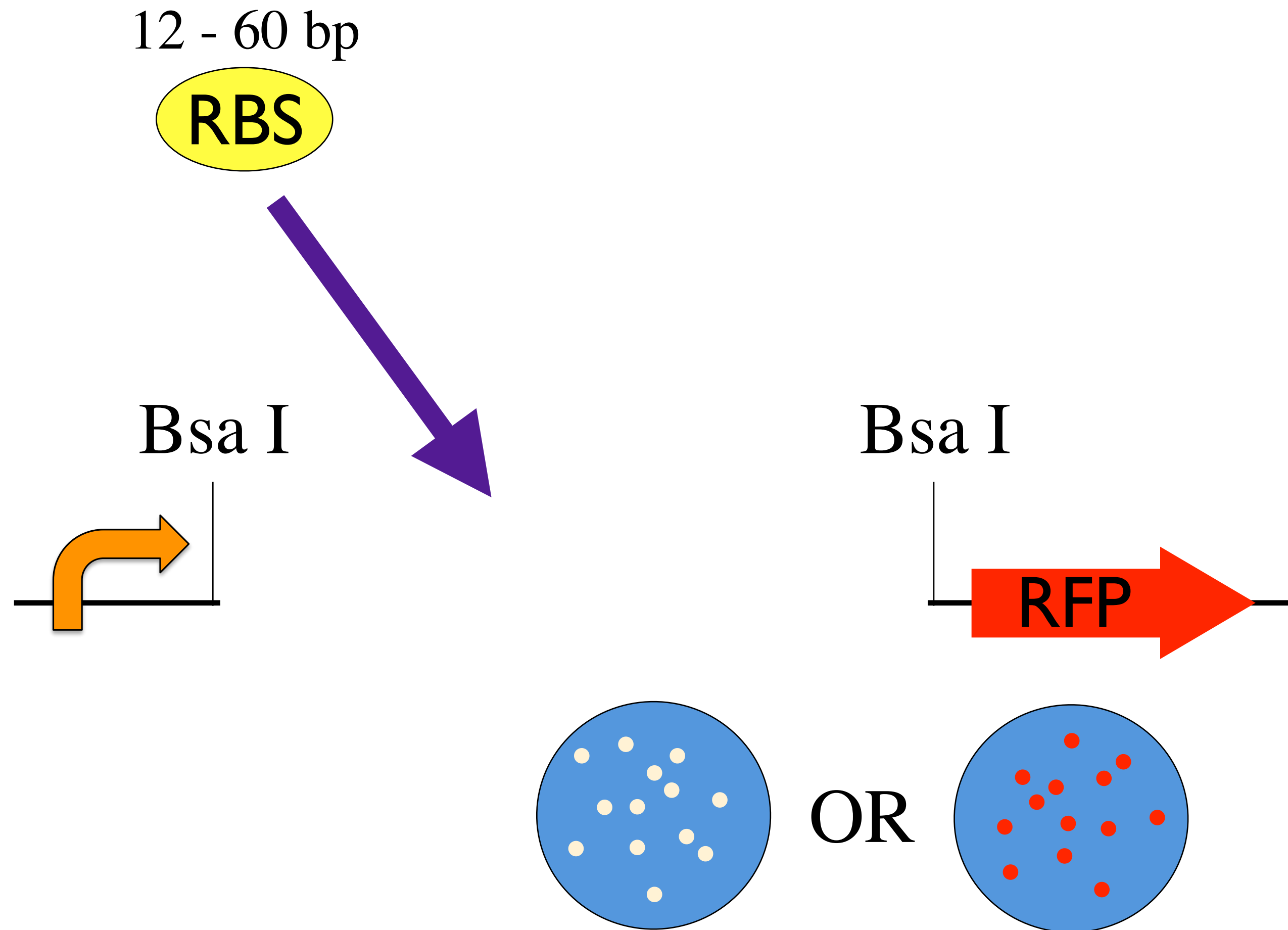
rClone Red

J119###



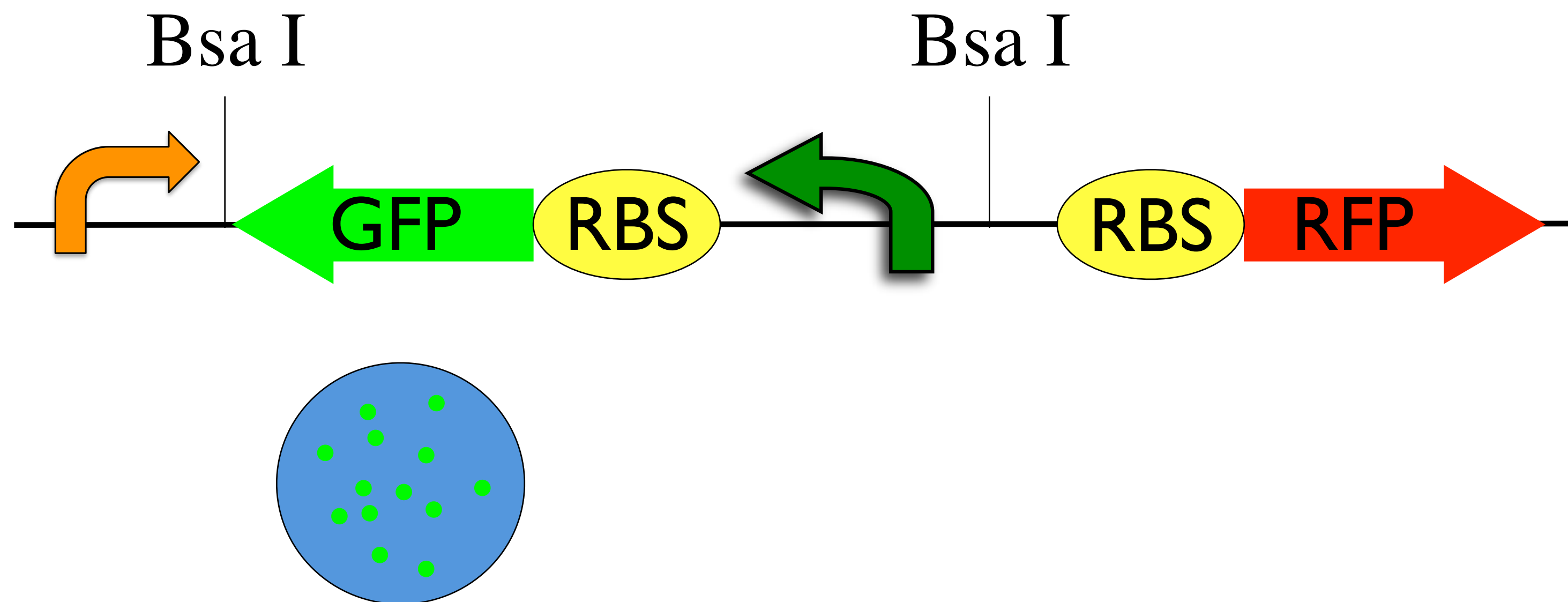
rClone Red

J119###



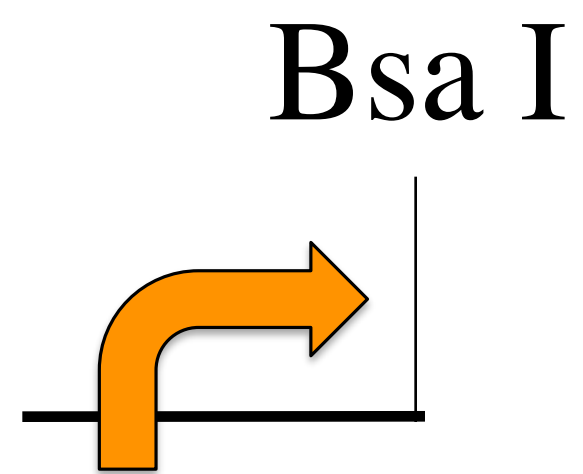
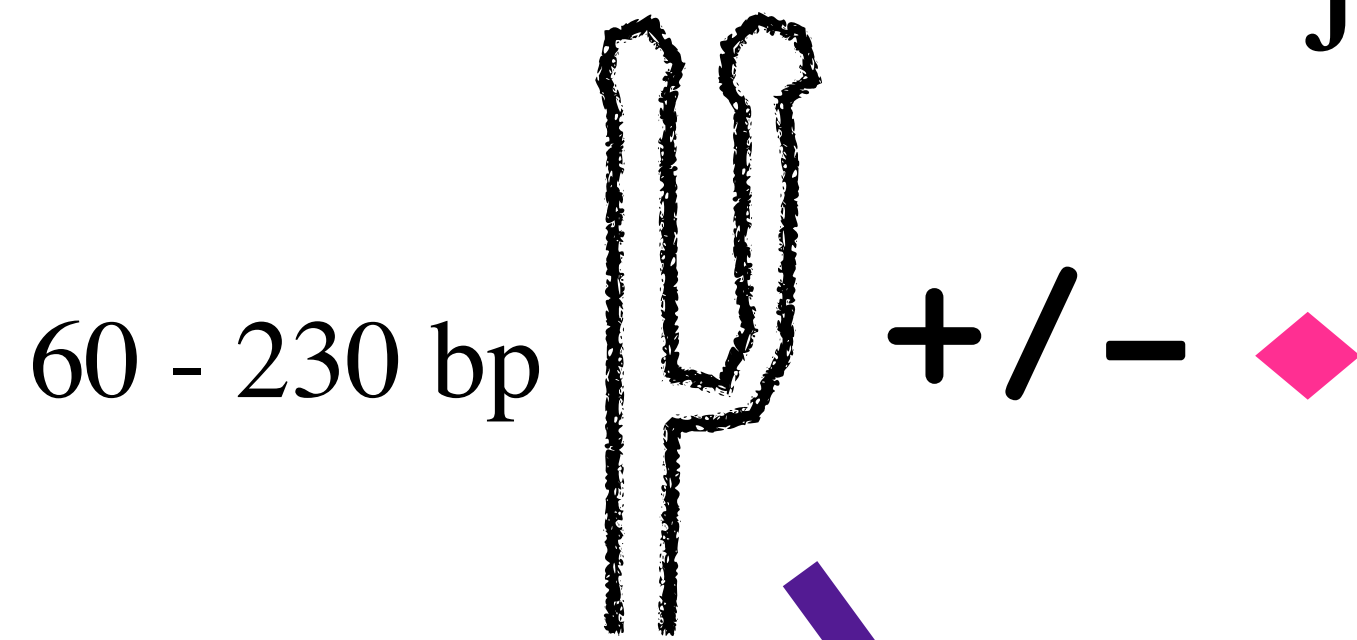
tClone Red

J119361

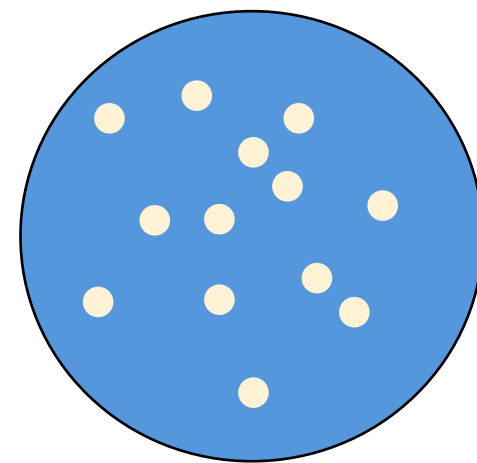
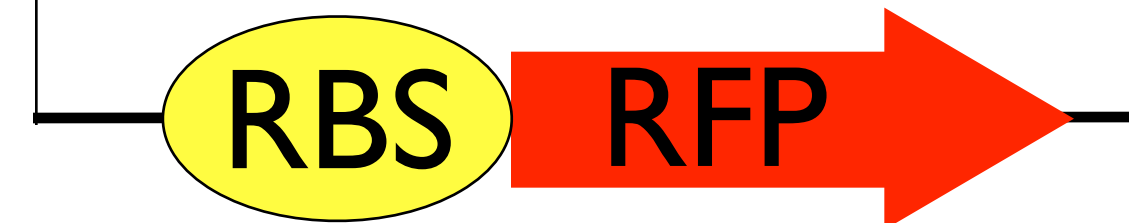


tClone Red

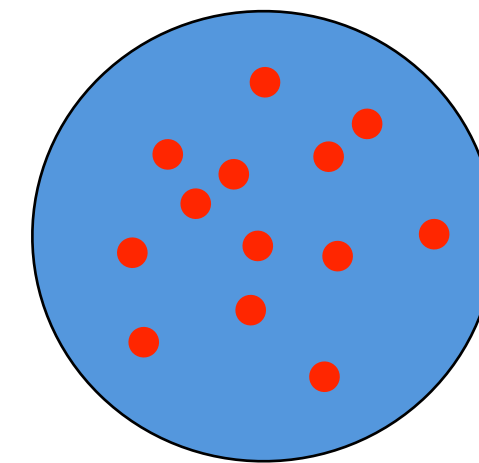
J119361



Bsa I

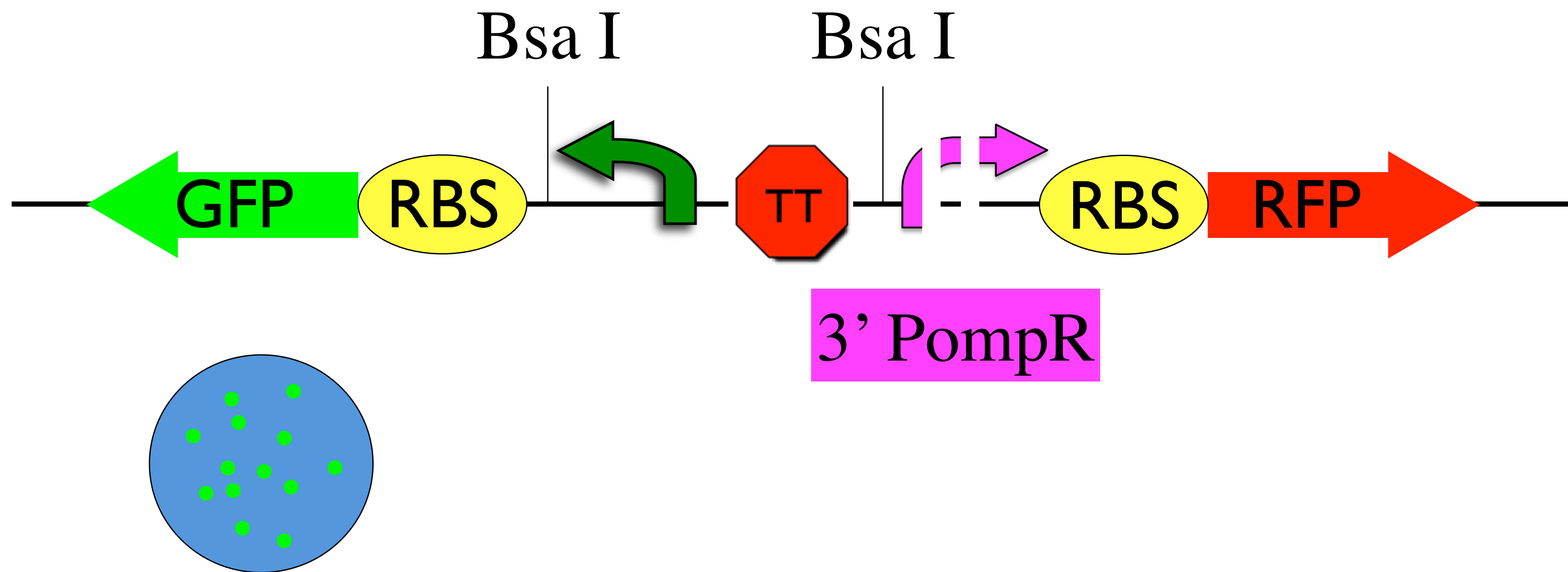


OR



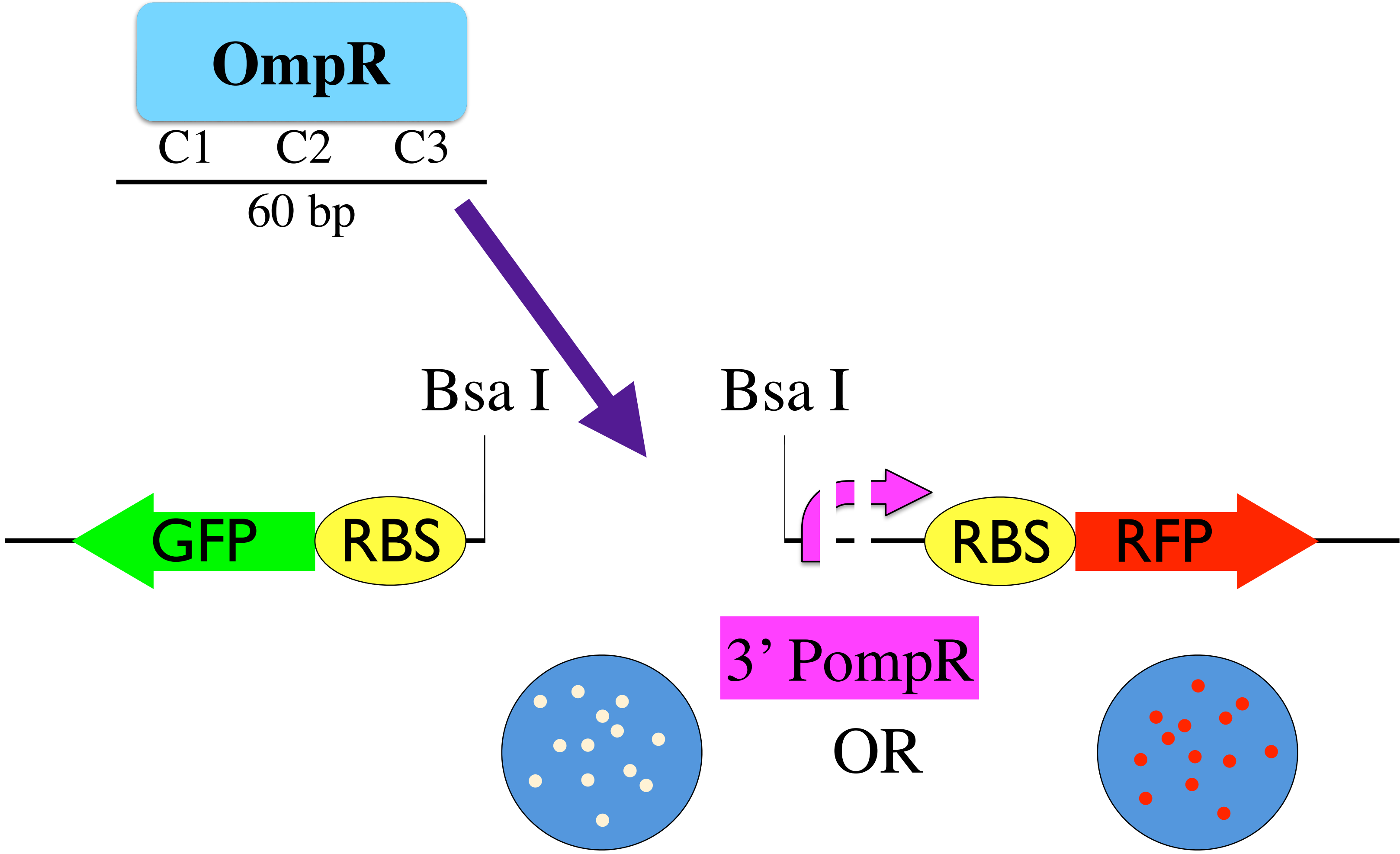
actClone Red

J100204



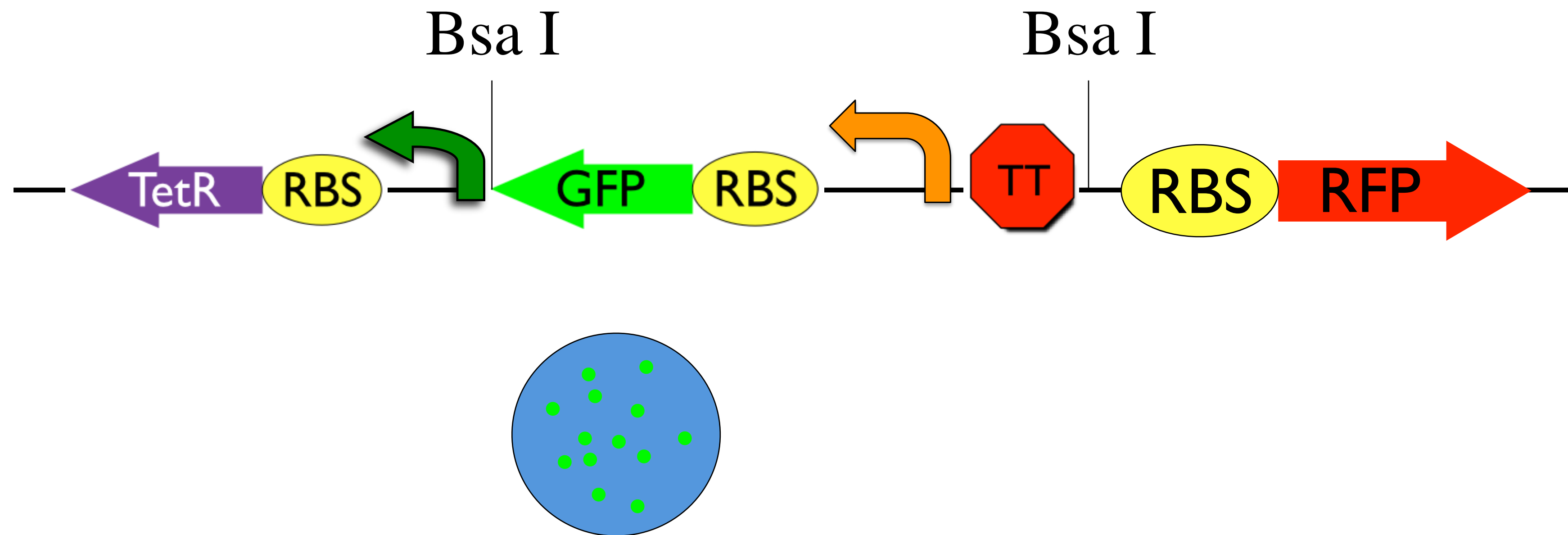
actClone Red

J100204



repClone Red

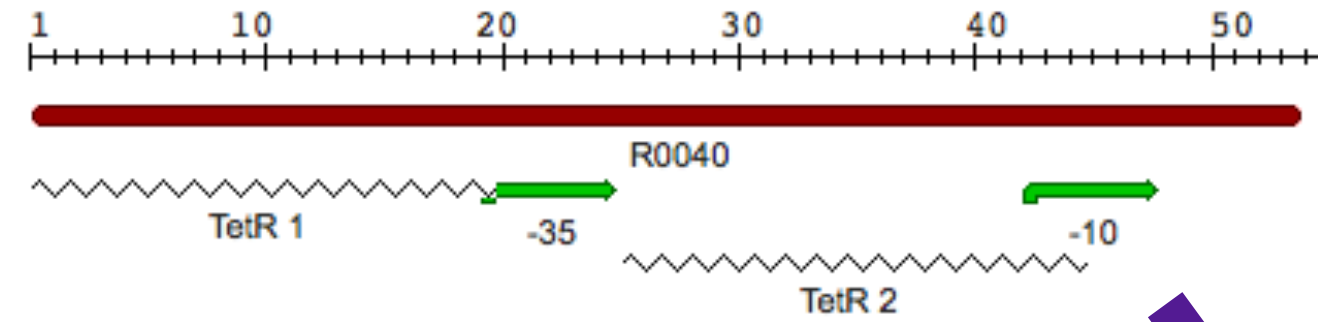
J100205



repClone Red

J100205

Ptet

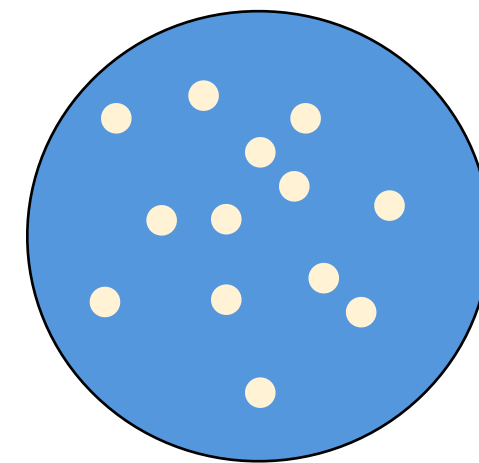


54 bp

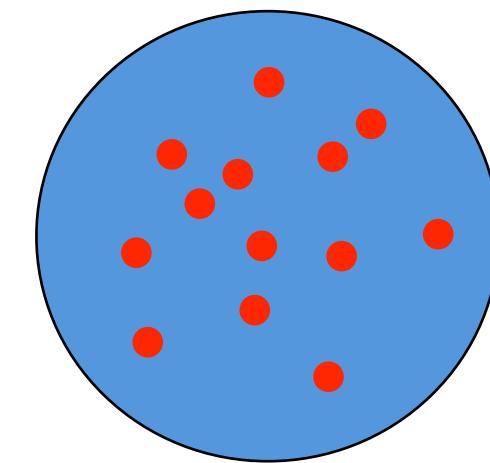
Bsa I



Bsa I



OR



**pClone: Synthetic Biology Tool Makes Promoter
Research Accessible to Beginning Biology Students.**
CBE Life Sciences Education. 2014. Vol. 13(2): 285 - 296.

We want to design a new method to produce medications more efficiently.

What is the definition of evolution?

What is the definition of evolution?

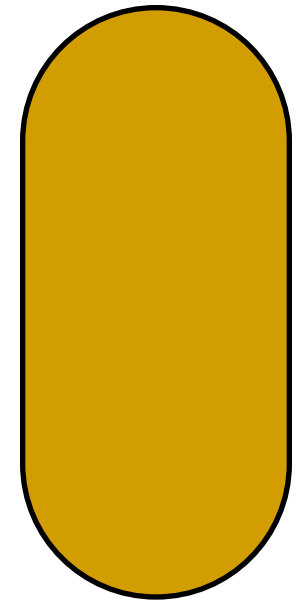
change in allele frequency in a population over time

How does natural selection work?

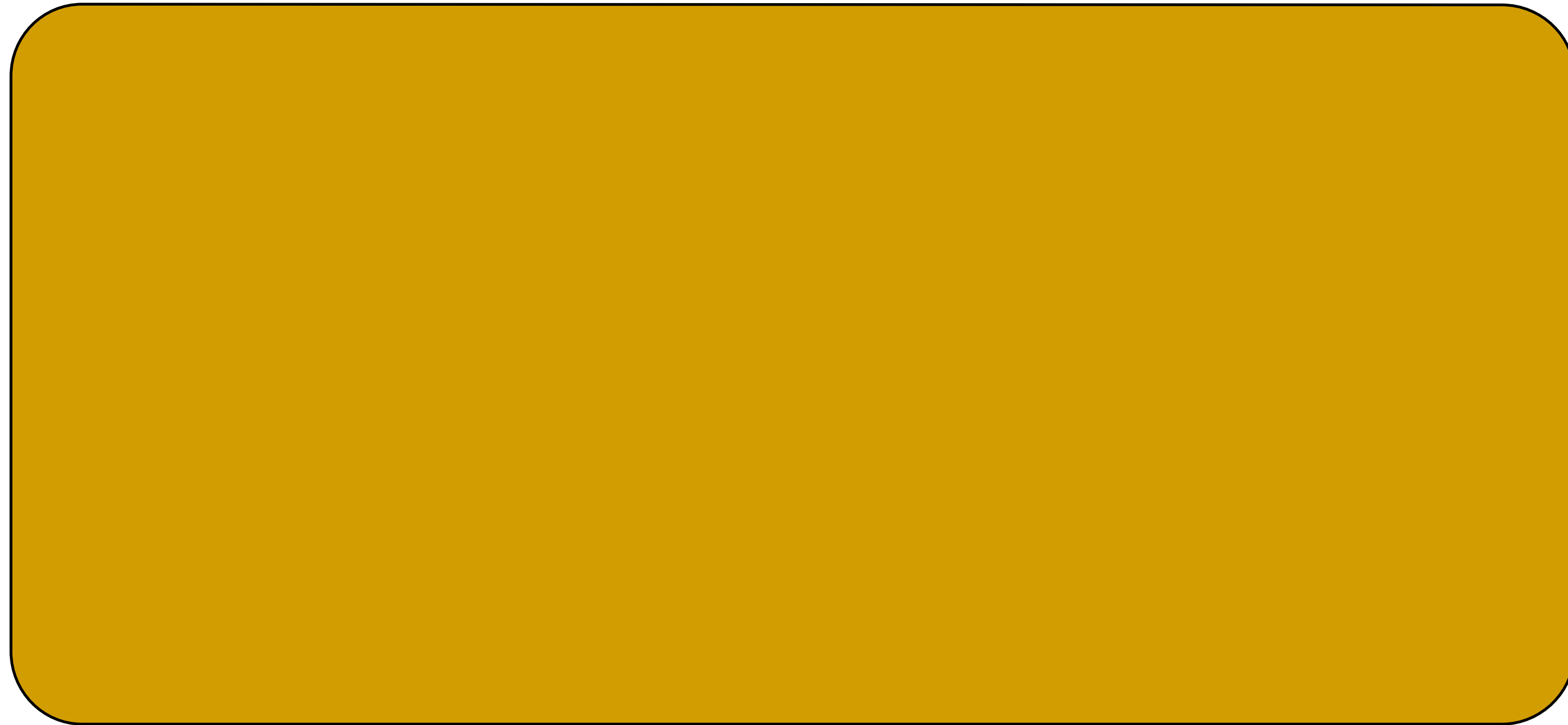
How does natural selection work?

1. over production
2. variation in the population
3. competition for limited resources
4. selective advantage
5. reproduction

Make *E. coli* Optimize Drug Production



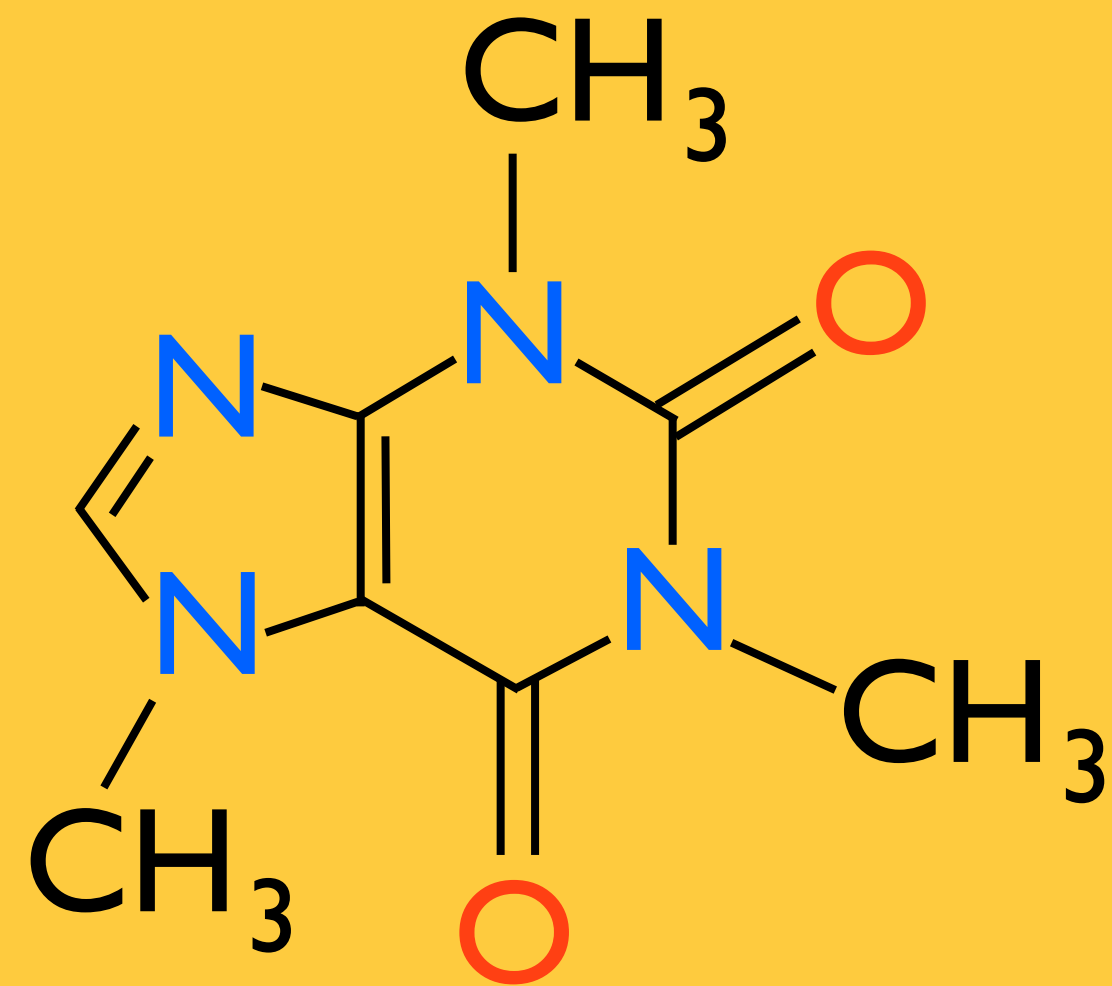
Make *E. coli* Optimize Drug Production



Make *E. coli* Optimize Drug Production

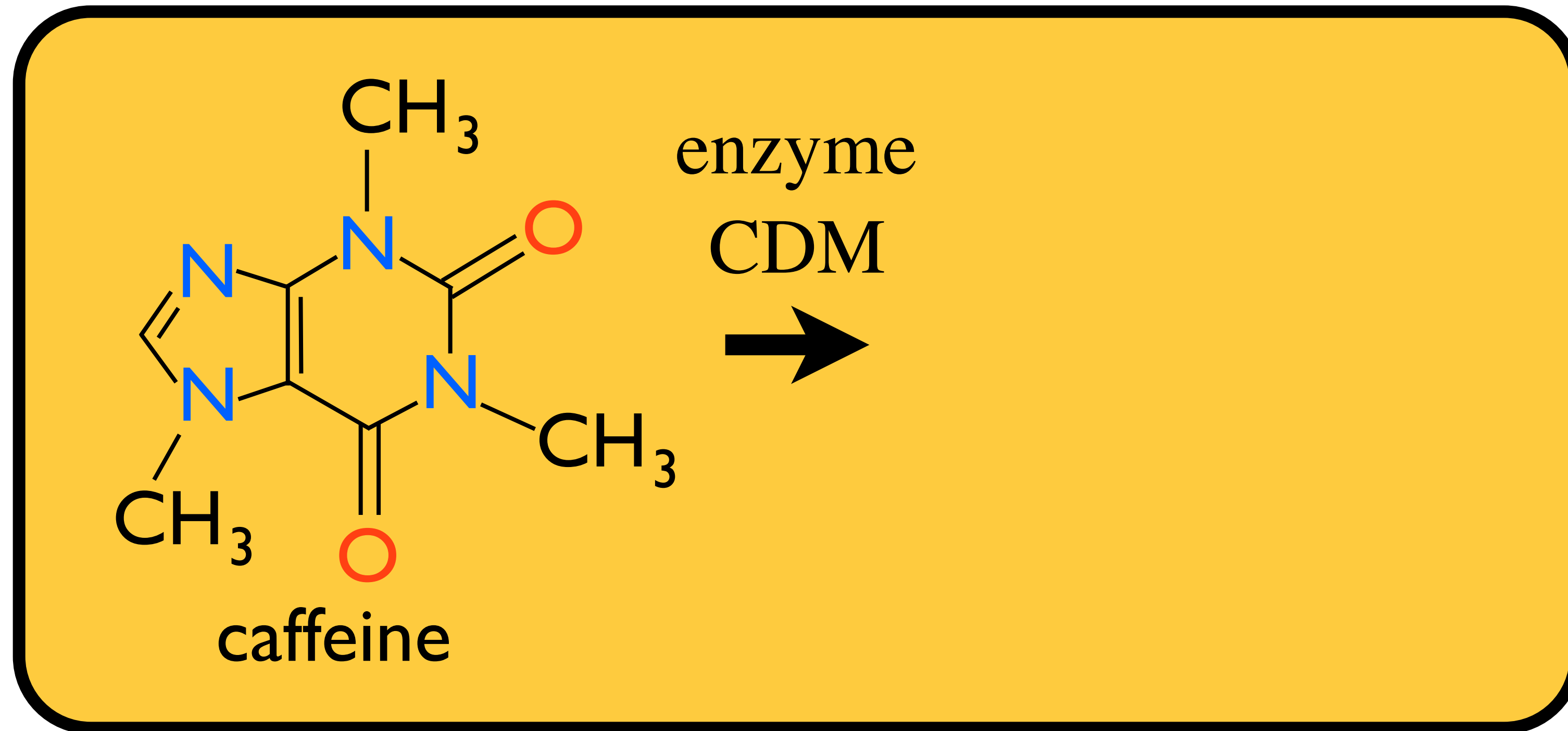


Make *E. coli* Optimize Drug Production

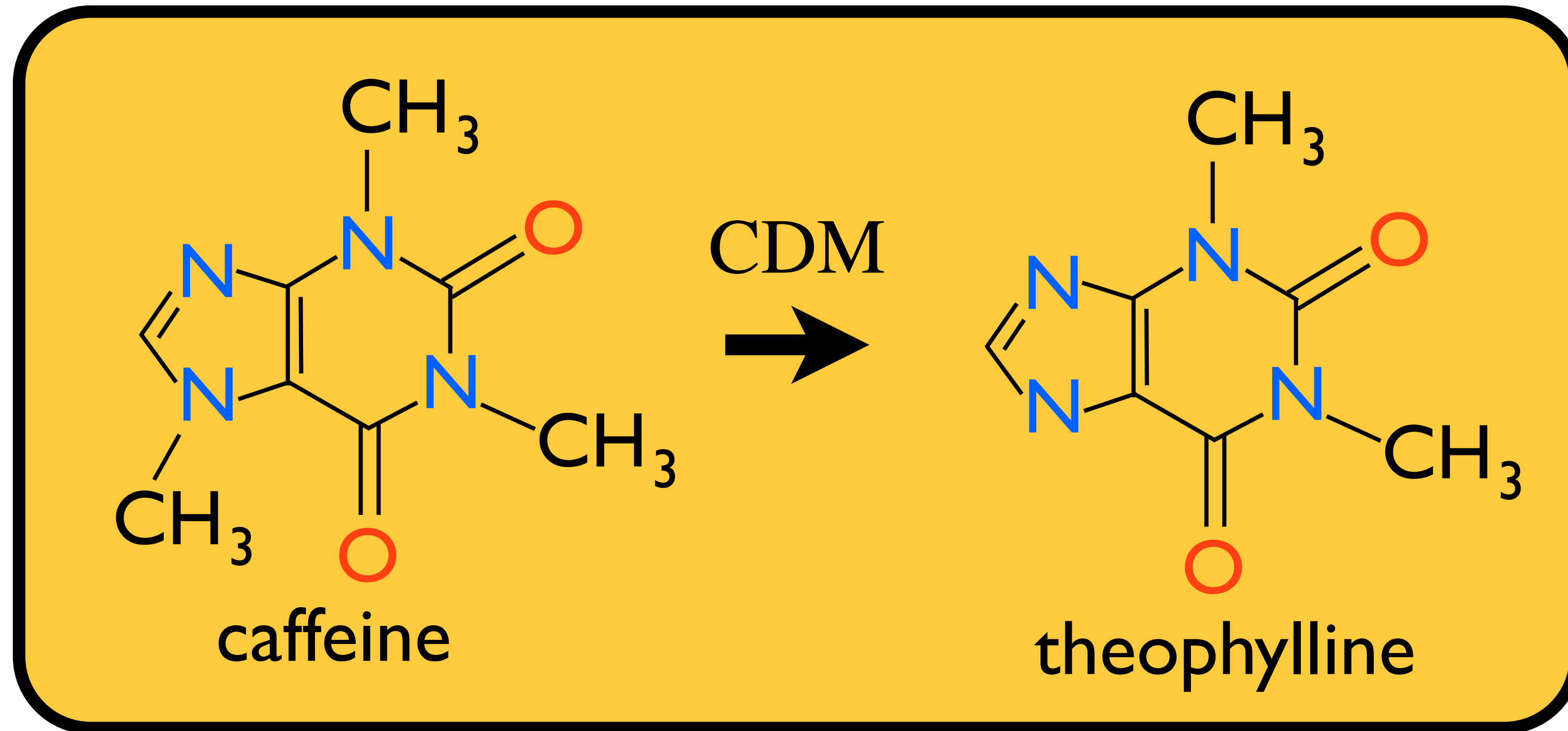


caffeine

Make *E. coli* Optimize Drug Production

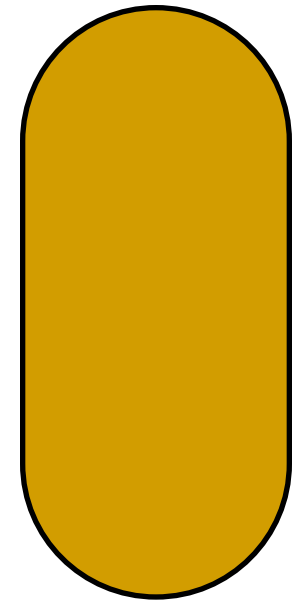


Make *E. coli* Optimize Drug Production

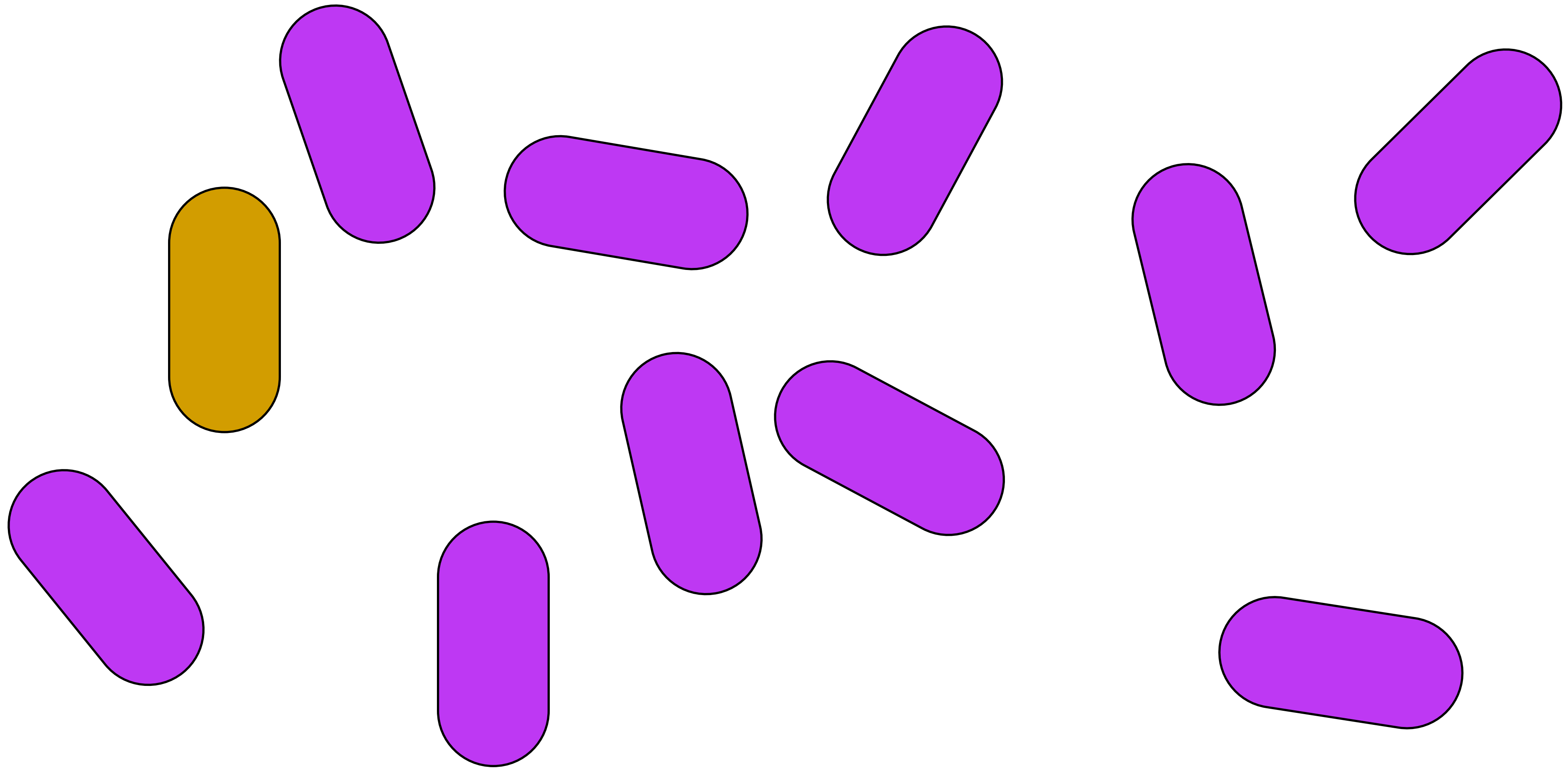


asthma medication

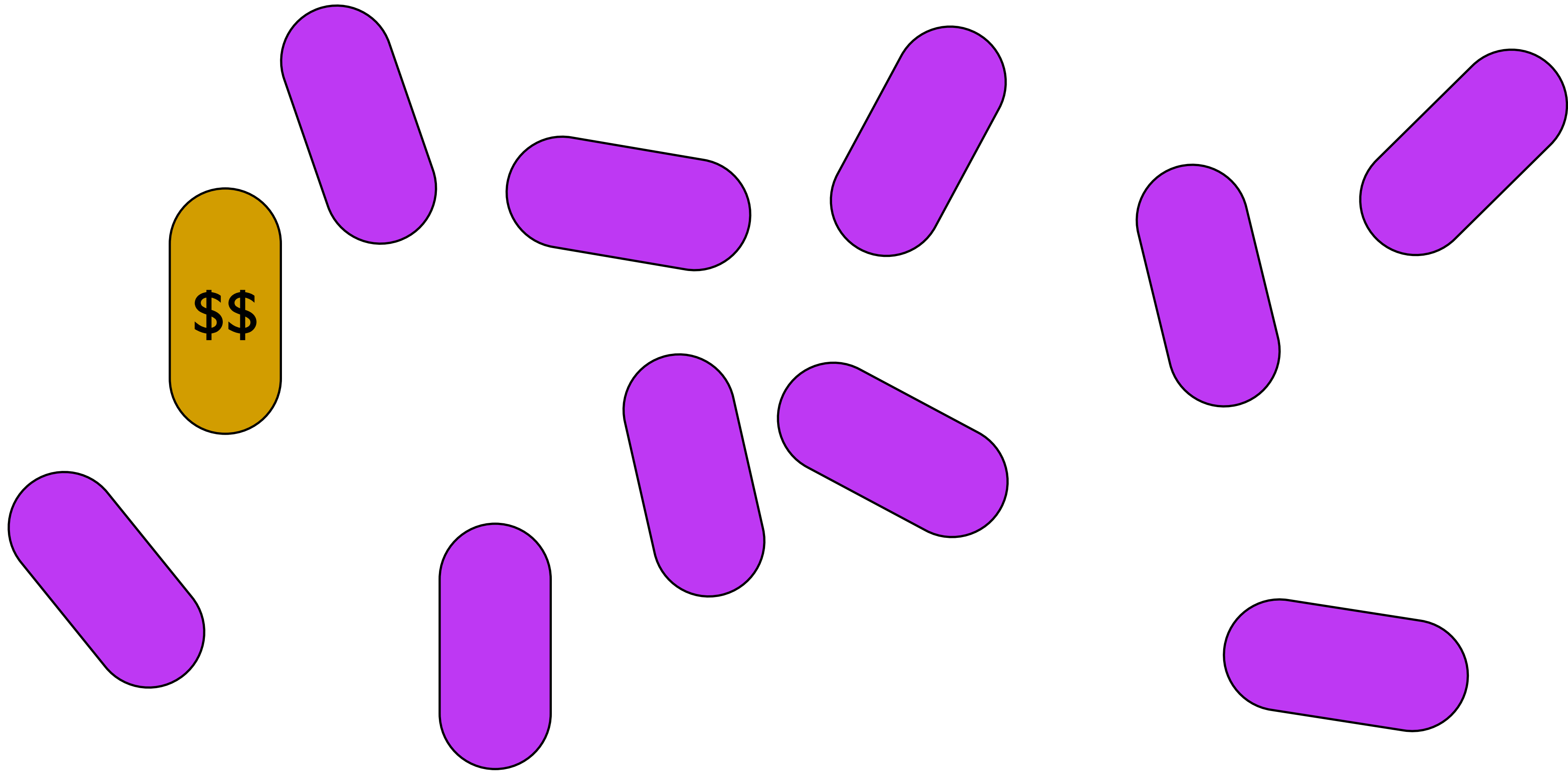
What Makes Optimization Difficult?



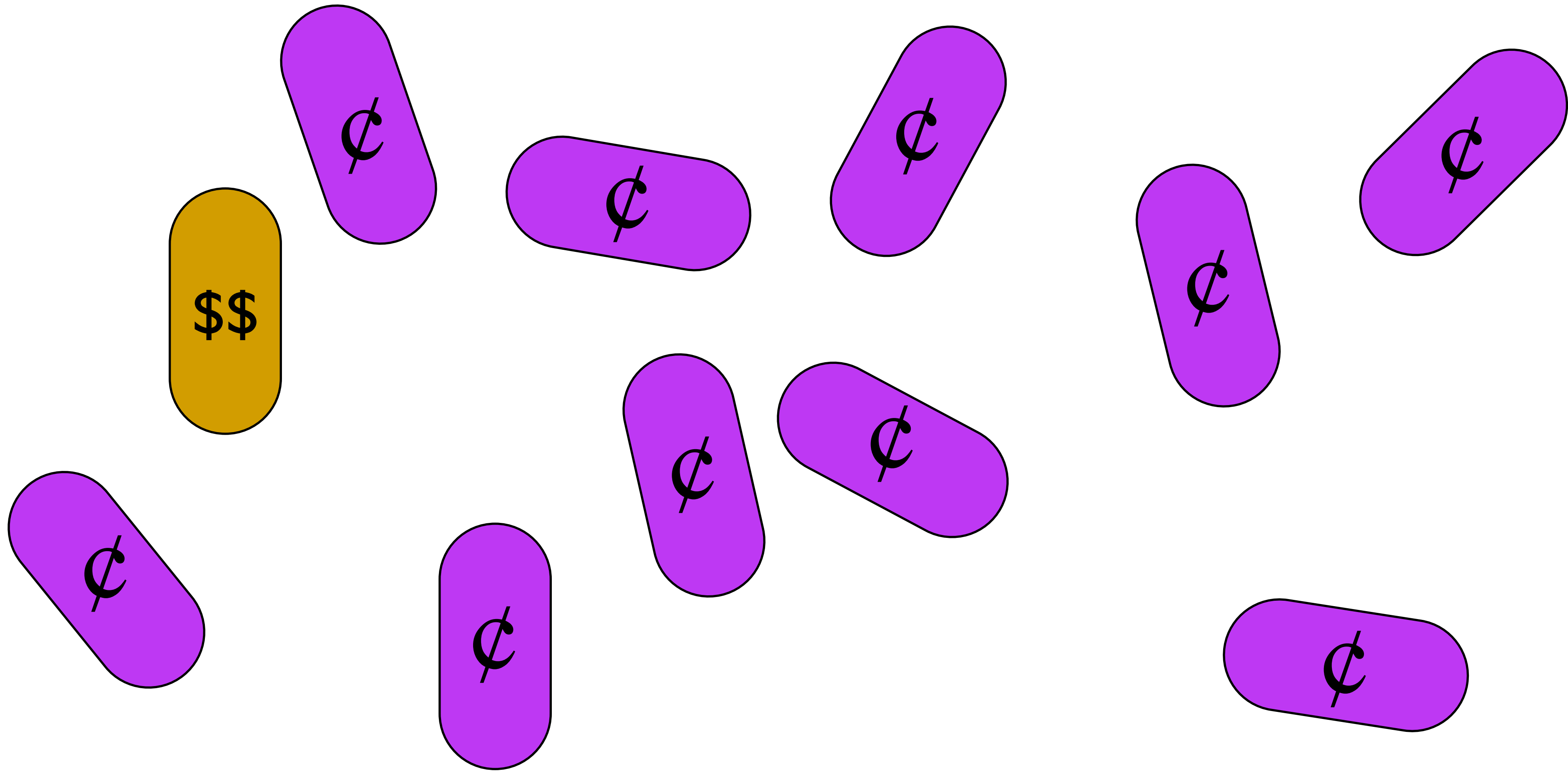
What Makes Optimization Difficult?



What Makes Optimization Difficult?



Natural Selection



Synthetic Selection



Synthetic Fitness



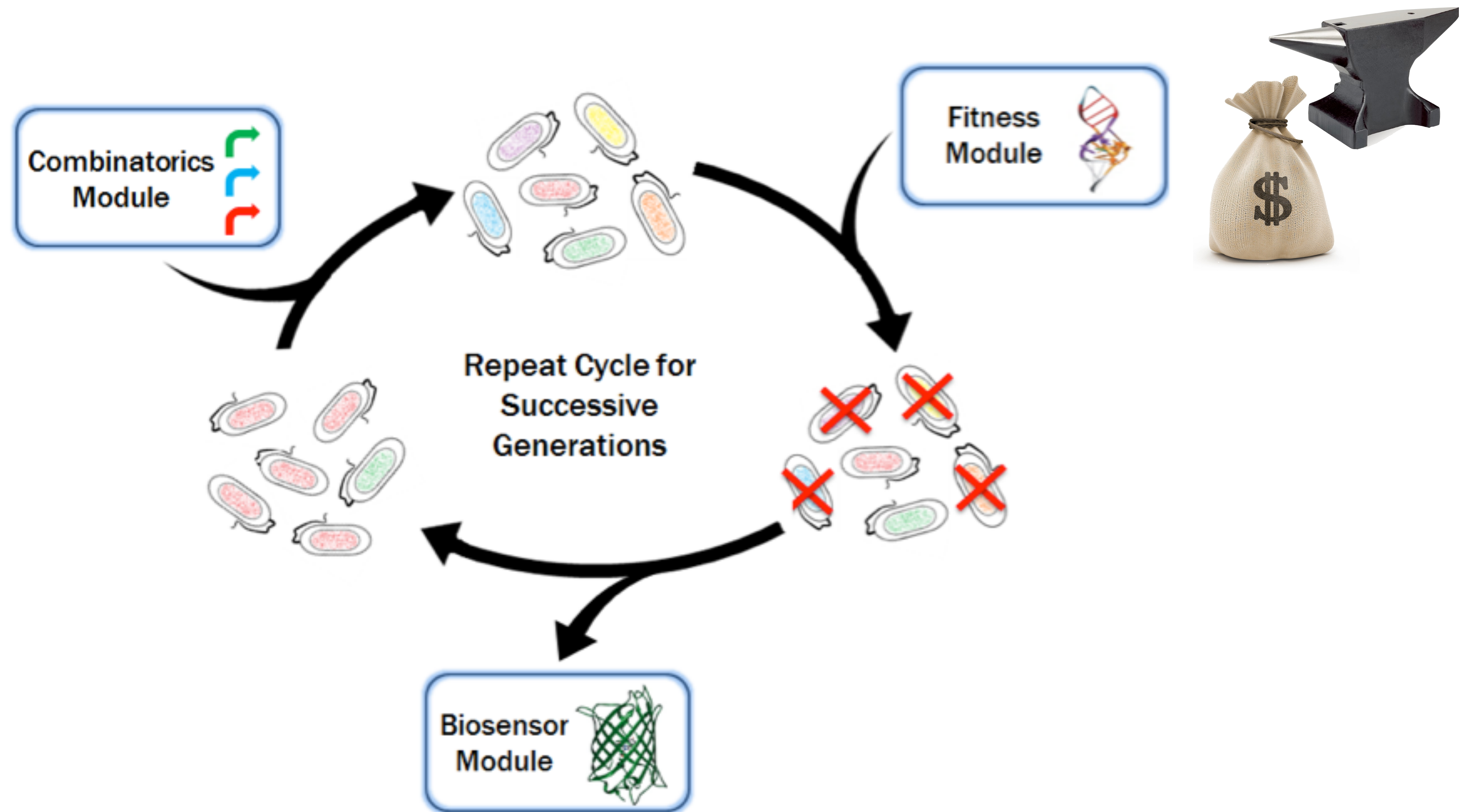
Synthetic Fitness



Engineering Programmed Evolution

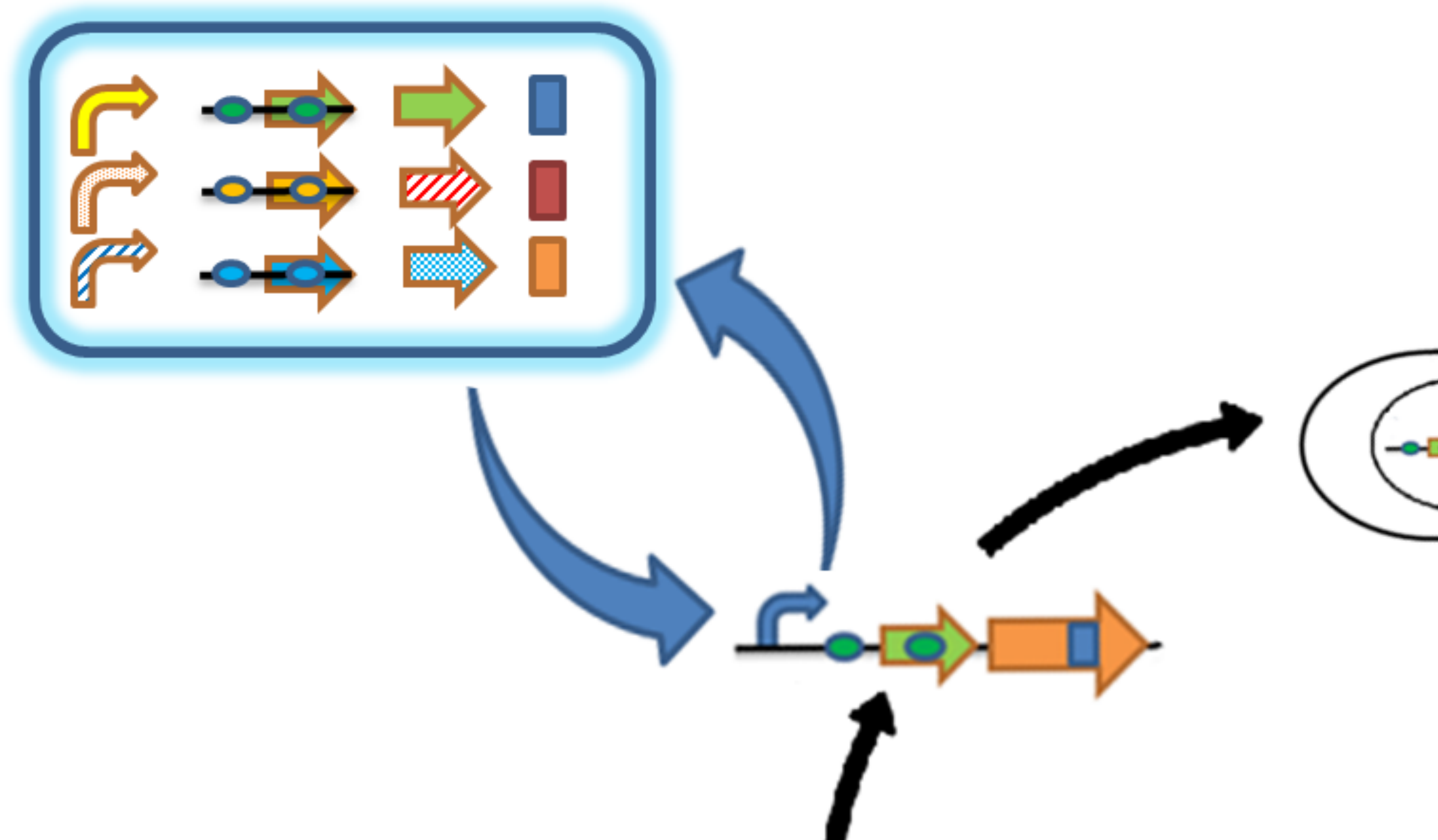


Programmed Evolution



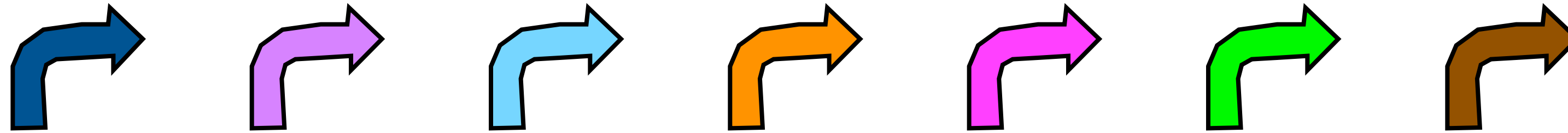
Programmed Evolution

Combinatorics Module

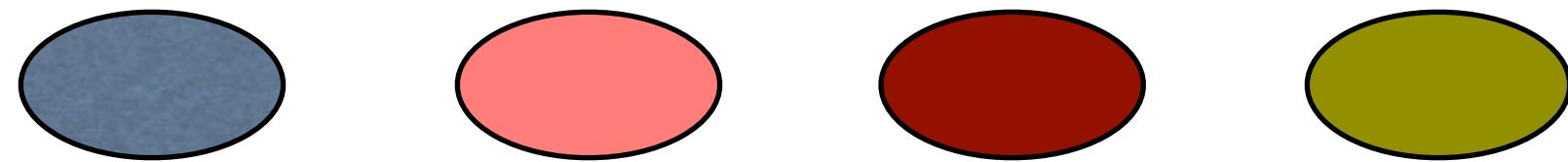


Combinatorics Cloning

Promoters (7)



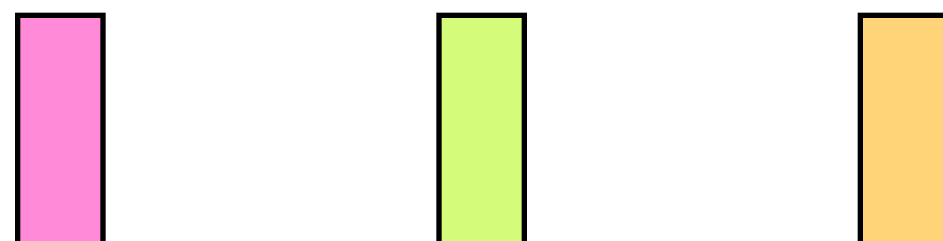
RBS (4)



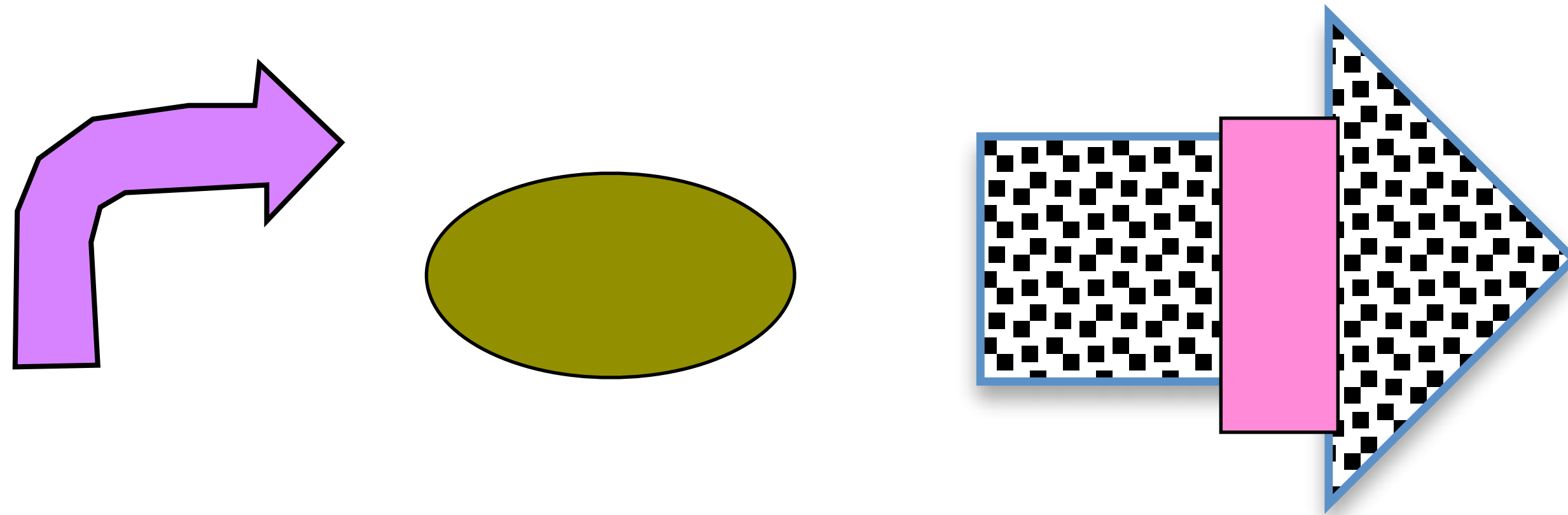
Allele (6)



Degradation tag (3)

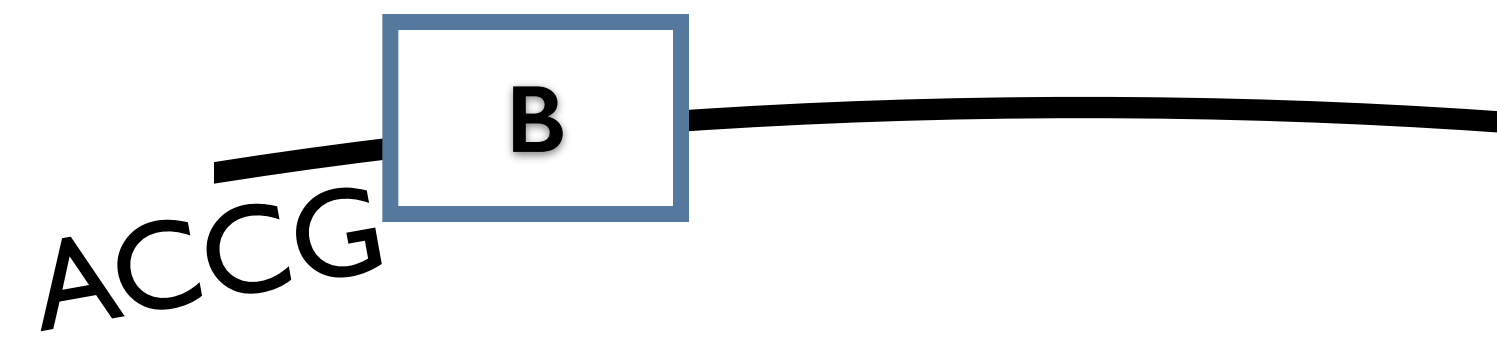
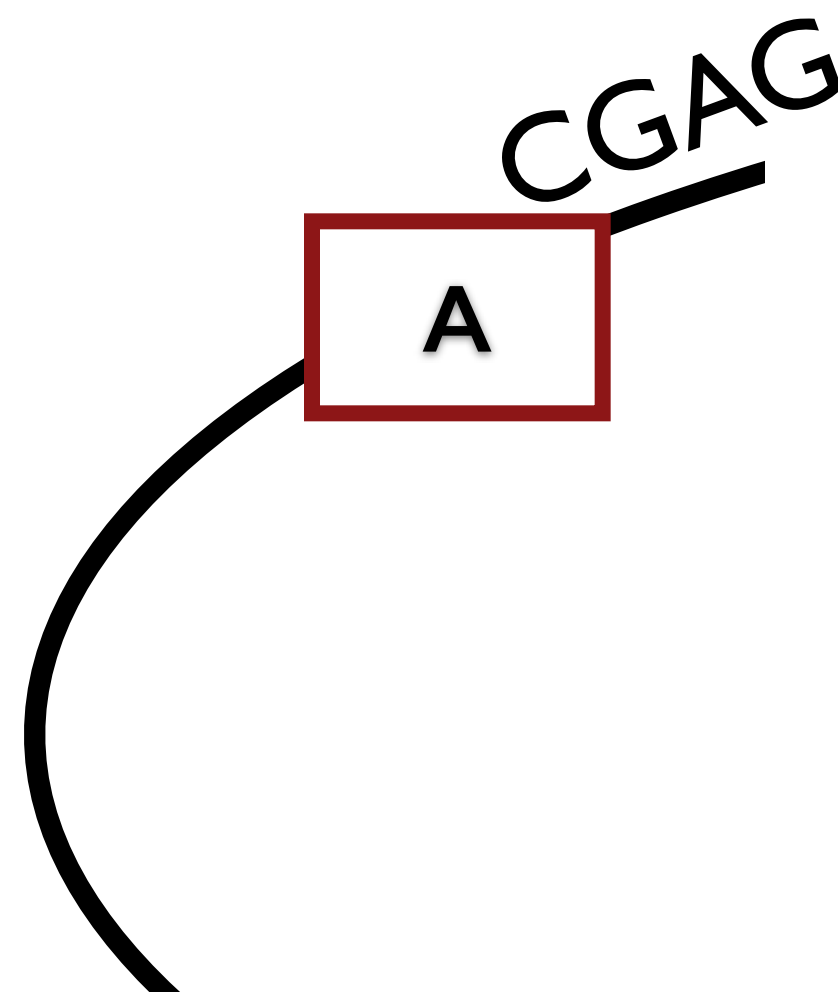
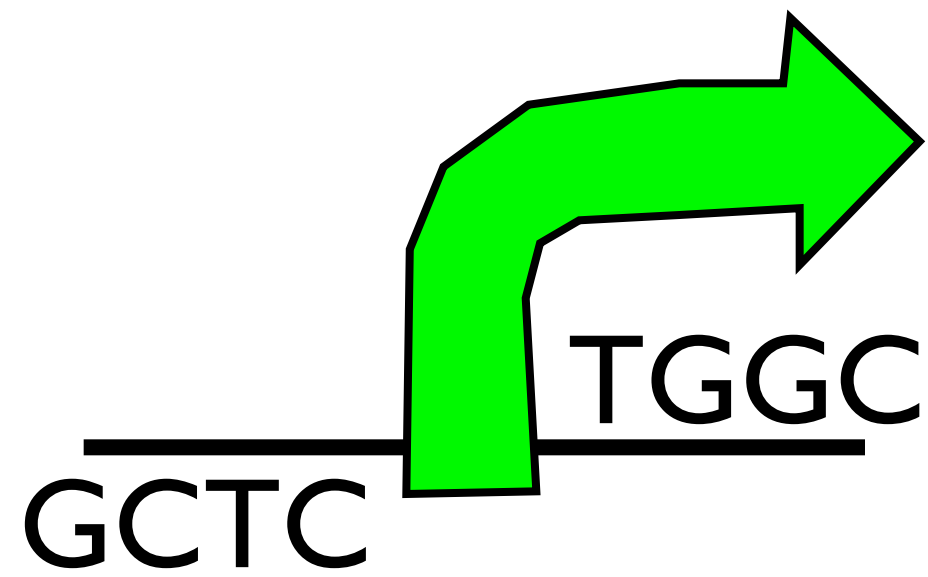
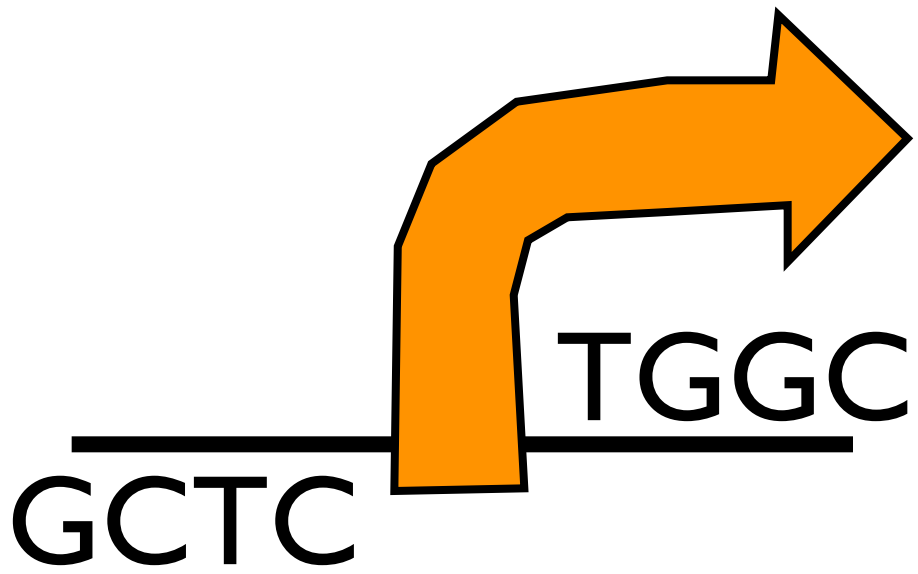
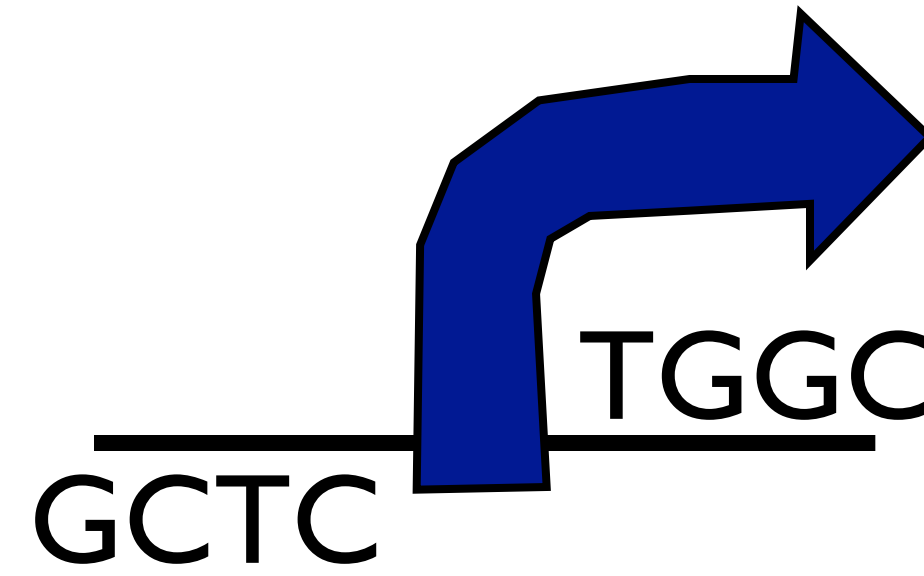
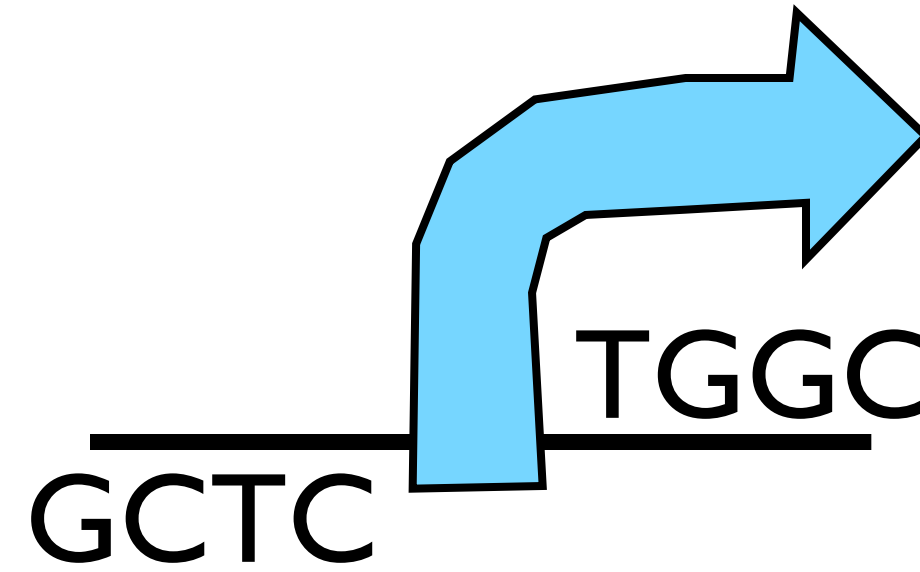
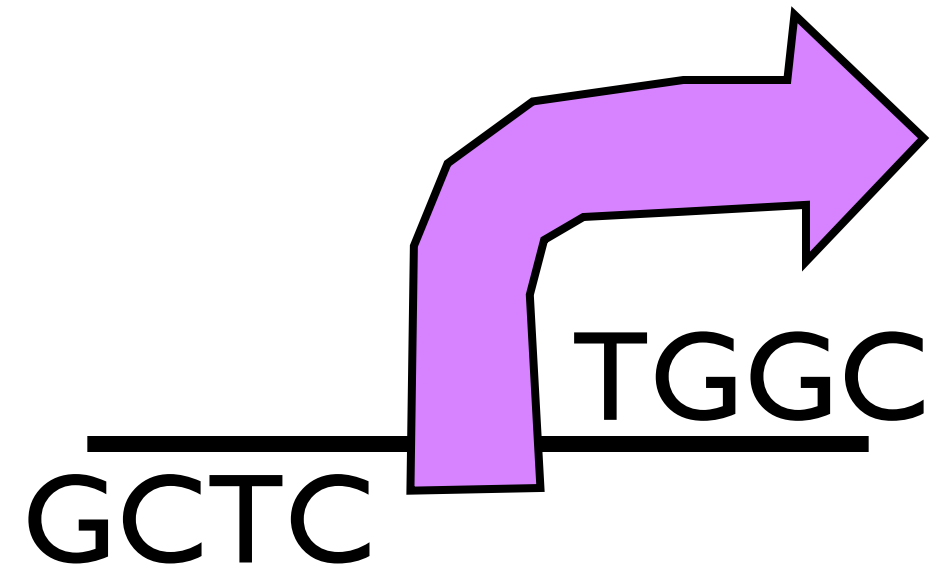


Combinatorics Cloning

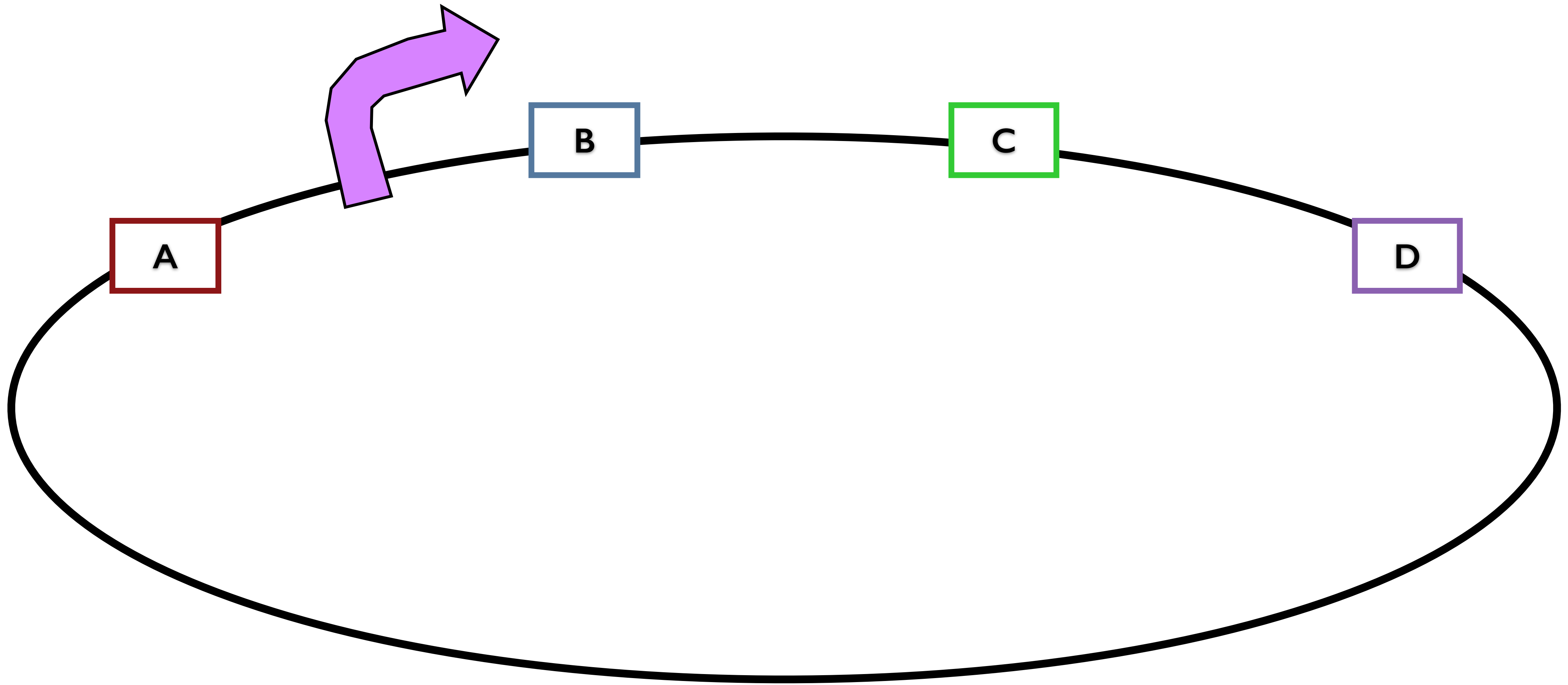


Total # constructs
 $= 8 \times 4 \times 6 \times 3 = 576$

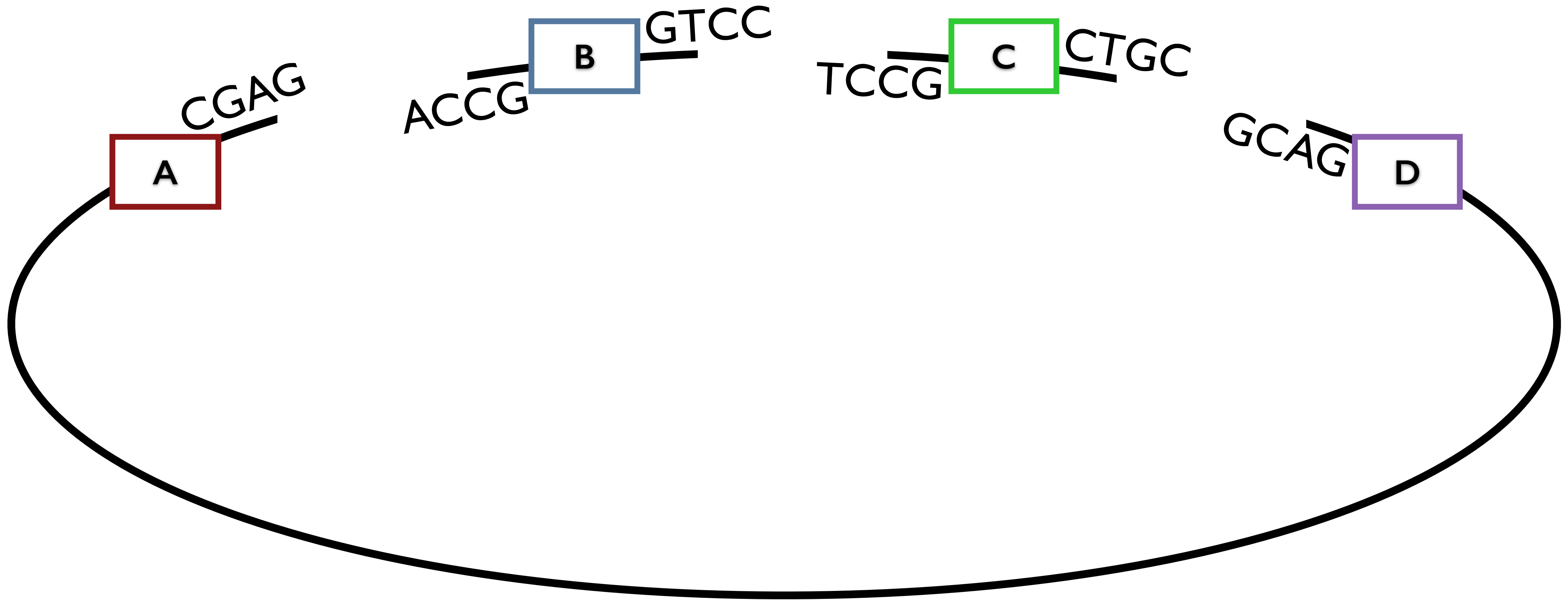
Combinatorics Cloning



Combinatorics Cloning



Combinatorics Cloning



Finding Compatible Sticky Ends

GGAJET

Golden Gate Assembly Junction Evaluative Tool

Instructions

Sources

*Plasmid/Gene Sequences (FASTA format only):

>Sequence Name

<http://gcat.davidson.edu/SynBio13/GGAJET/>

* Restriction enzyme:

BsaI

Currently limited to BsaI

* Melting temperature (°C):

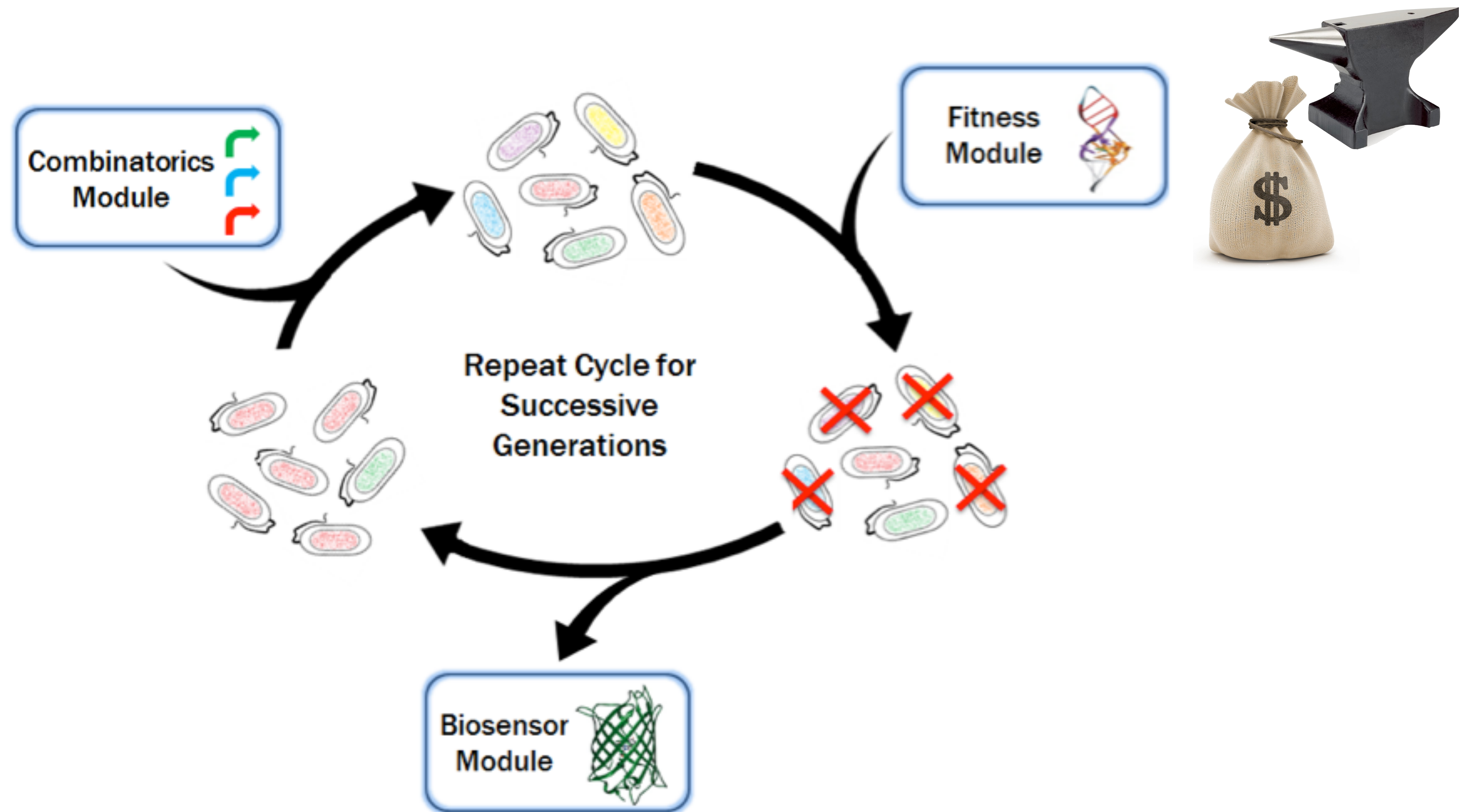
* Junction length (base pairs):

* Number of desired junctions:

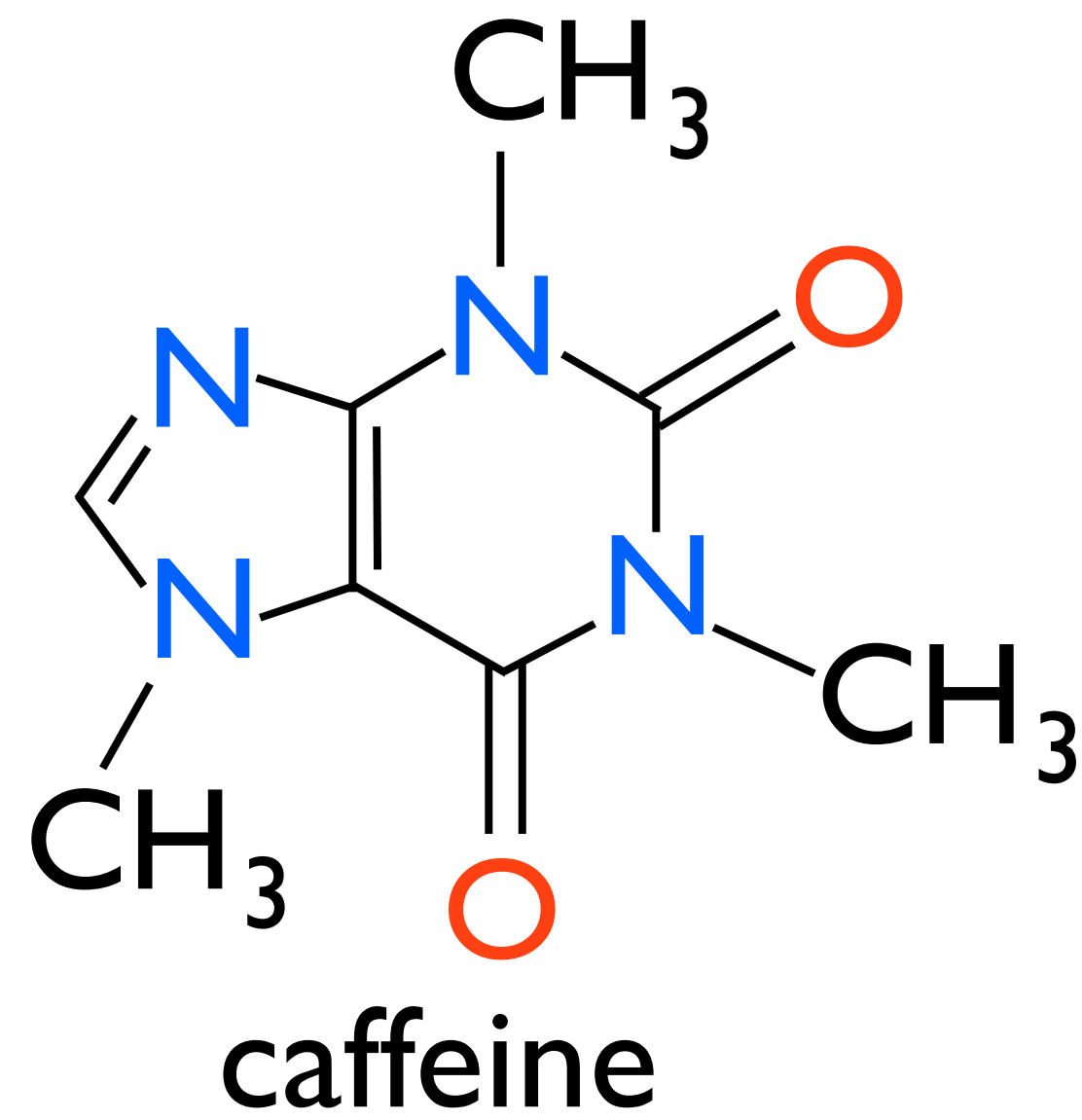
Currently limited to 4 junctions

PCR annealing temperature (°C):

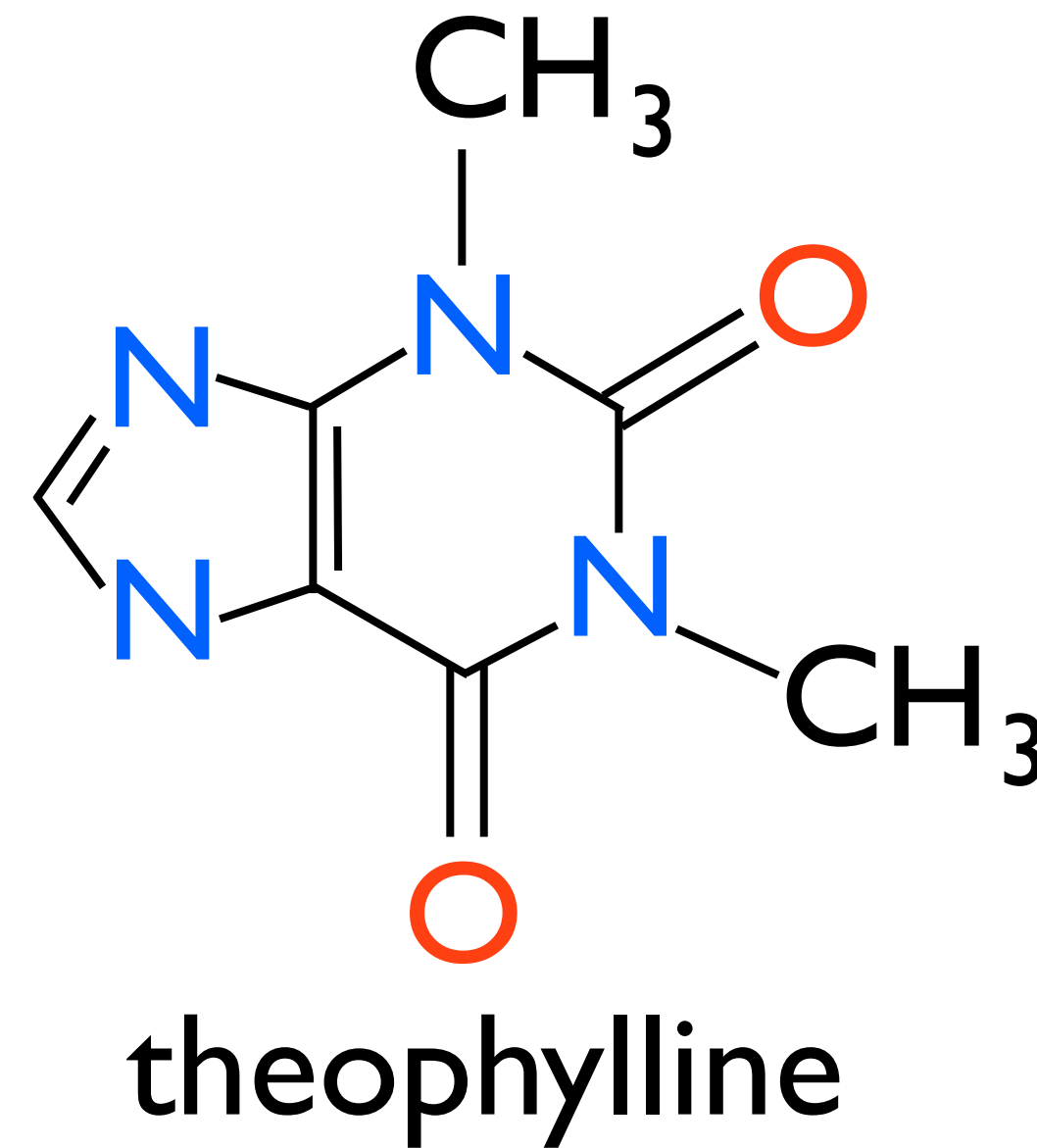
Programmed Evolution



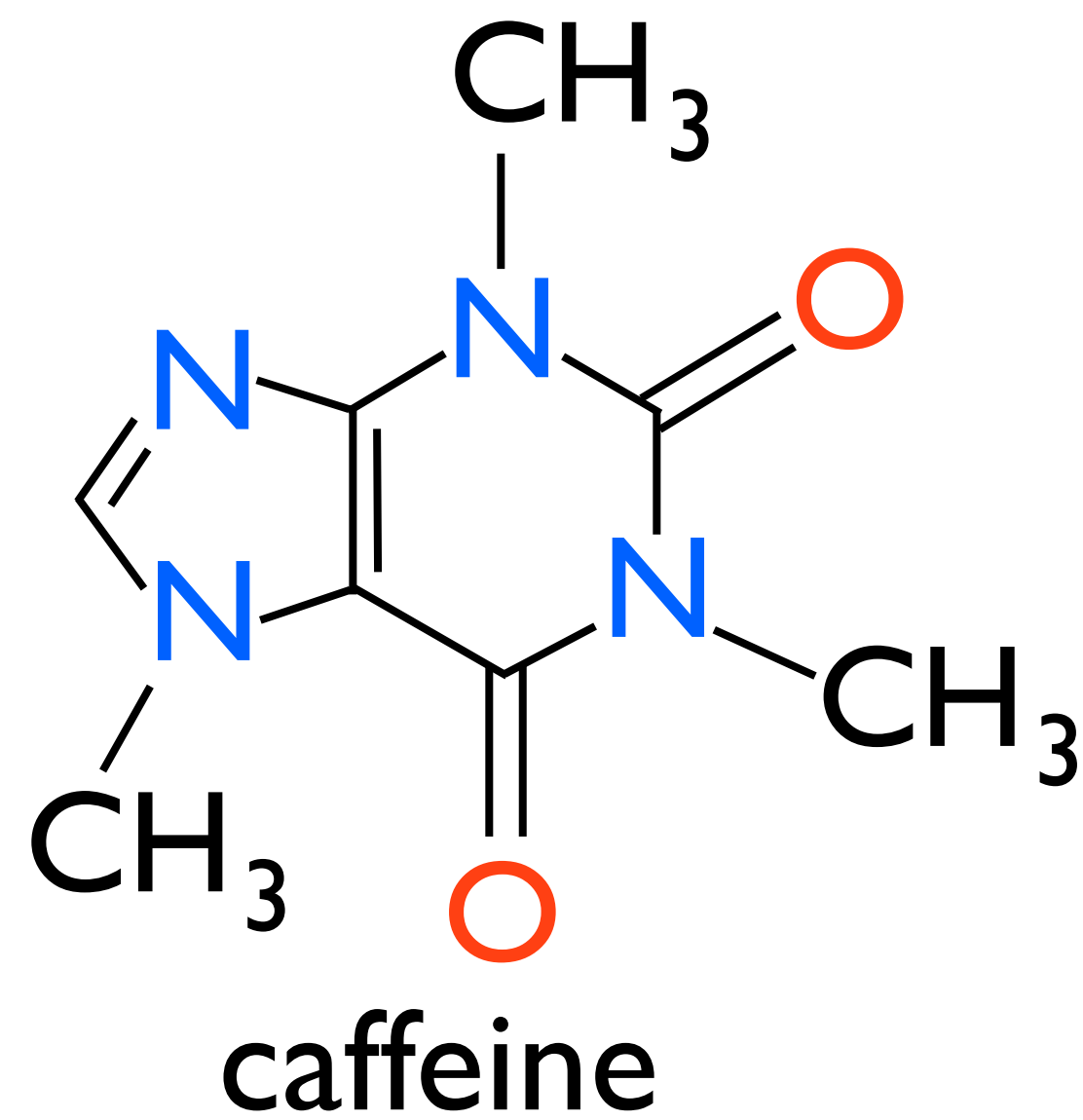
How to Build a Biosensor



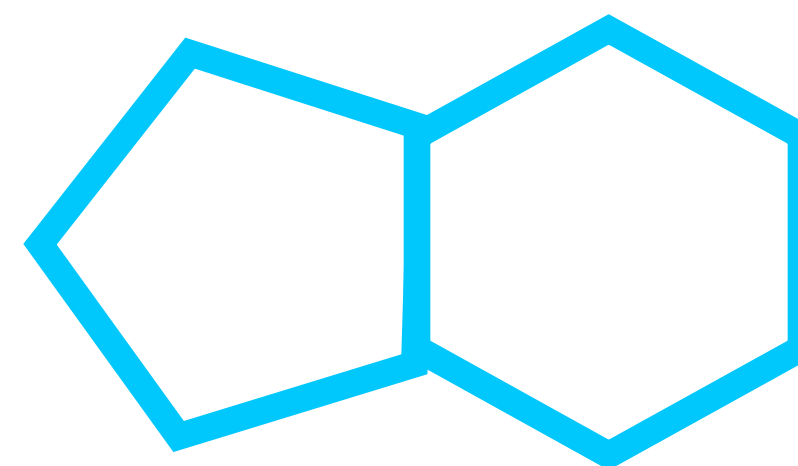
CDM
➔



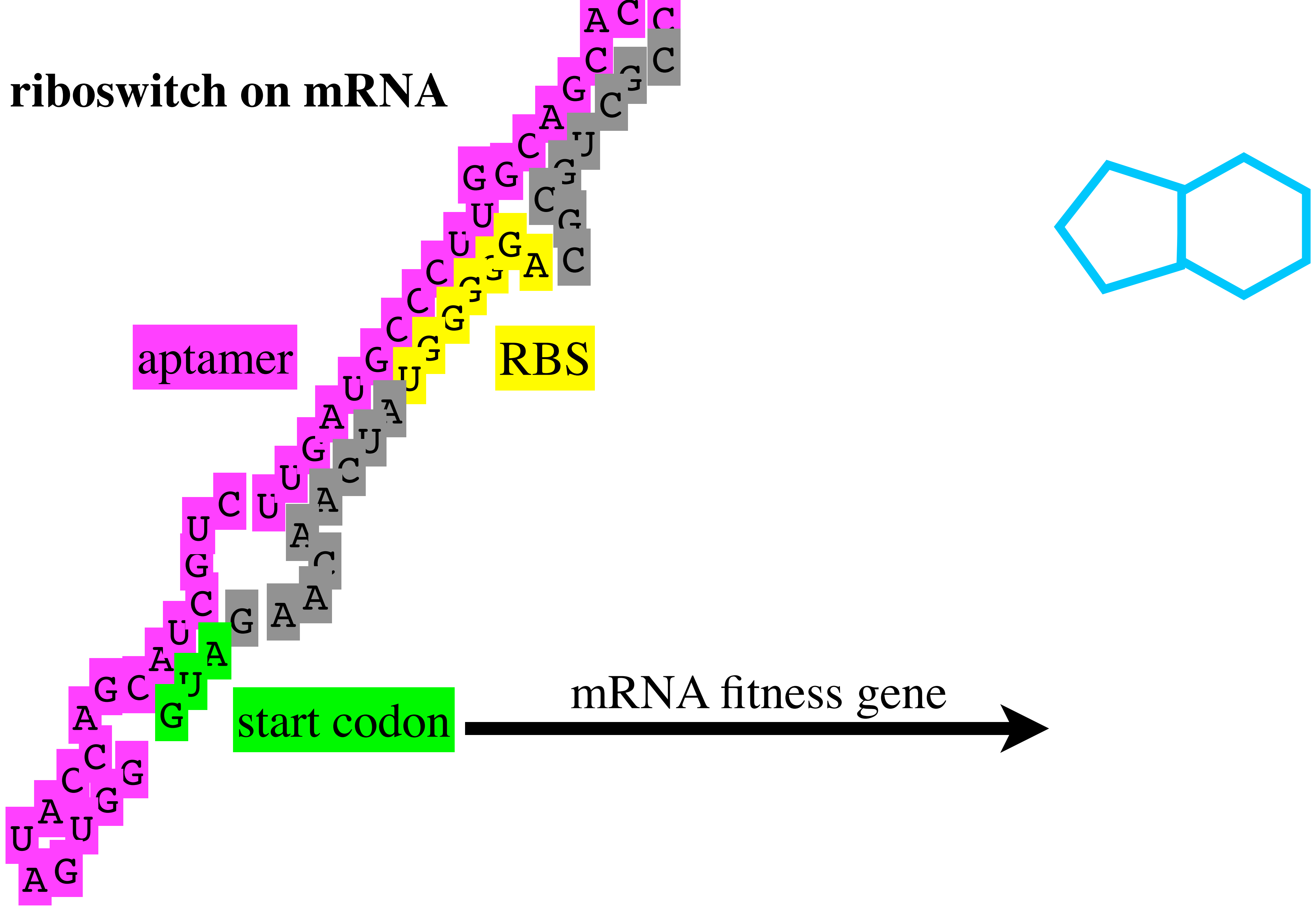
How to Build a Biosensor



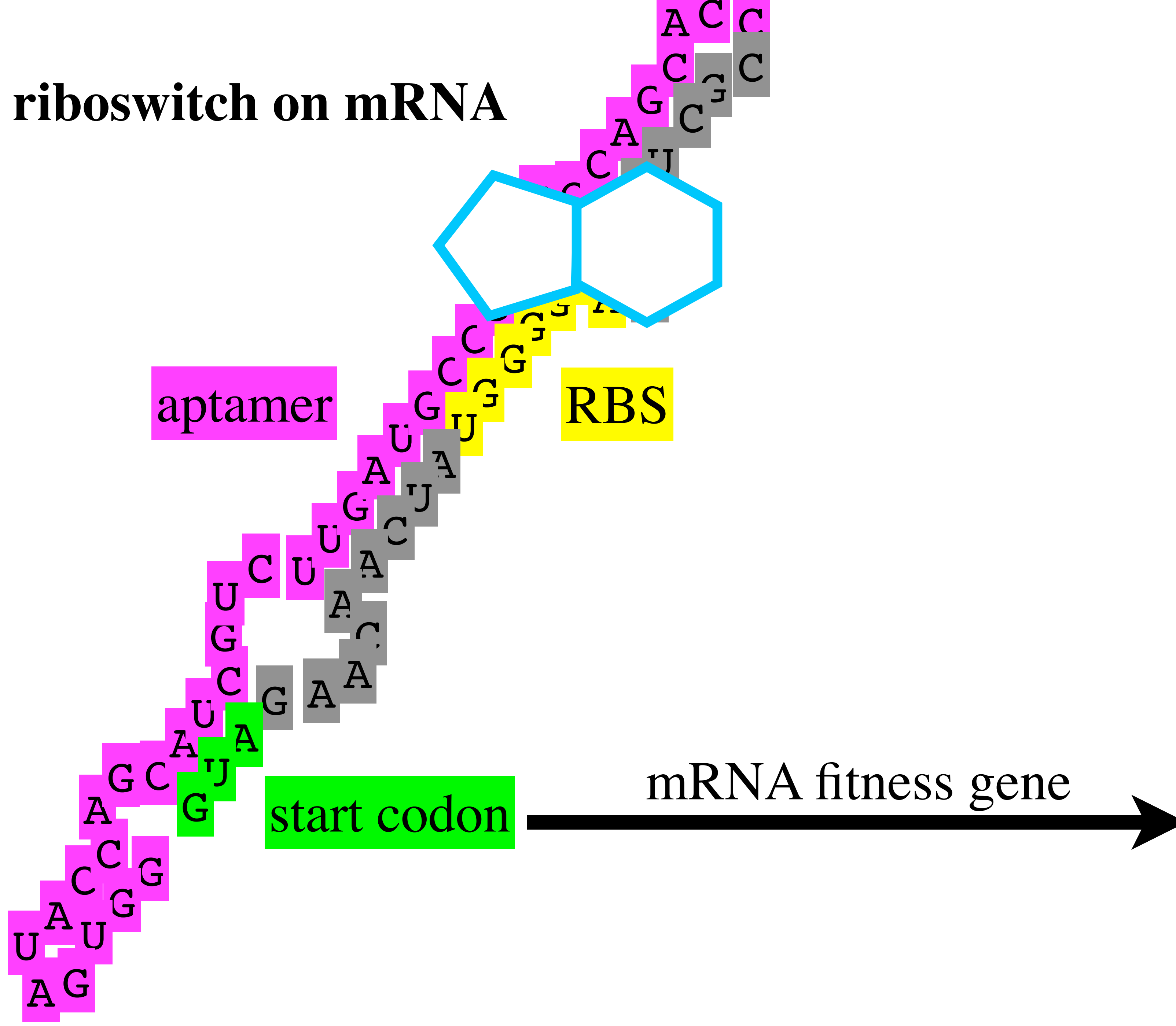
CDM
➔

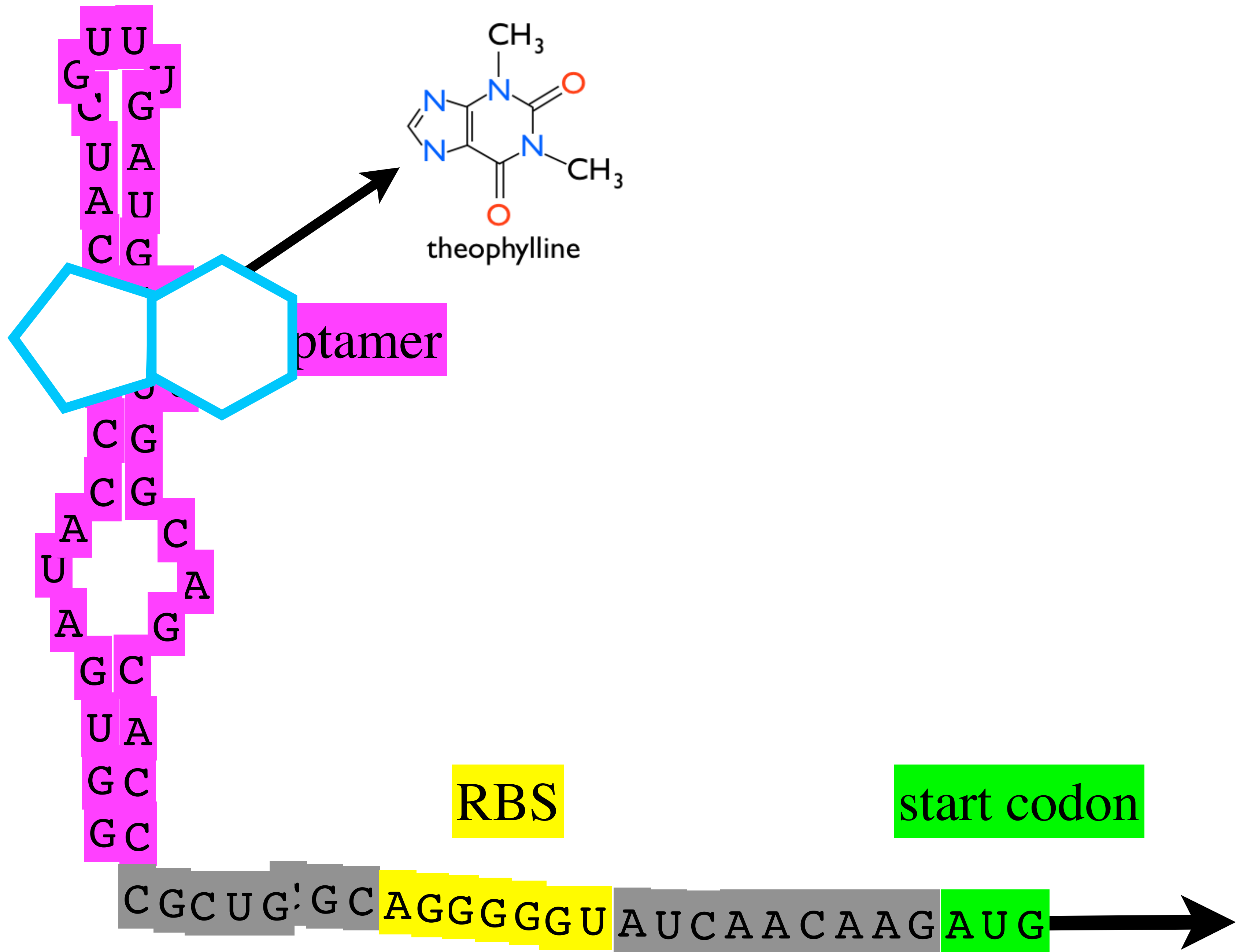


riboswitch on mRNA

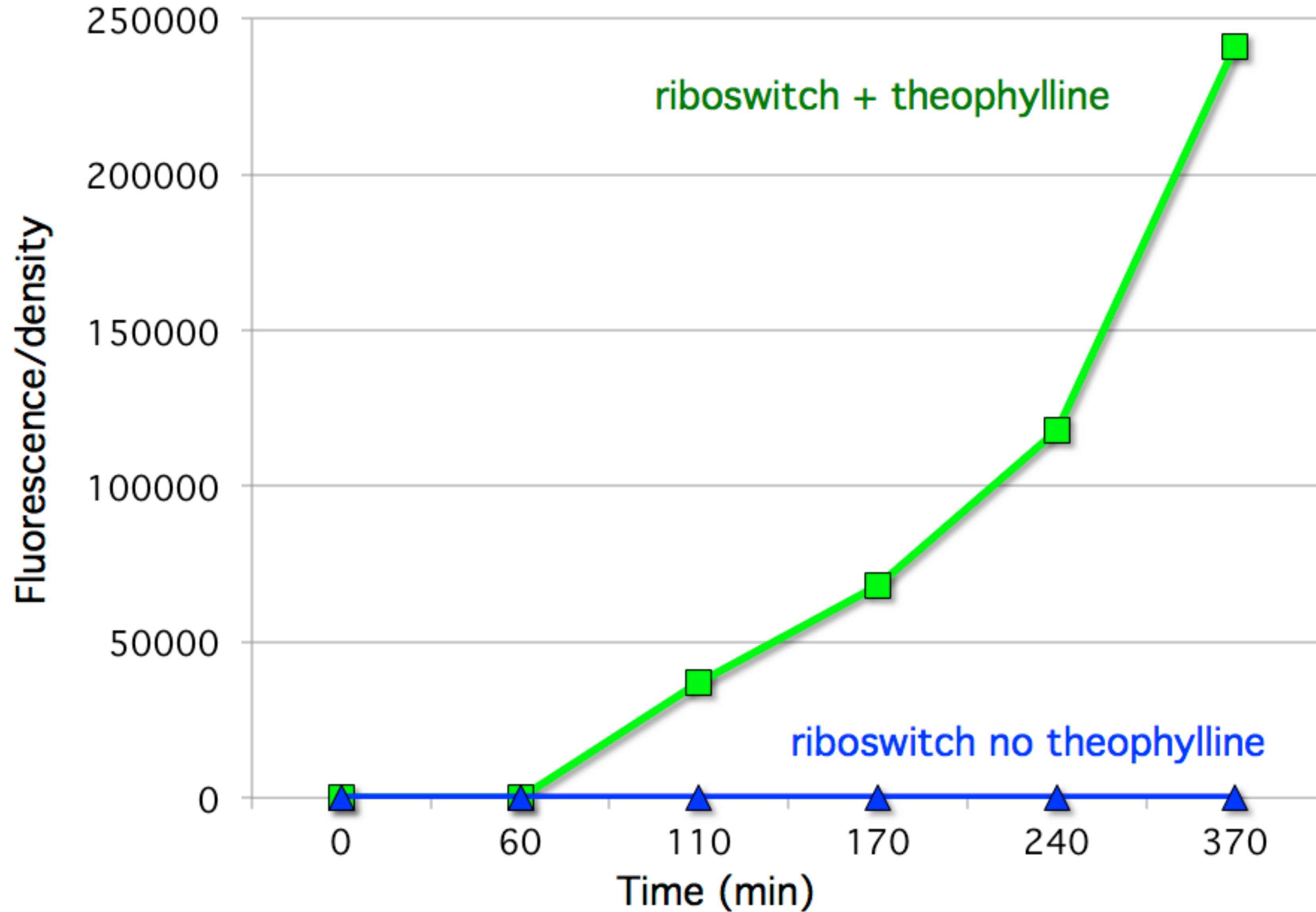


riboswitch on mRNA

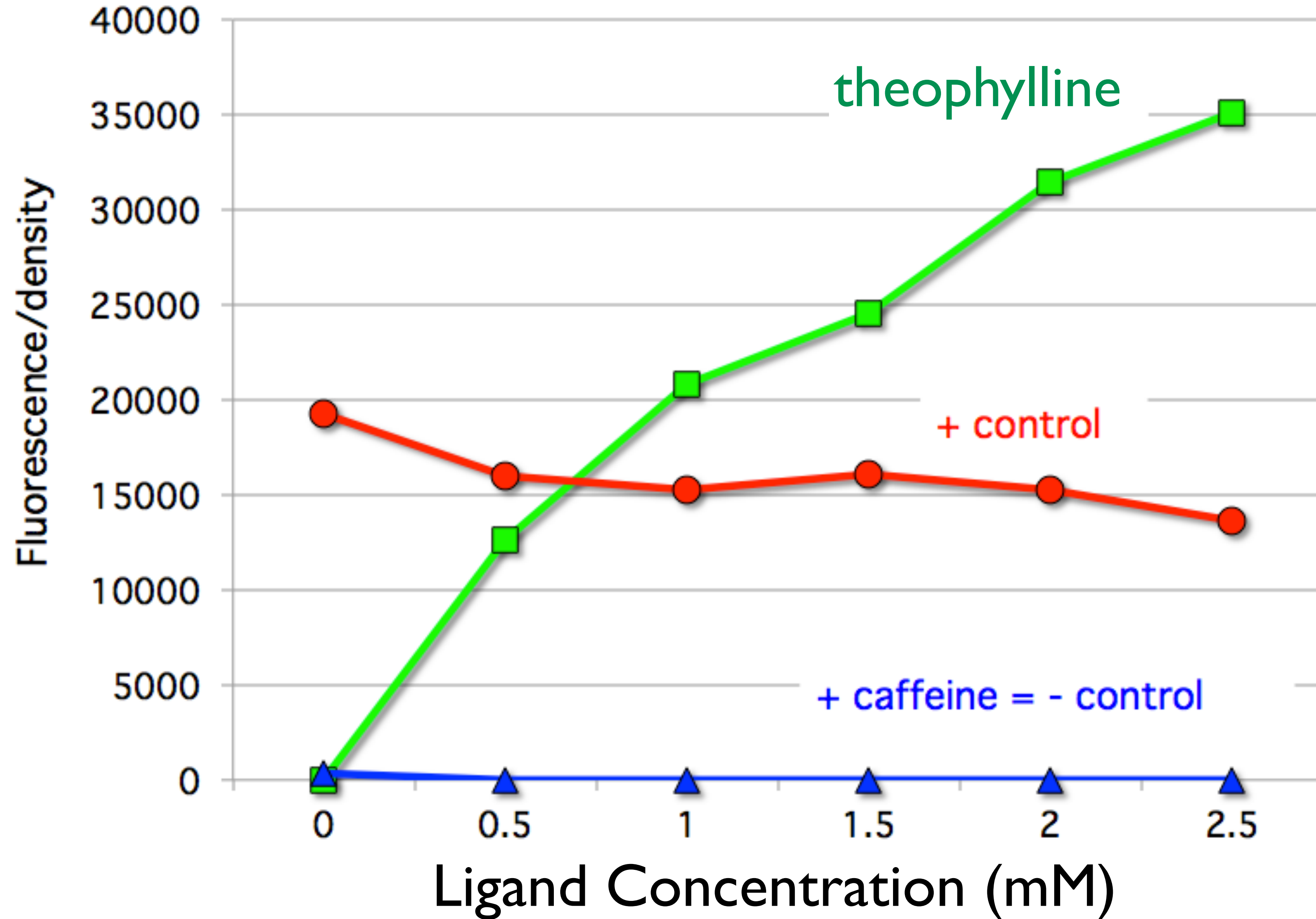




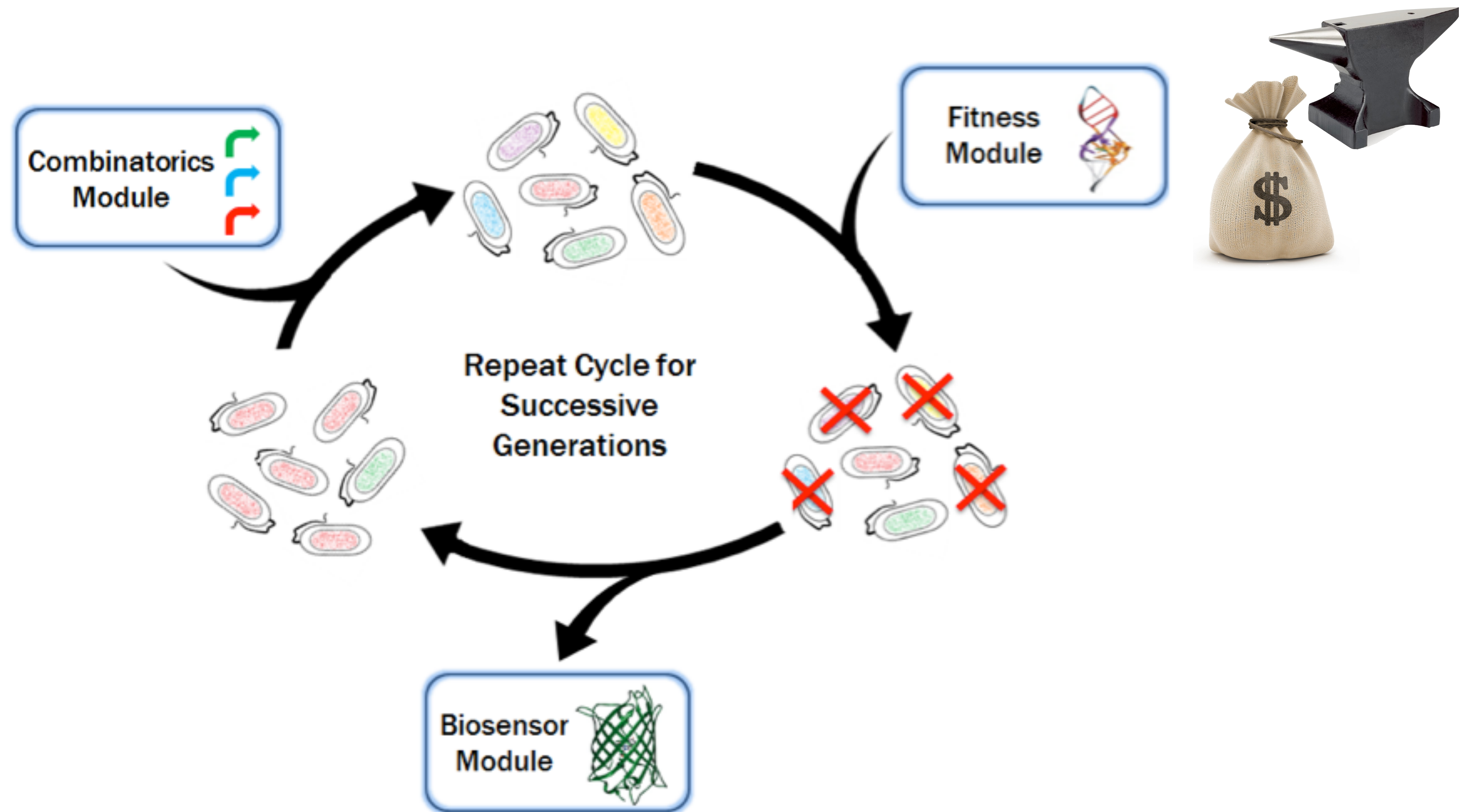
Biosensor Detects Theophylline



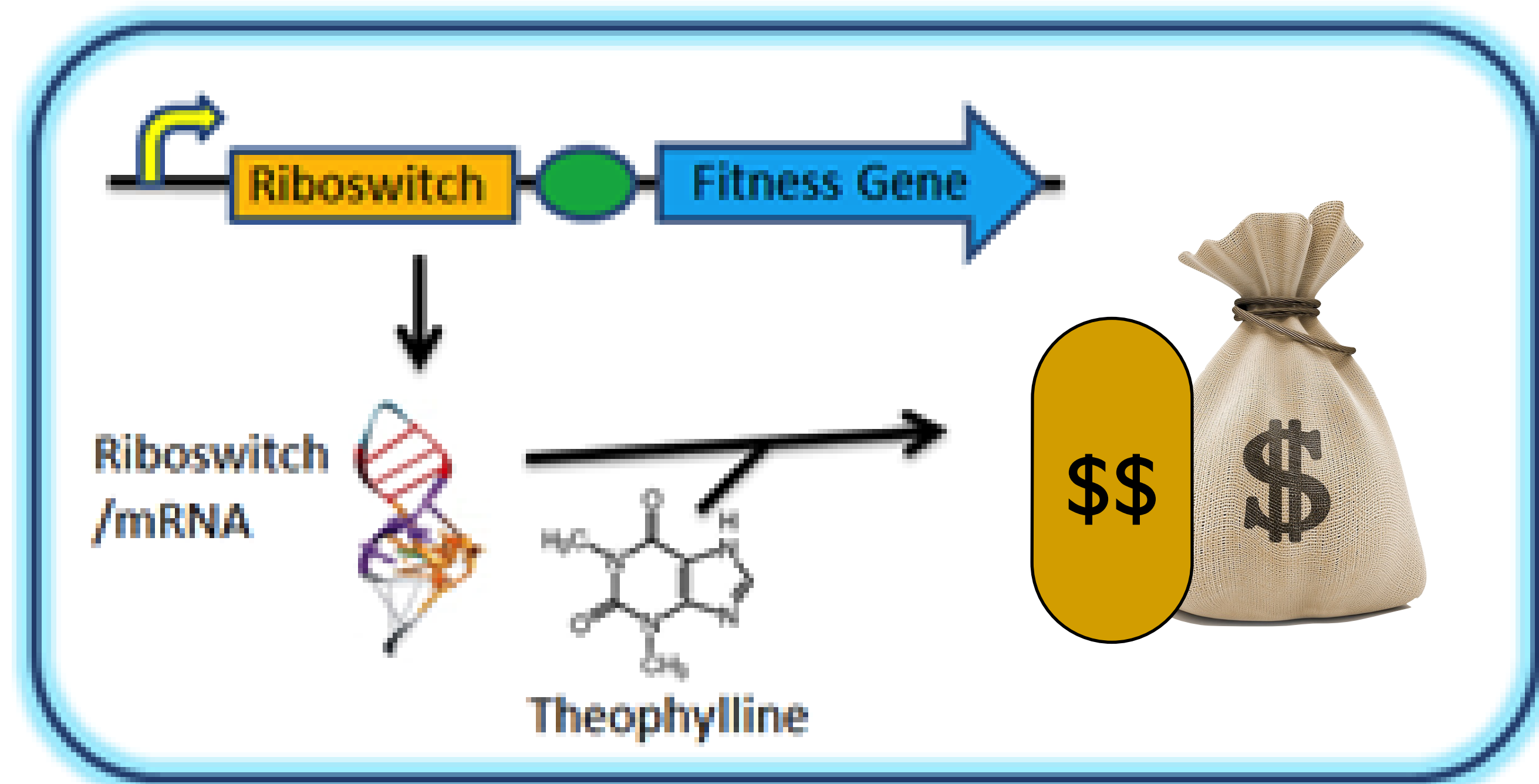
Biosensor Detects Theophylline



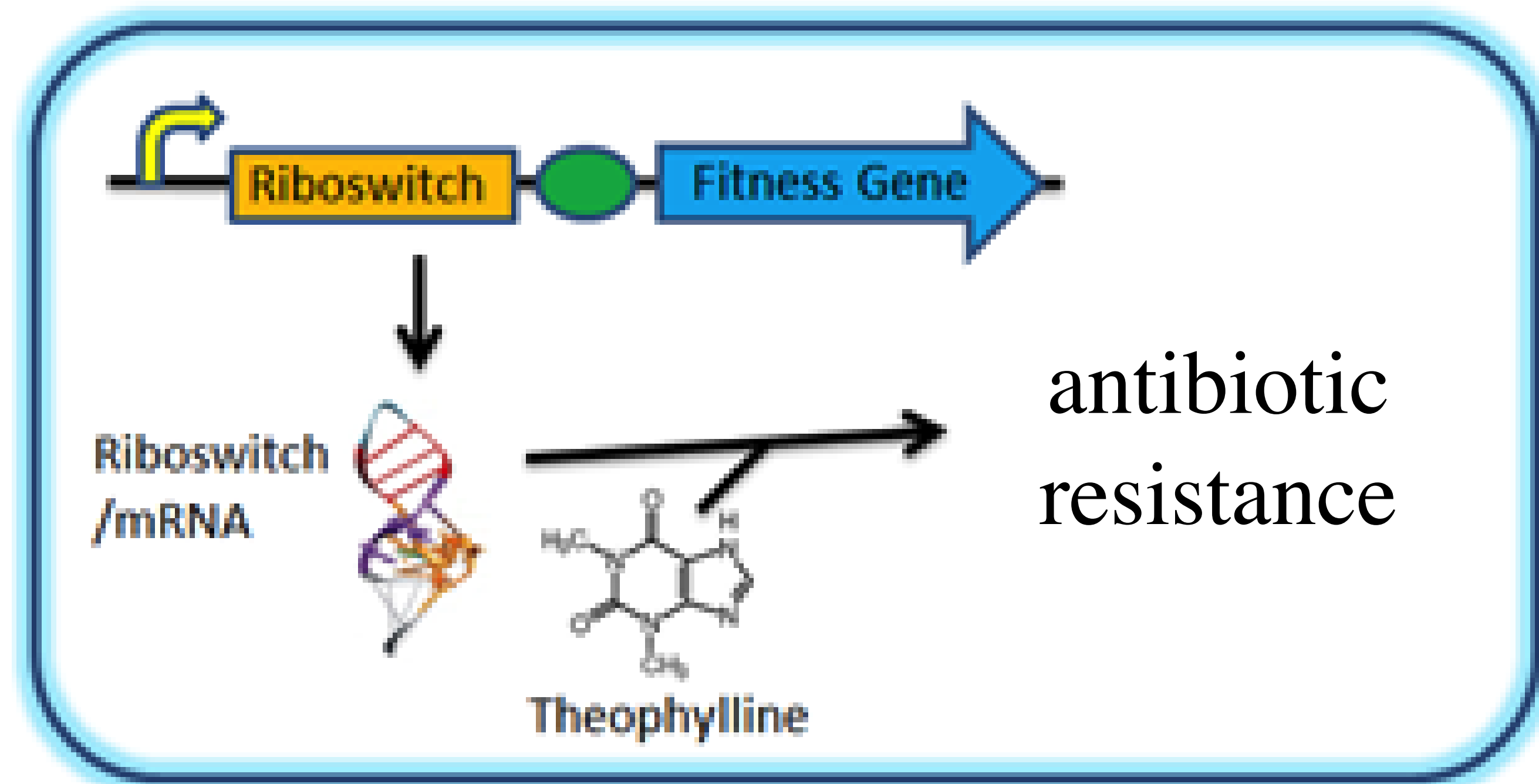
Programmed Evolution



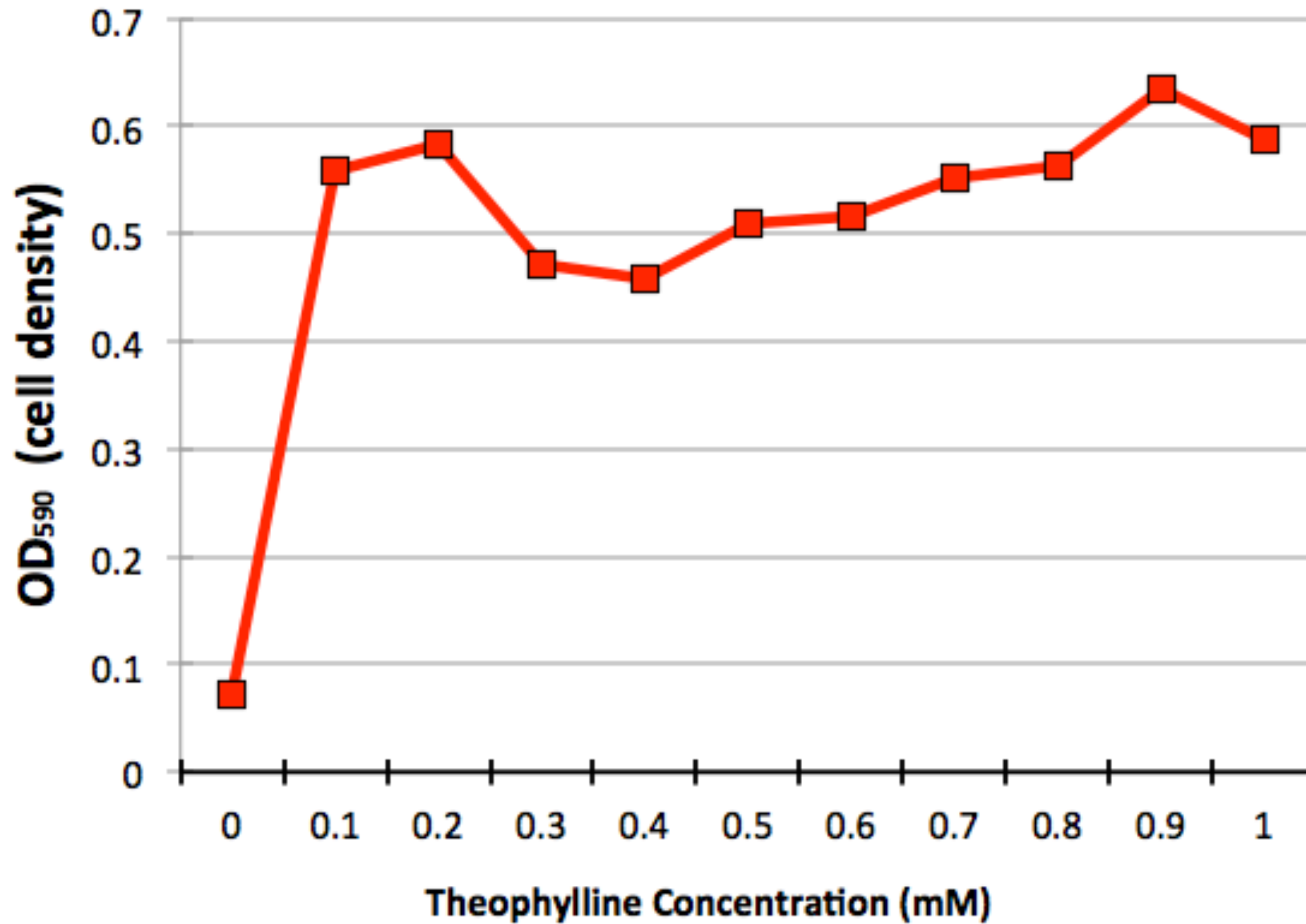
Fitness Module



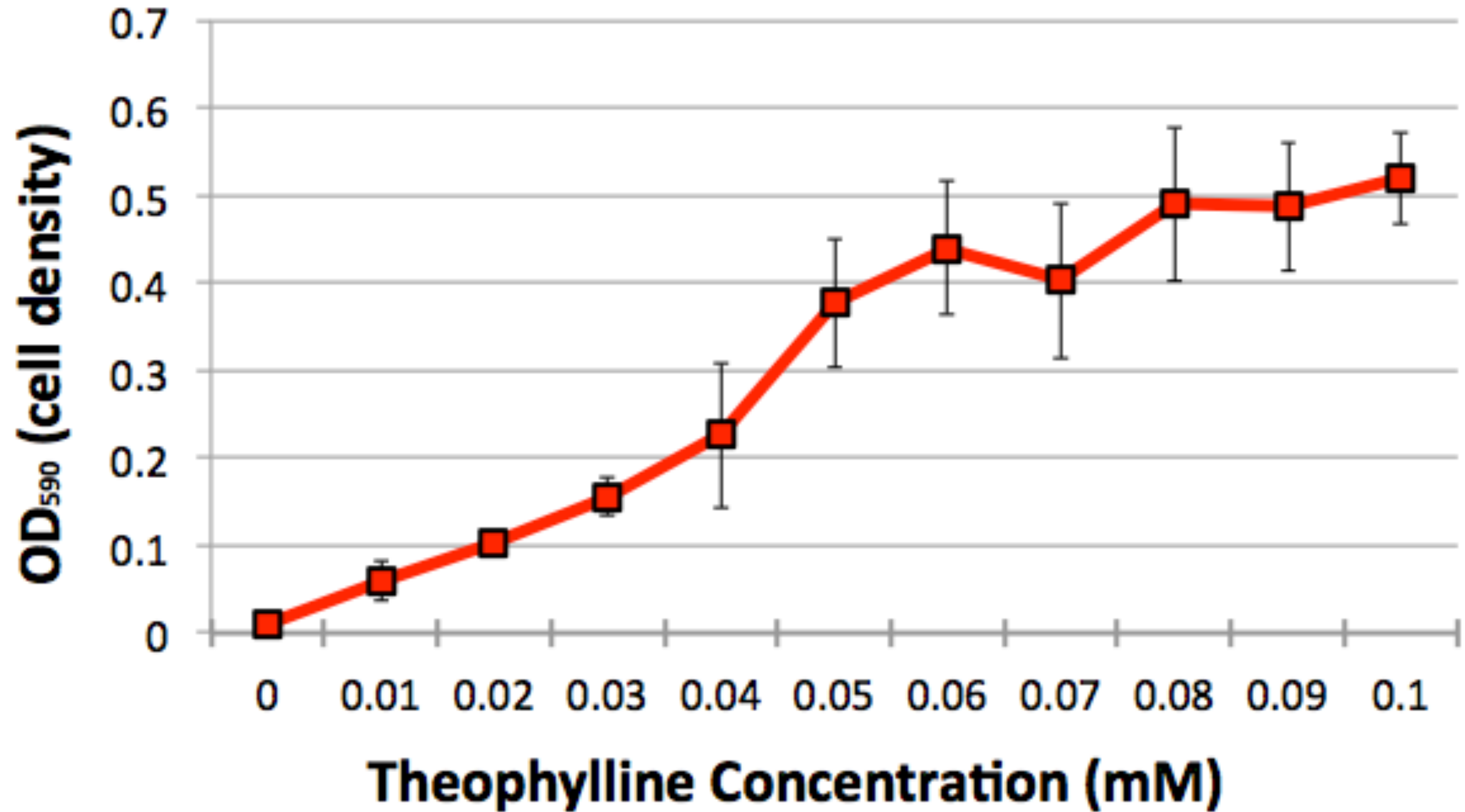
Fitness Module



Fitness Gene Sensitivity

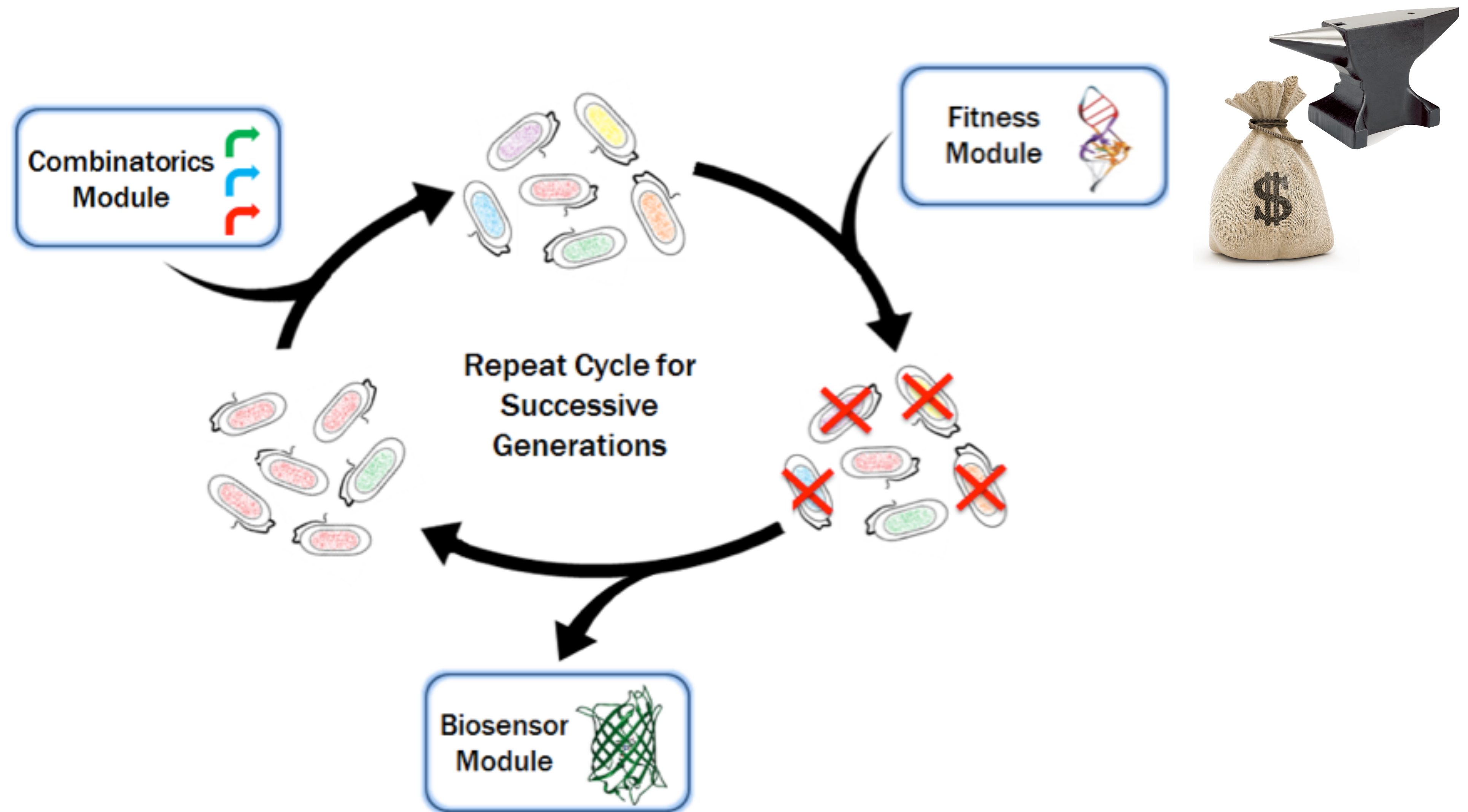


Fitness Gene Sensitivity



average +/- SEM

Programmed Evolution



How does natural selection work?

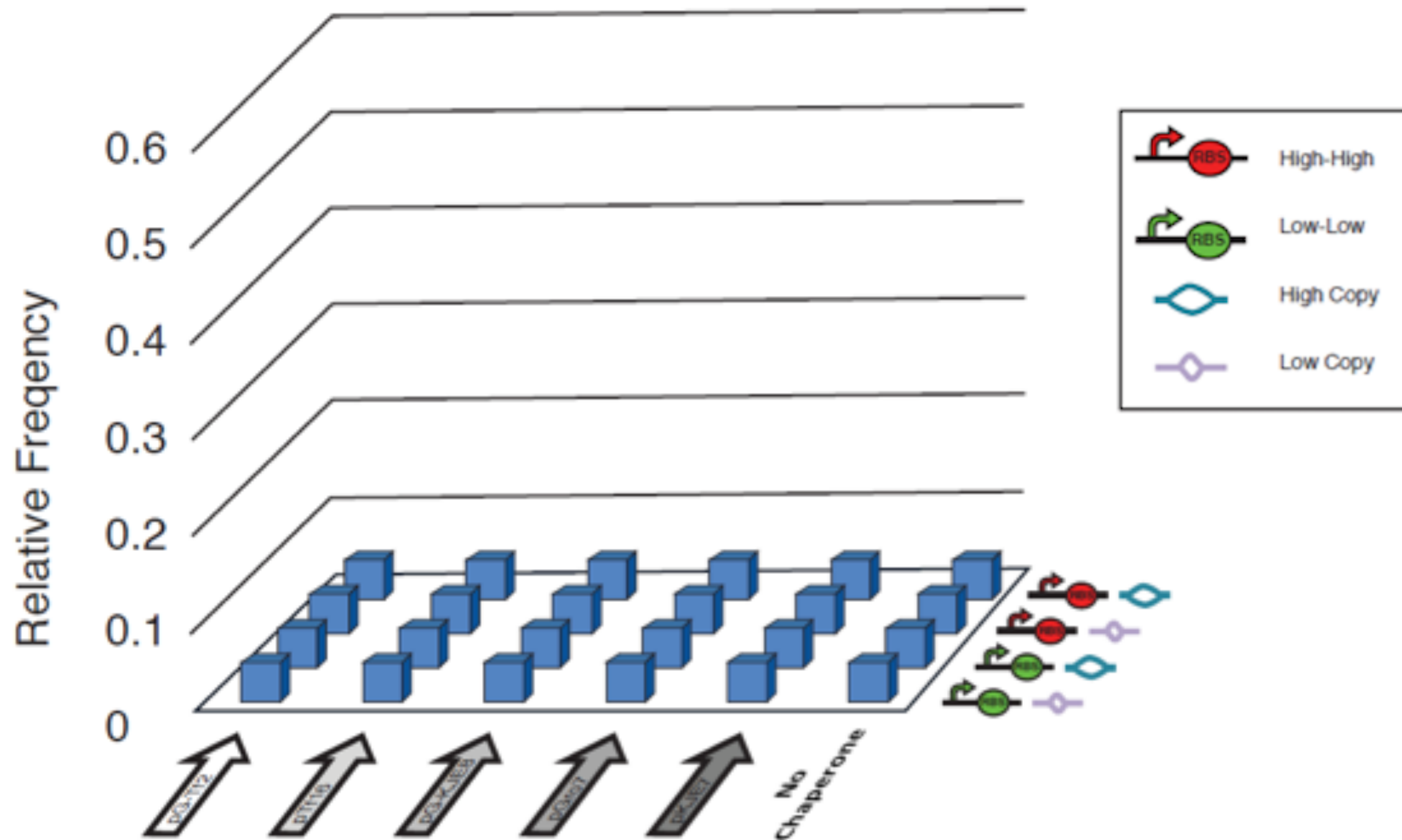
1. over production
2. variation in the population
3. competition for limited resources
4. selective advantage
5. reproduction

How does natural selection work?

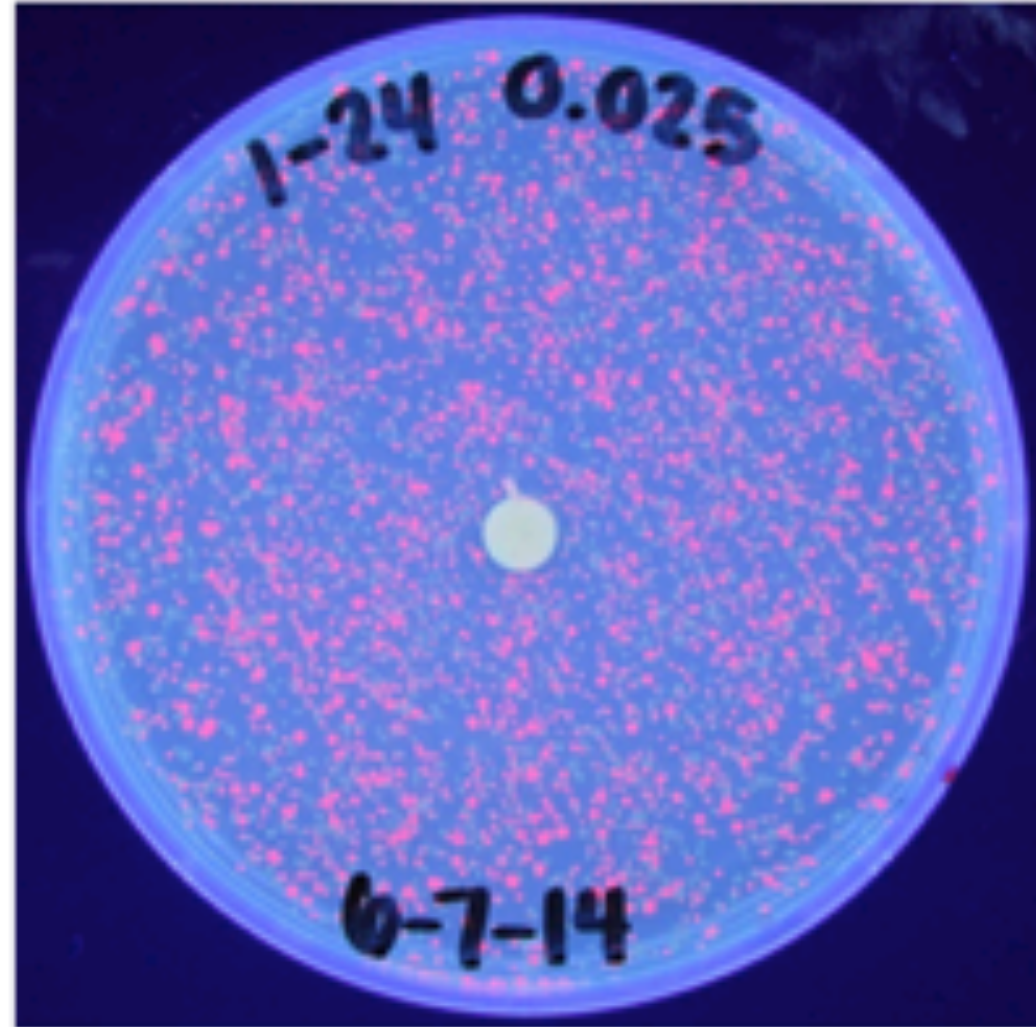
1. over production
2. **variation in the population**
3. competition for limited resources
4. selective advantage
5. reproduction

First Programmed Evolution Results

input 24 genotypes, equal proportions



First Programmed Evolution Results

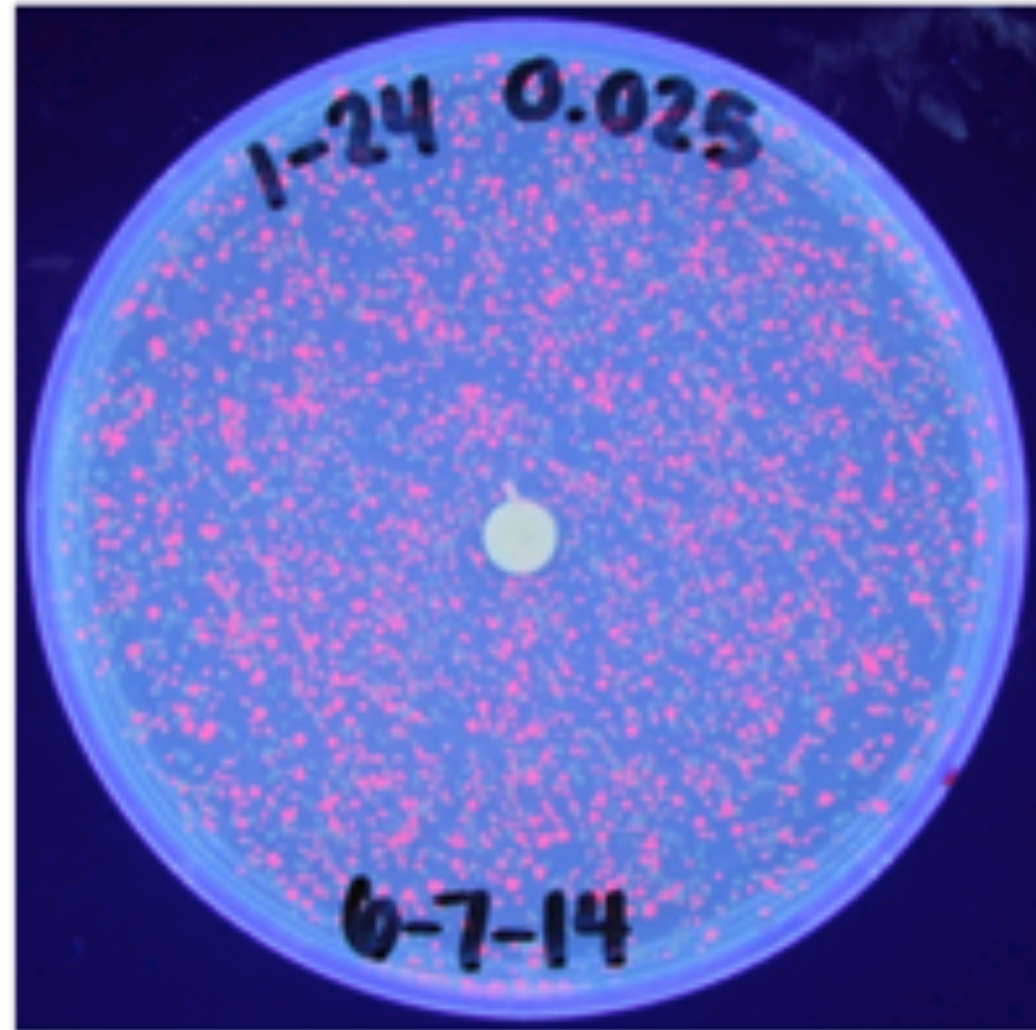


LB + Amp

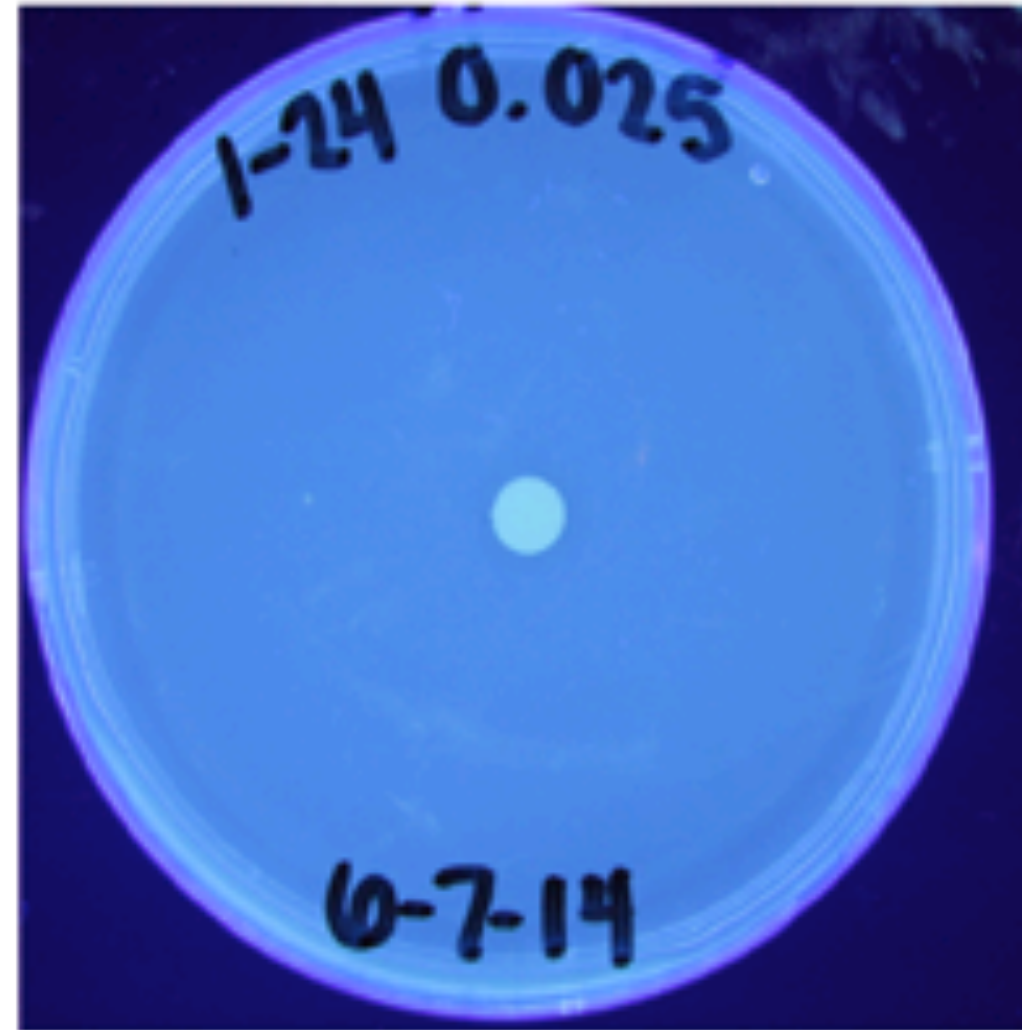
H₂O

Disk

First Programmed Evolution Results

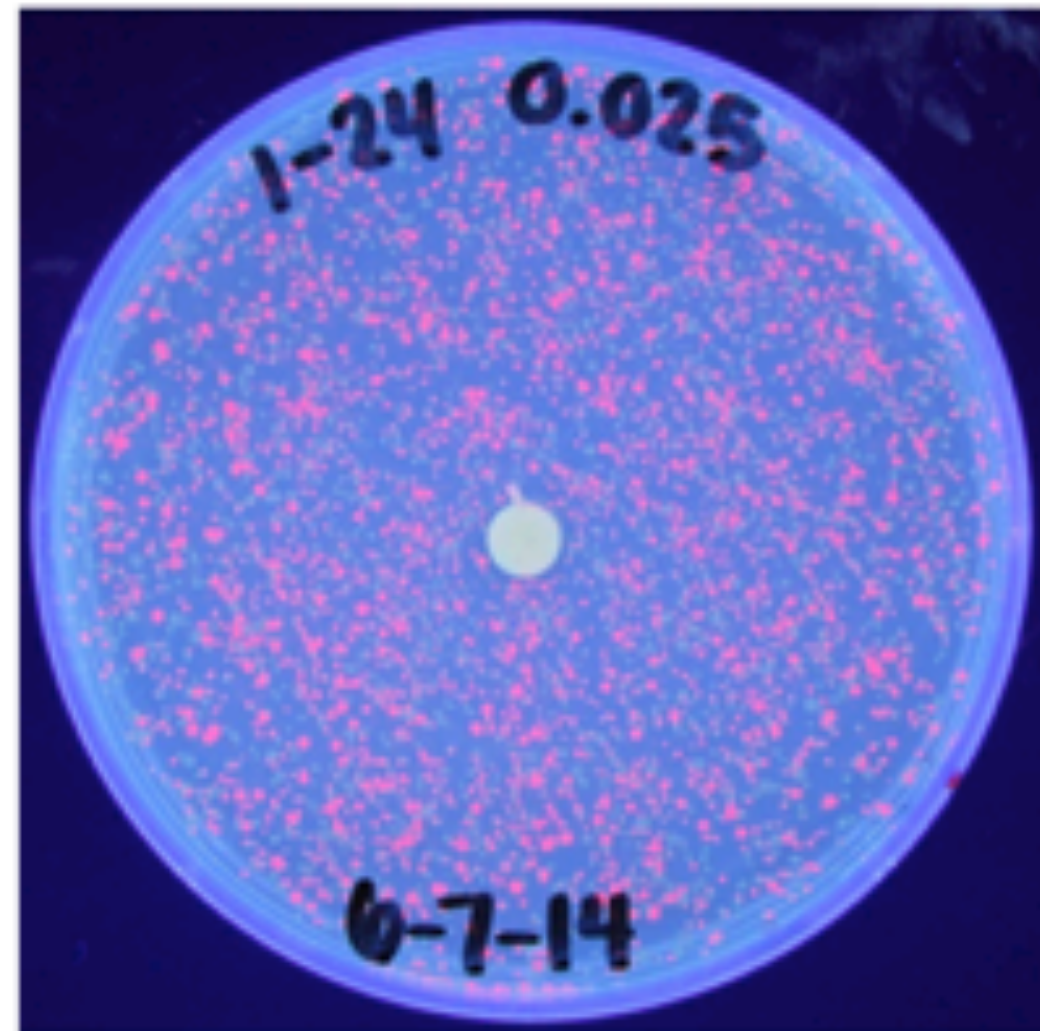


LB + Amp
H₂O
Disk

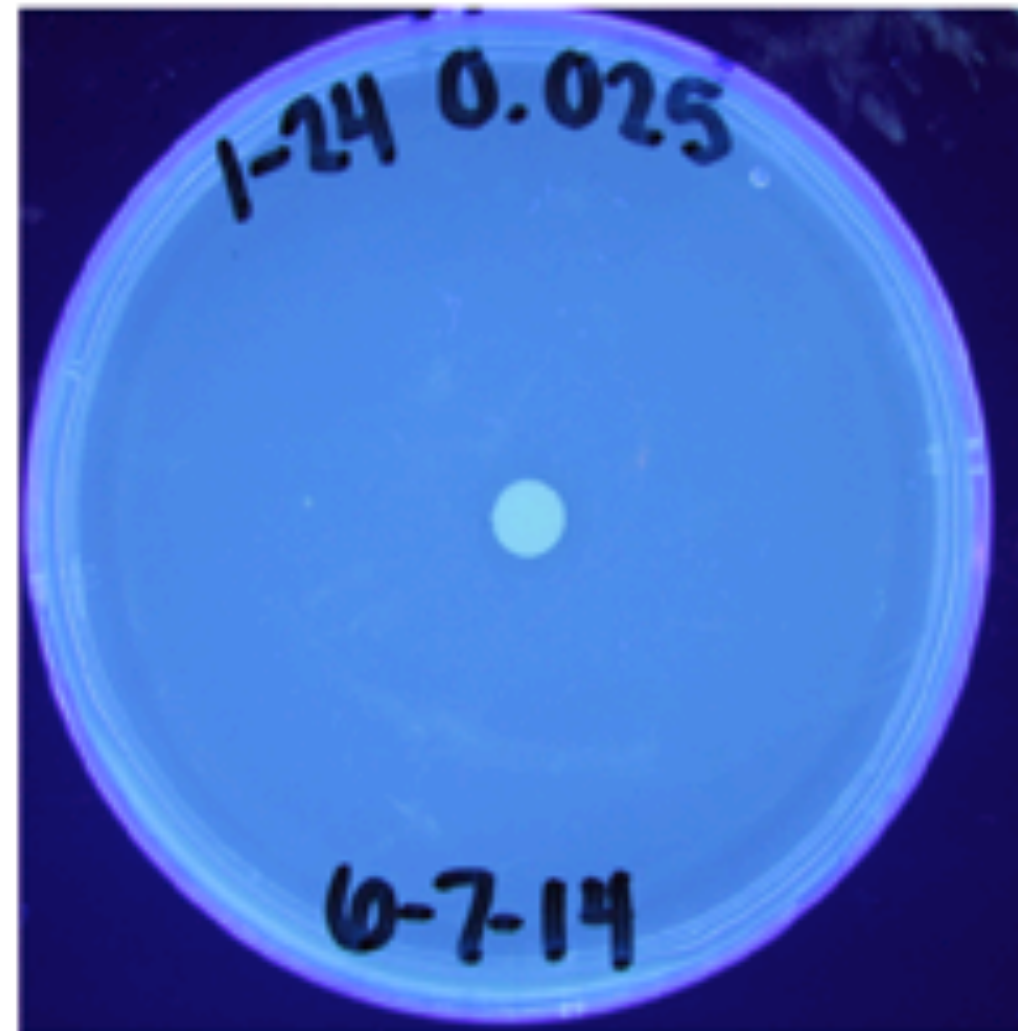


LB + Tet
H₂O
Disk

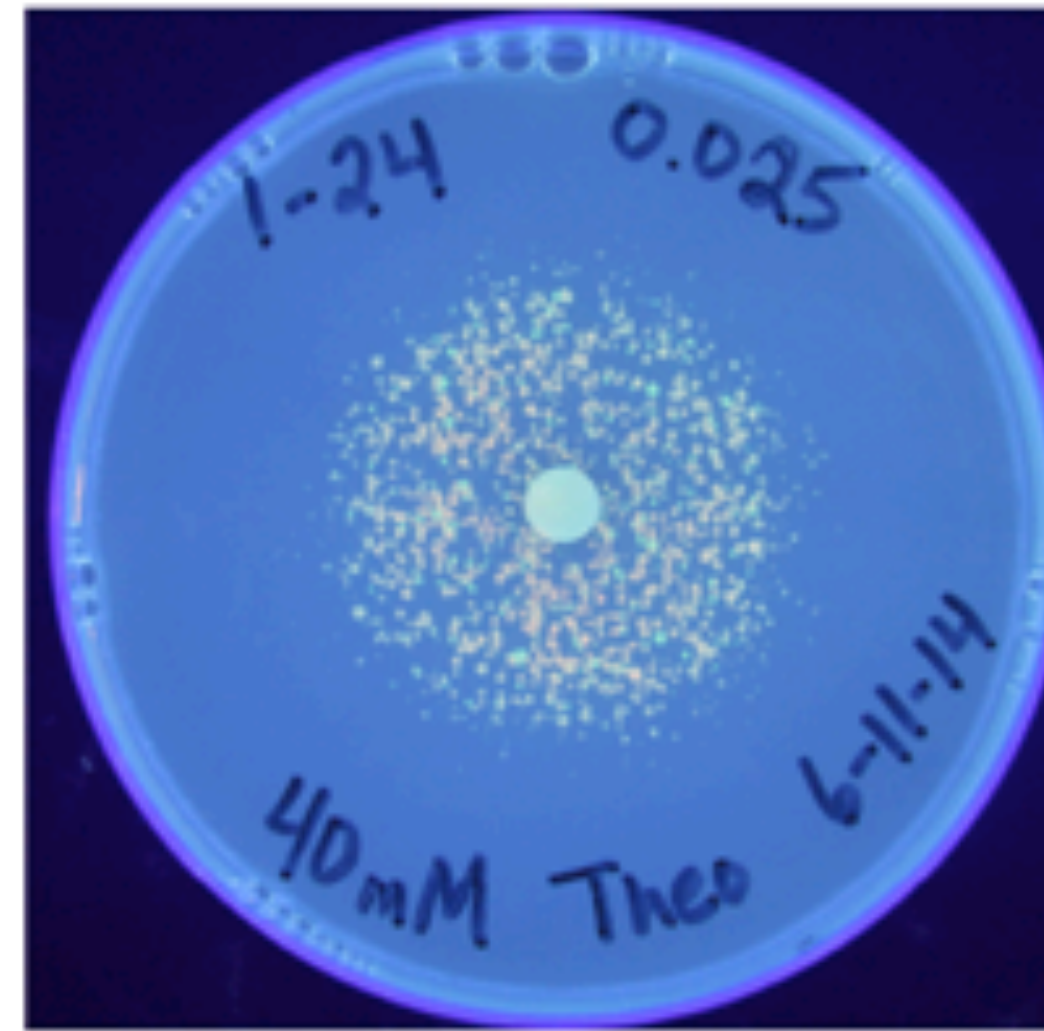
First Programmed Evolution Results



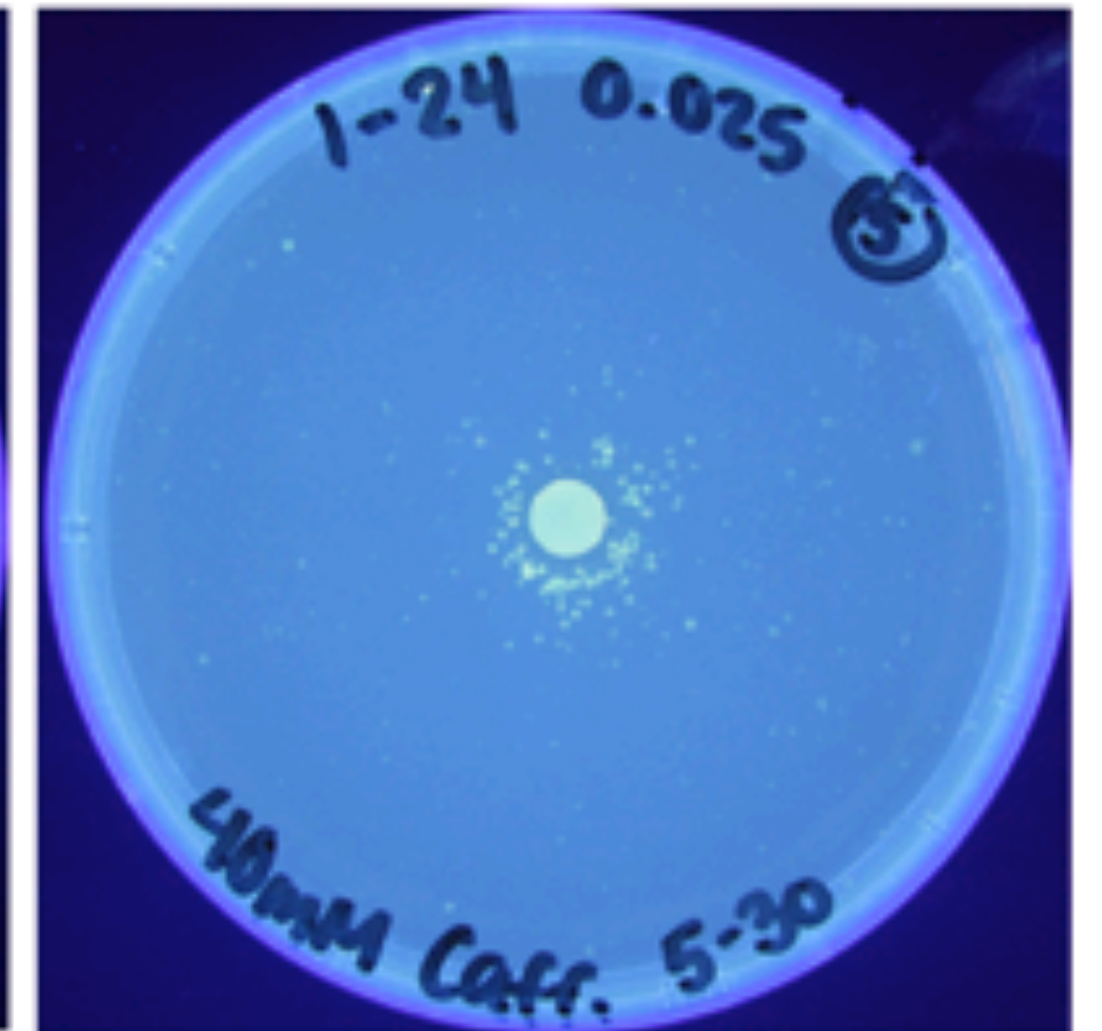
LB + Amp
H₂O
Disk



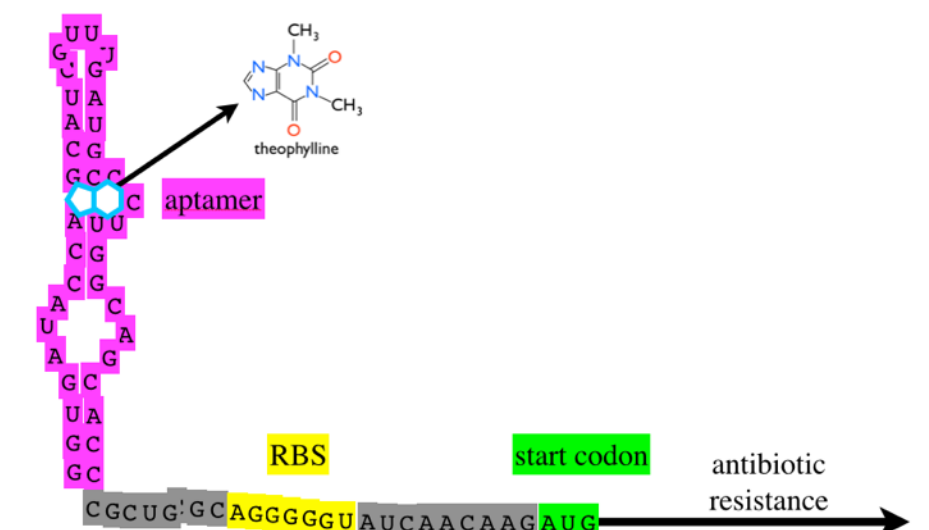
LB + Tet
H₂O
Disk



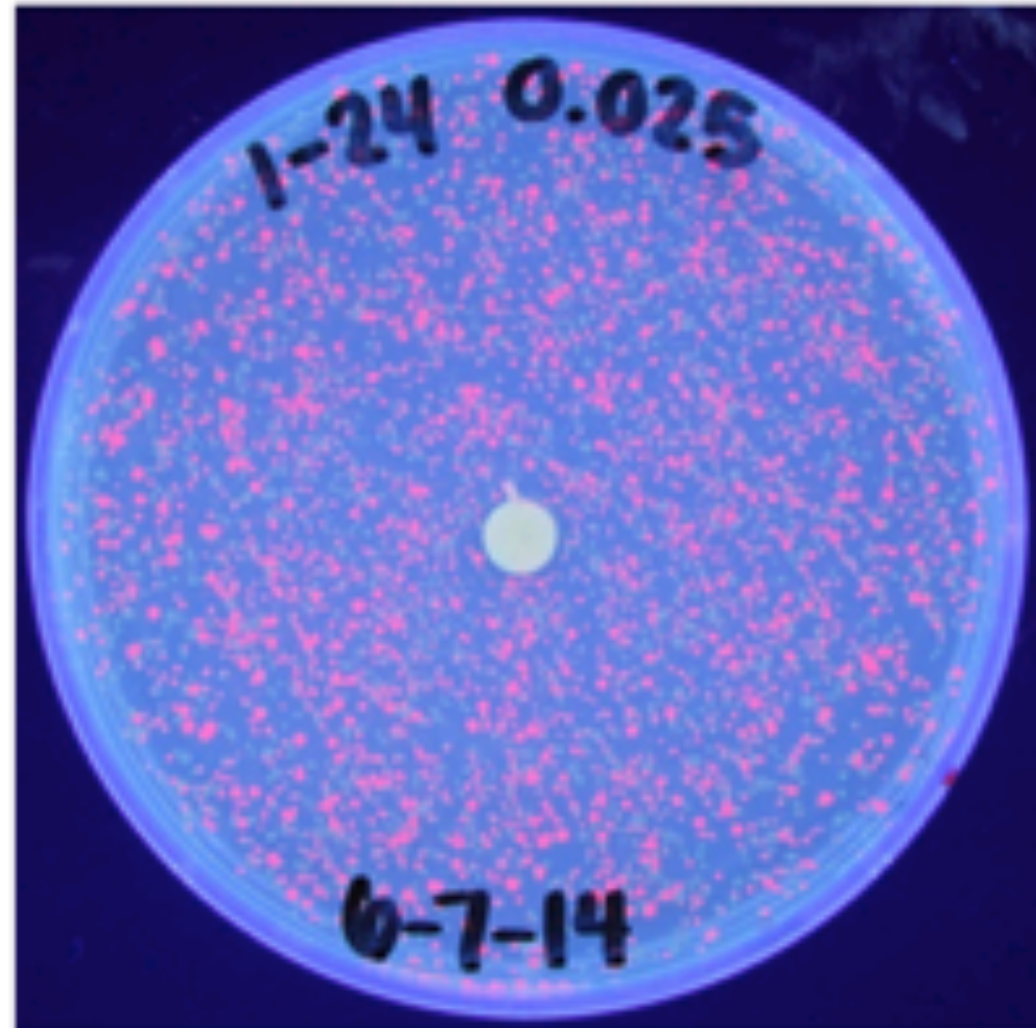
LB + Tet
40 mM Theophylline
Disk



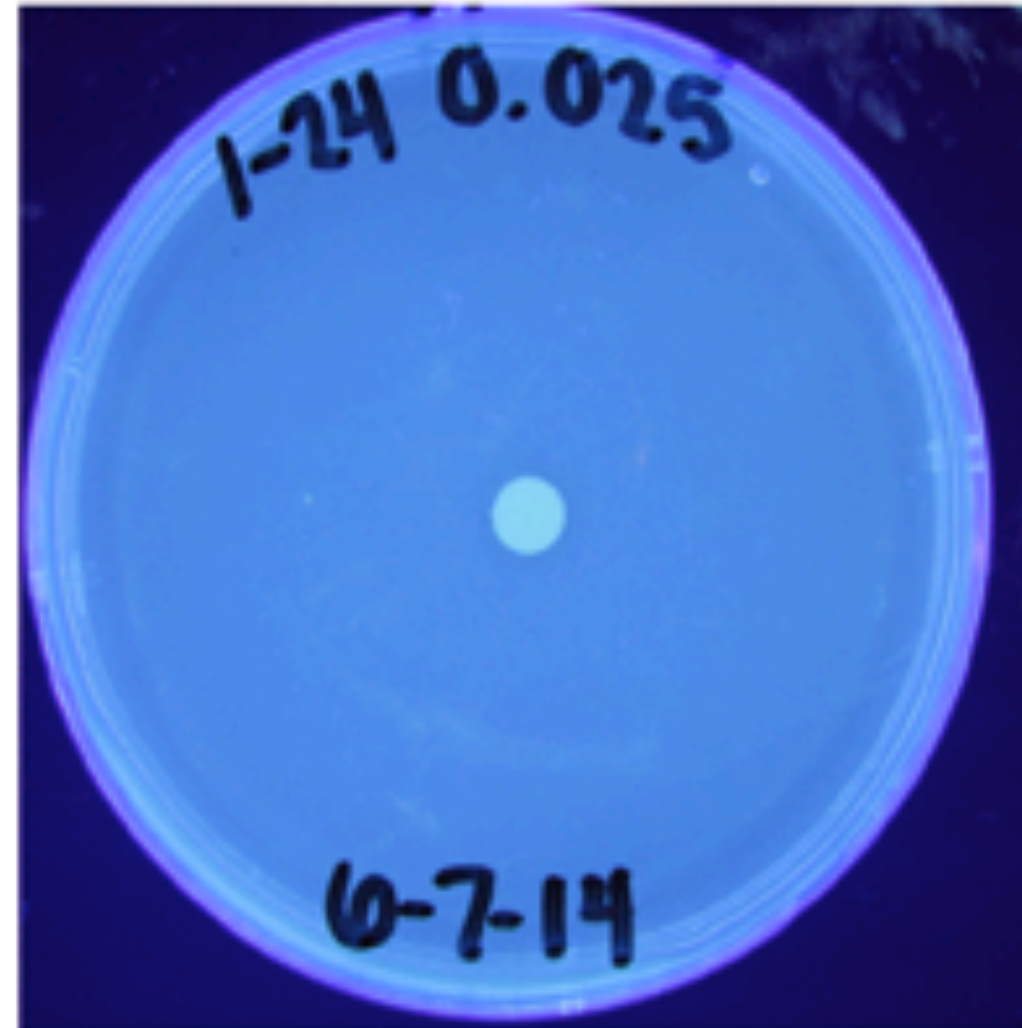
LB + Tet
40 mM Caffeine
Disk



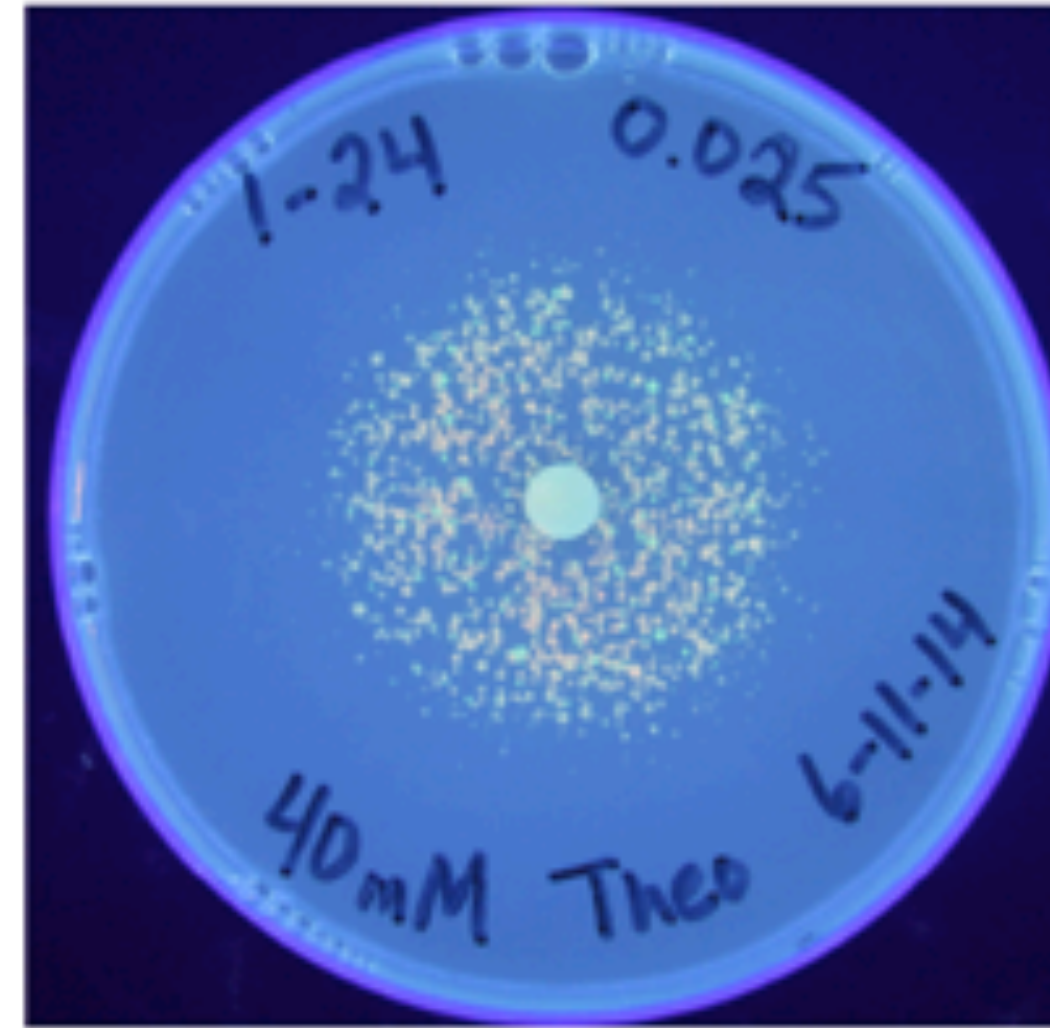
First Programmed Evolution Results



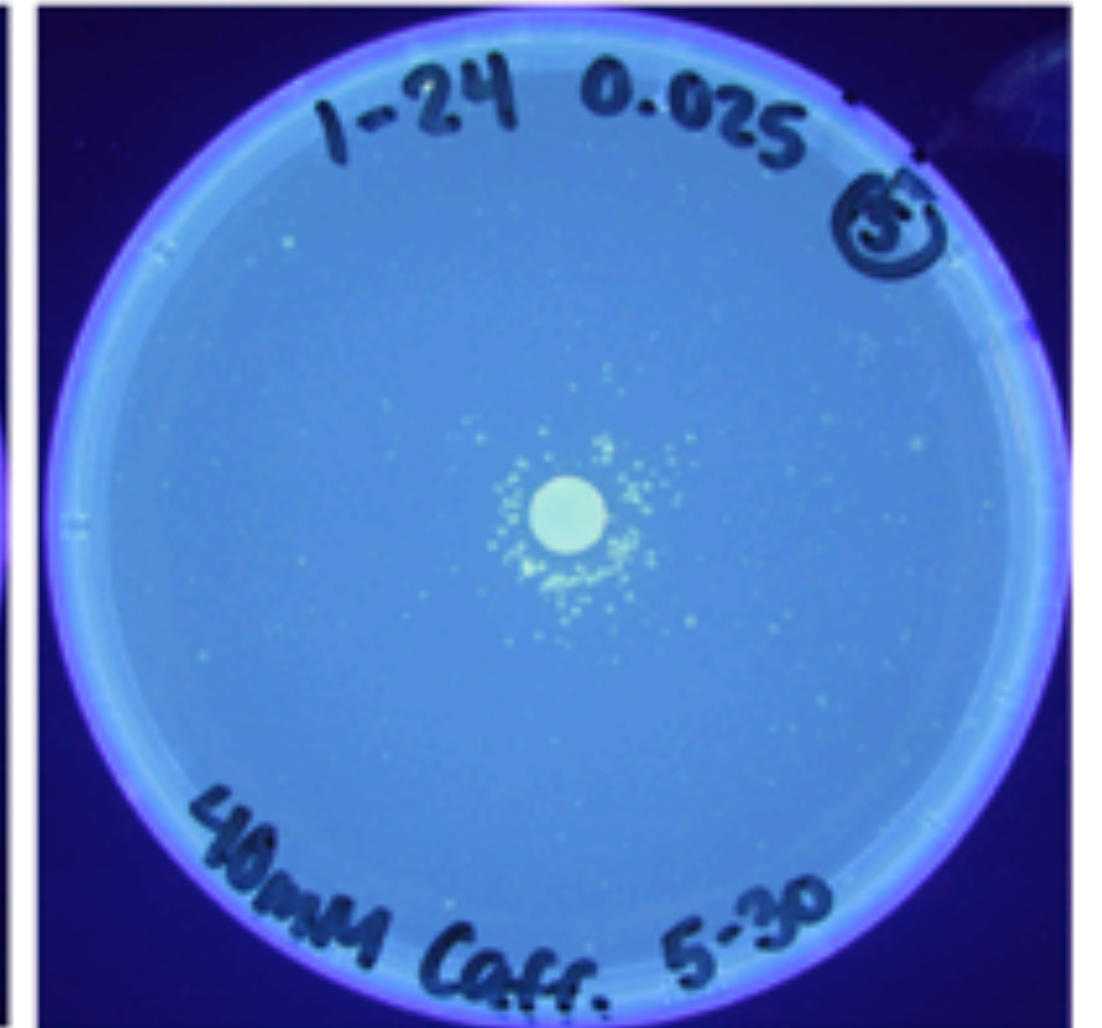
LB + Amp
H₂O
Disk



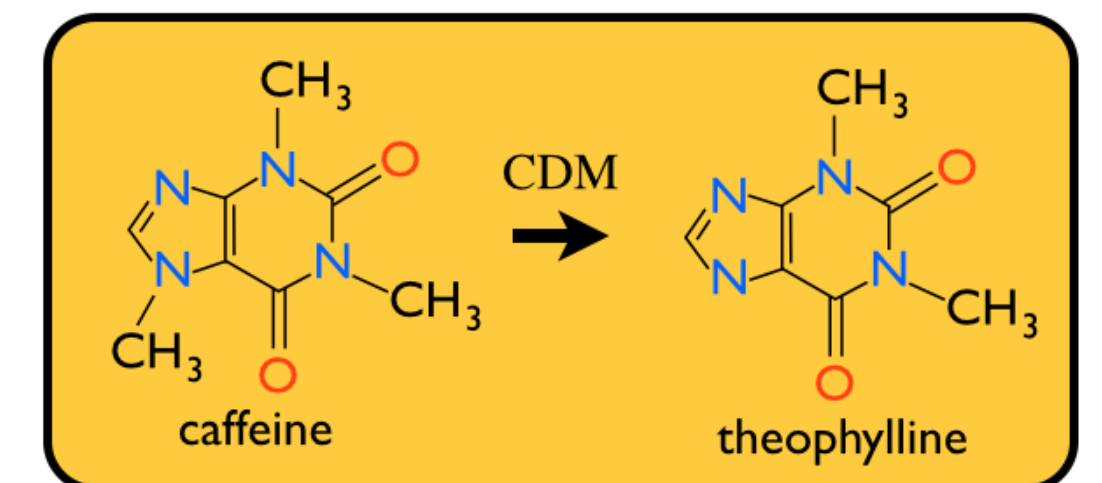
LB + Tet
H₂O
Disk



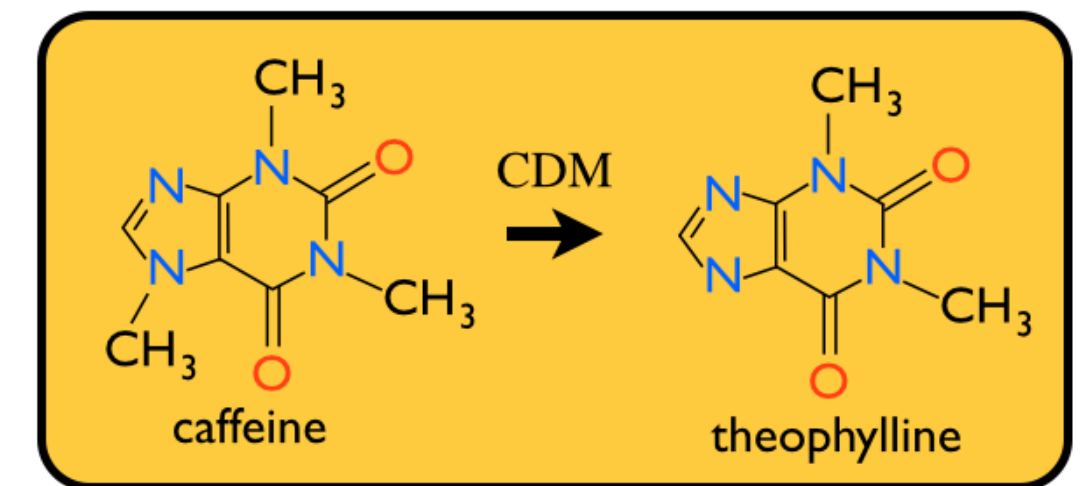
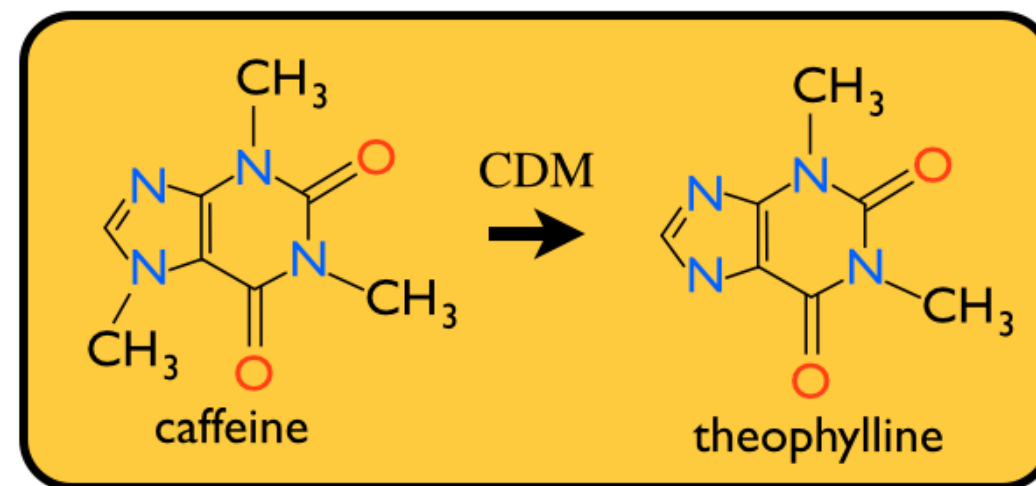
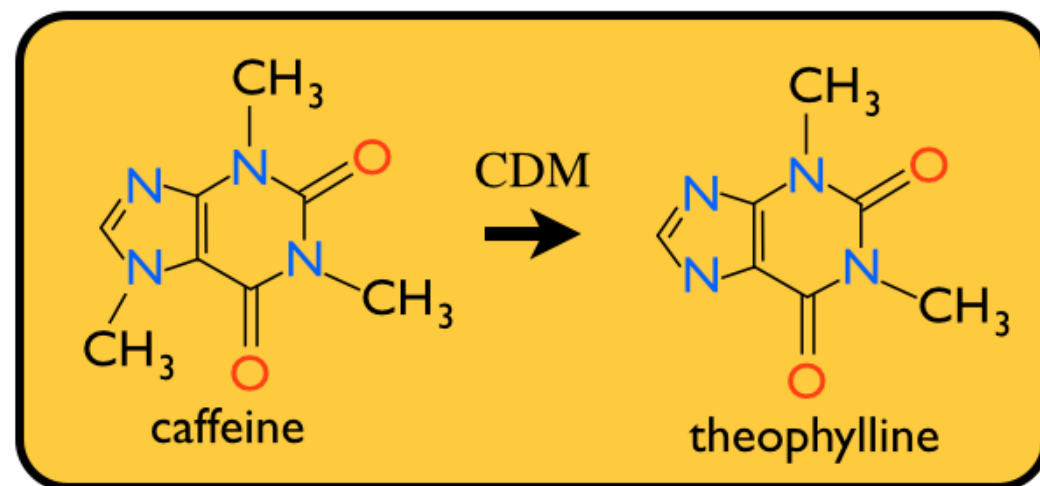
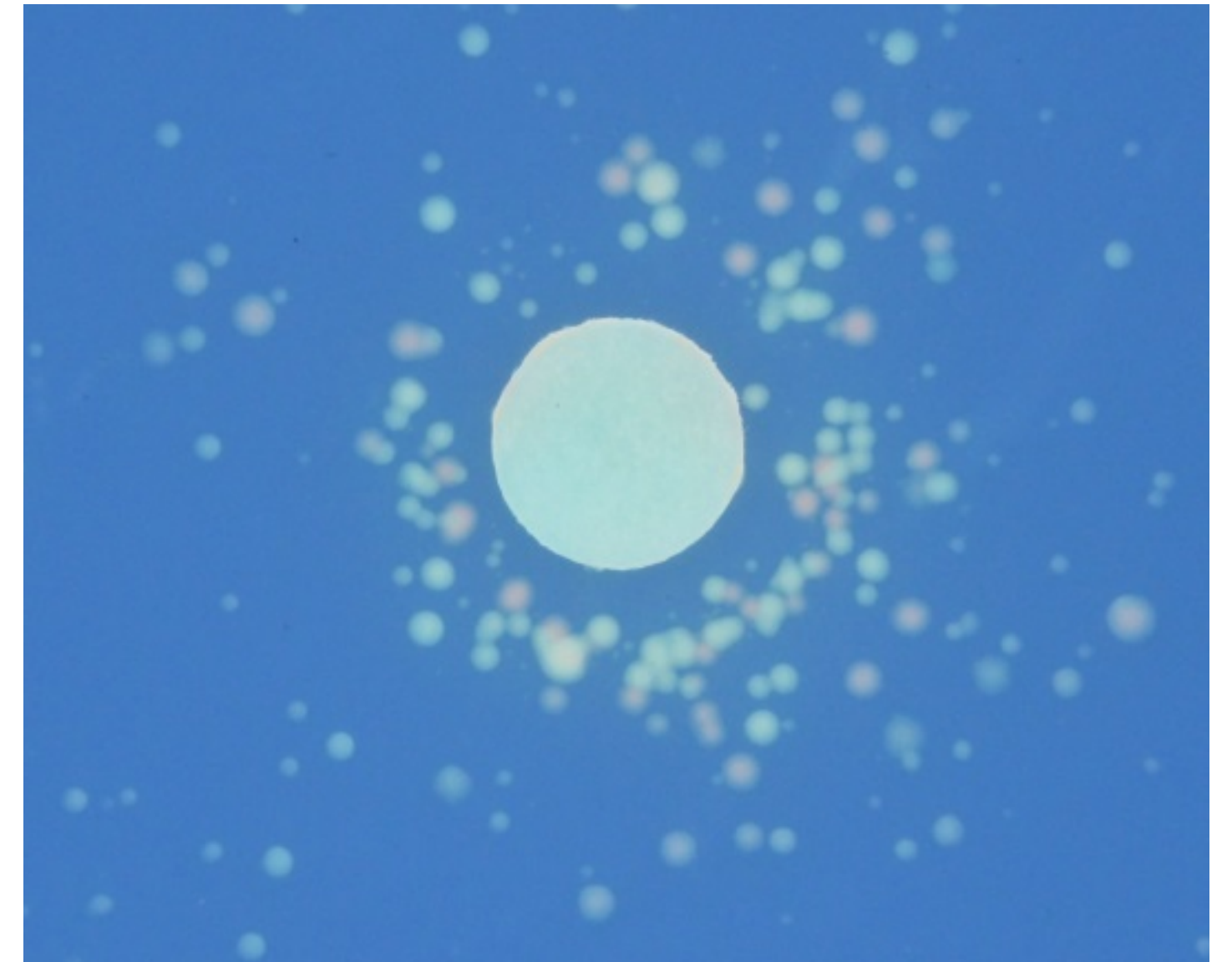
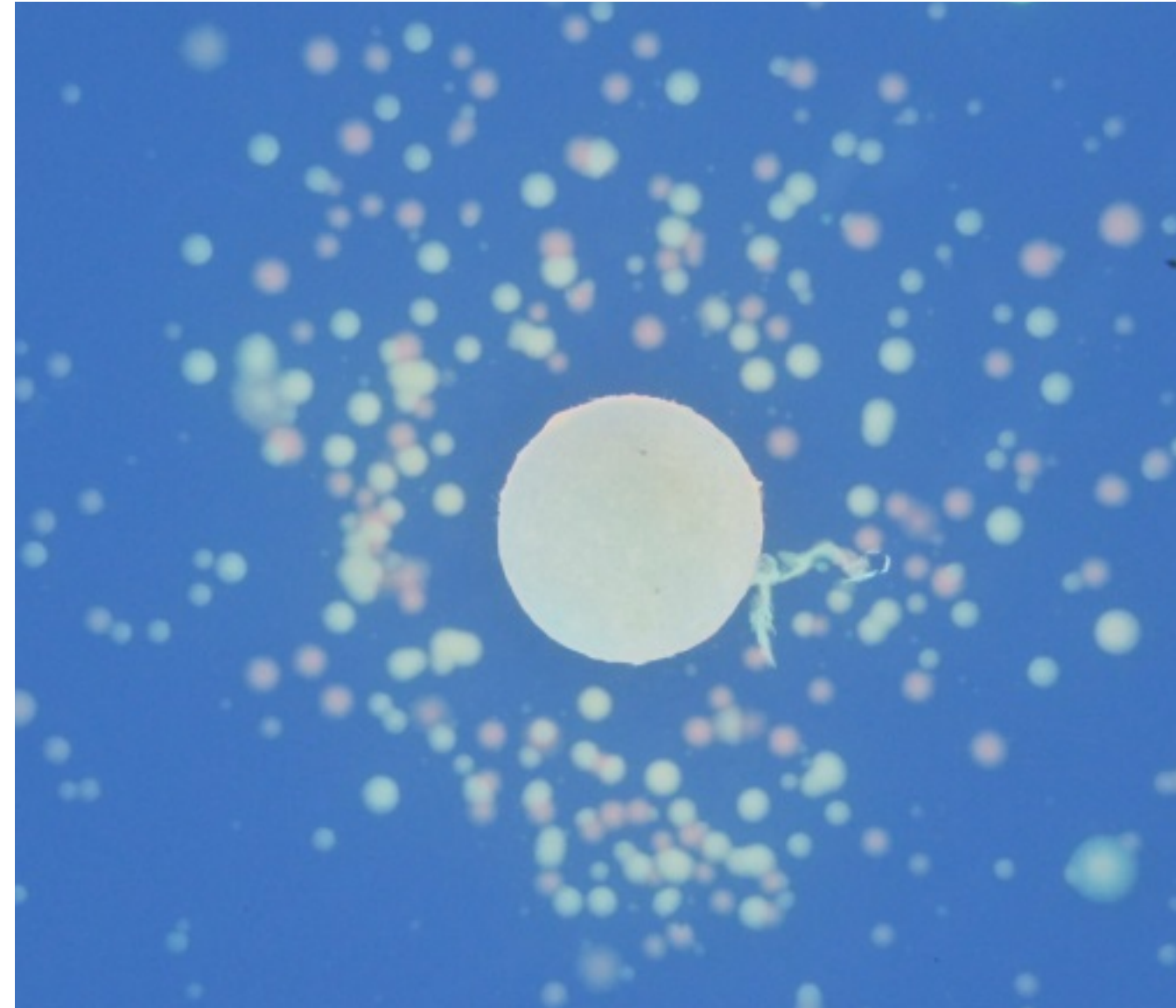
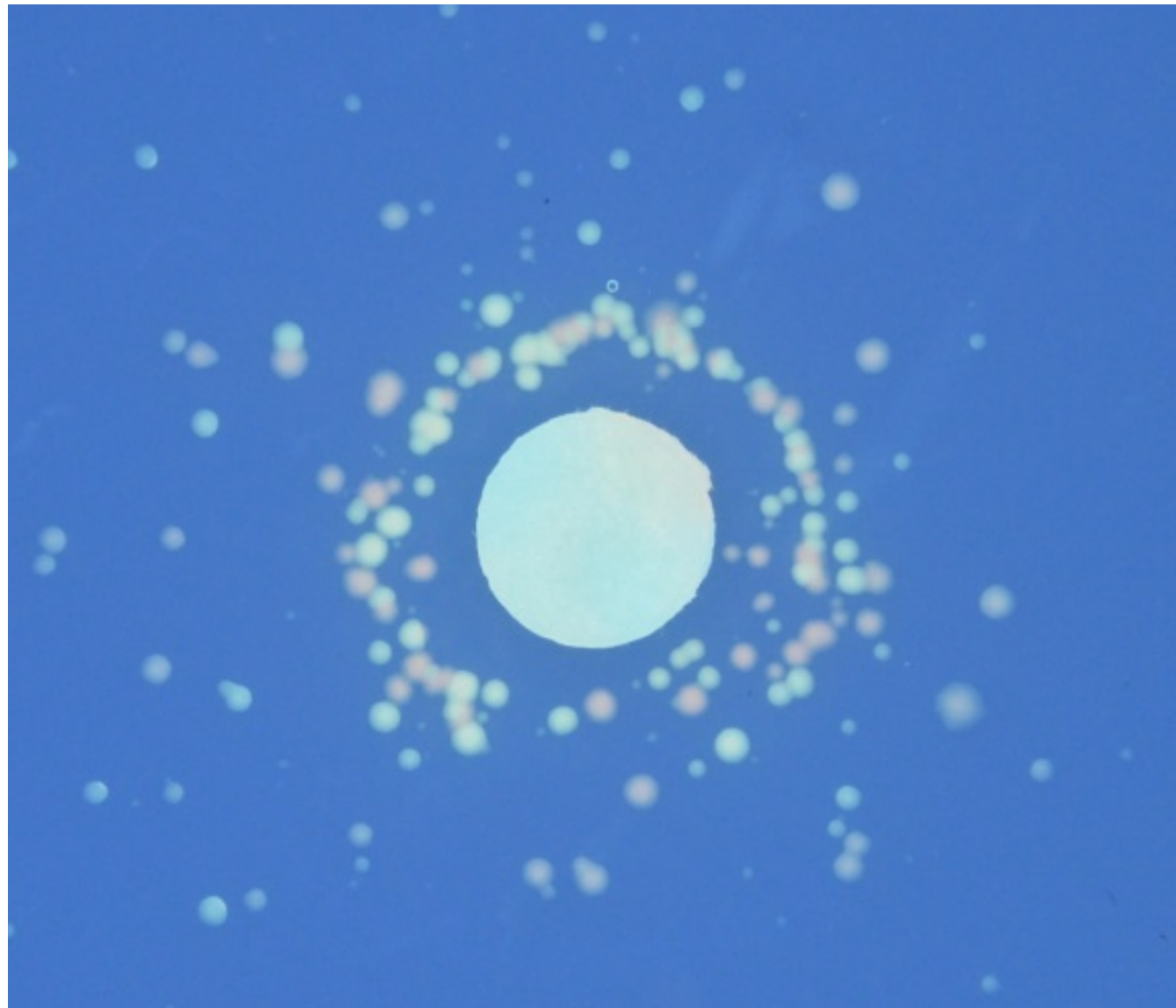
LB + Tet
40 mM Theophylline
Disk



LB + Tet
40 mM Caffeine
Disk

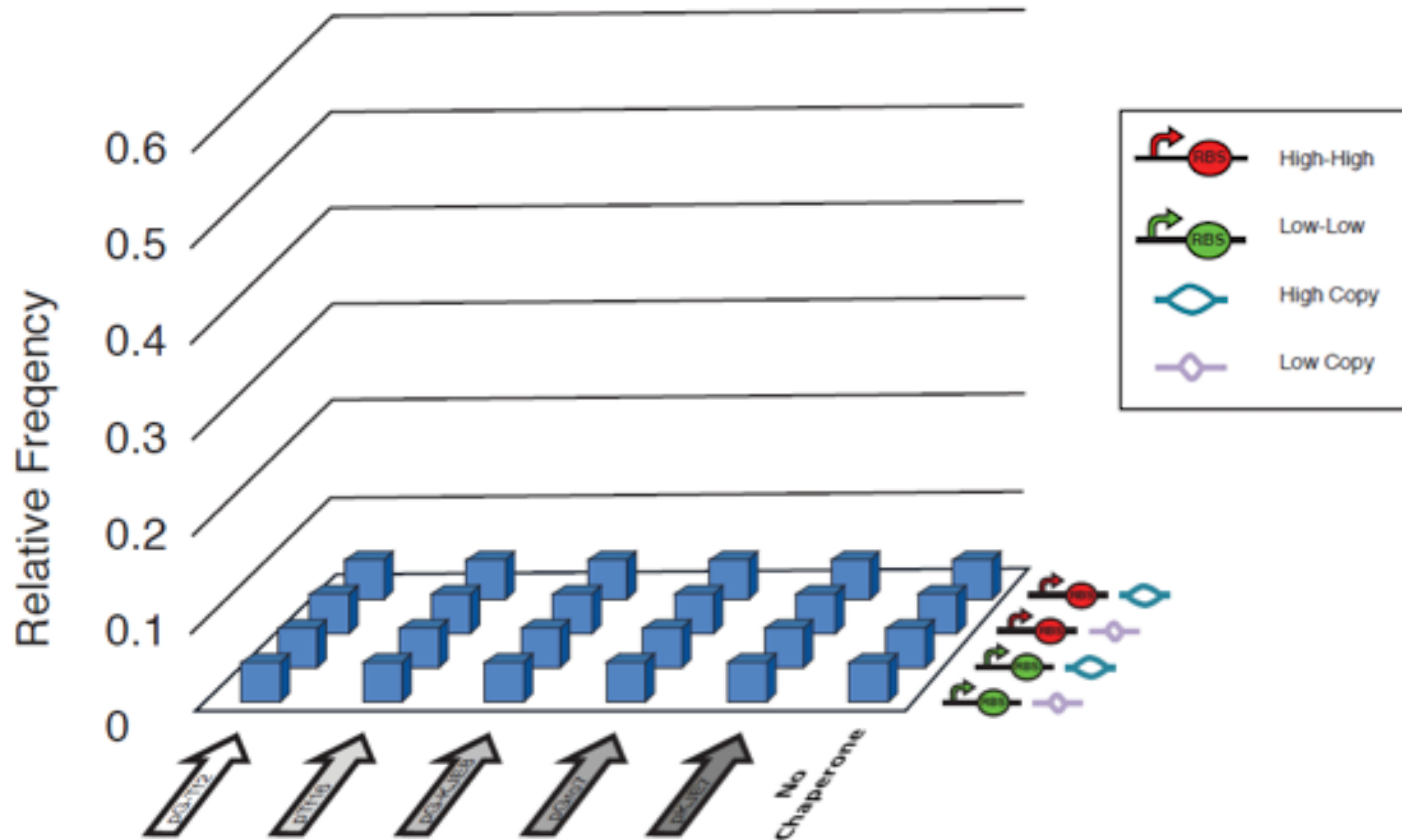


Replicated Programmed Evolution Results



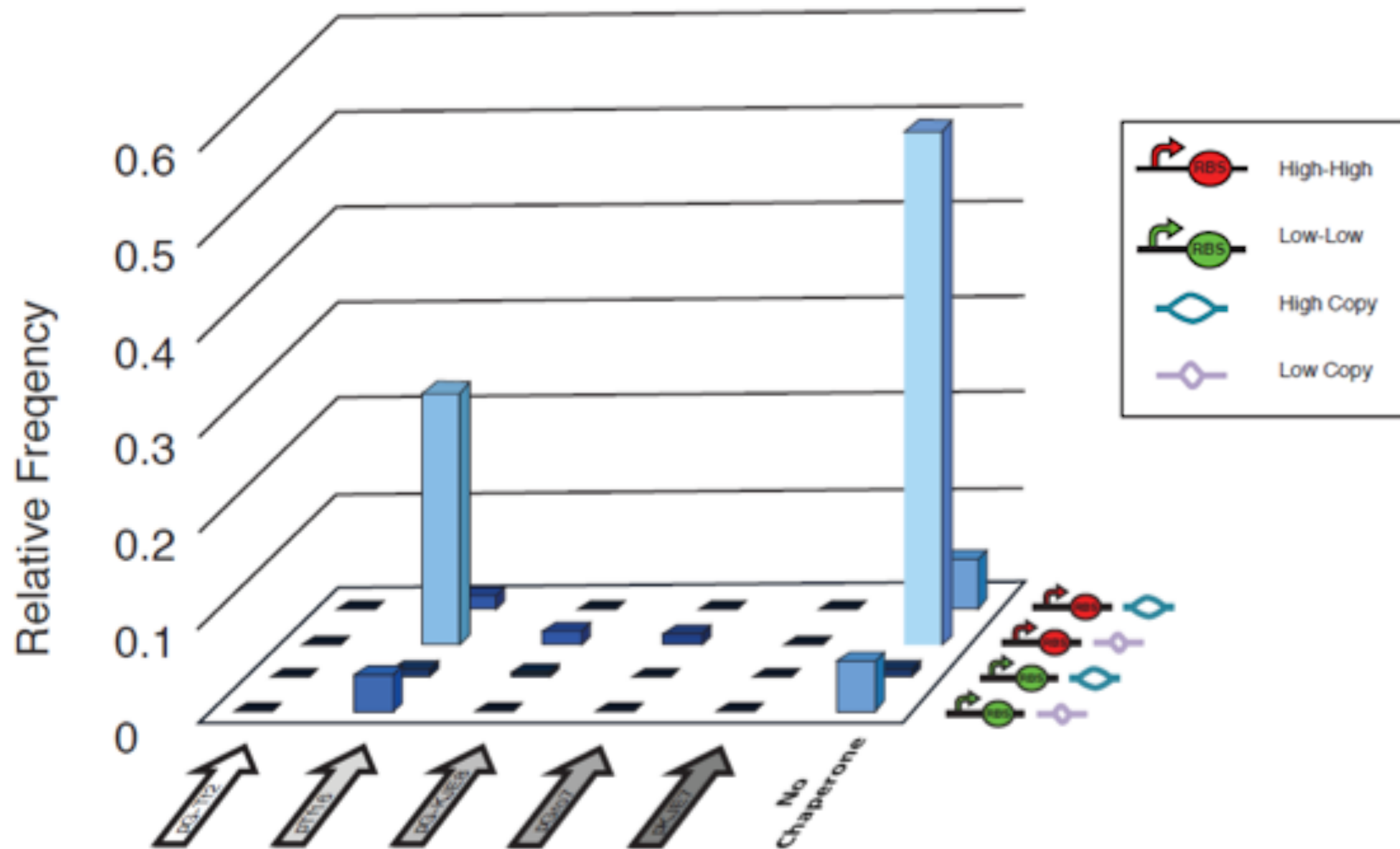
First Programmed Evolution Results

input 24 genotypes, equal proportions

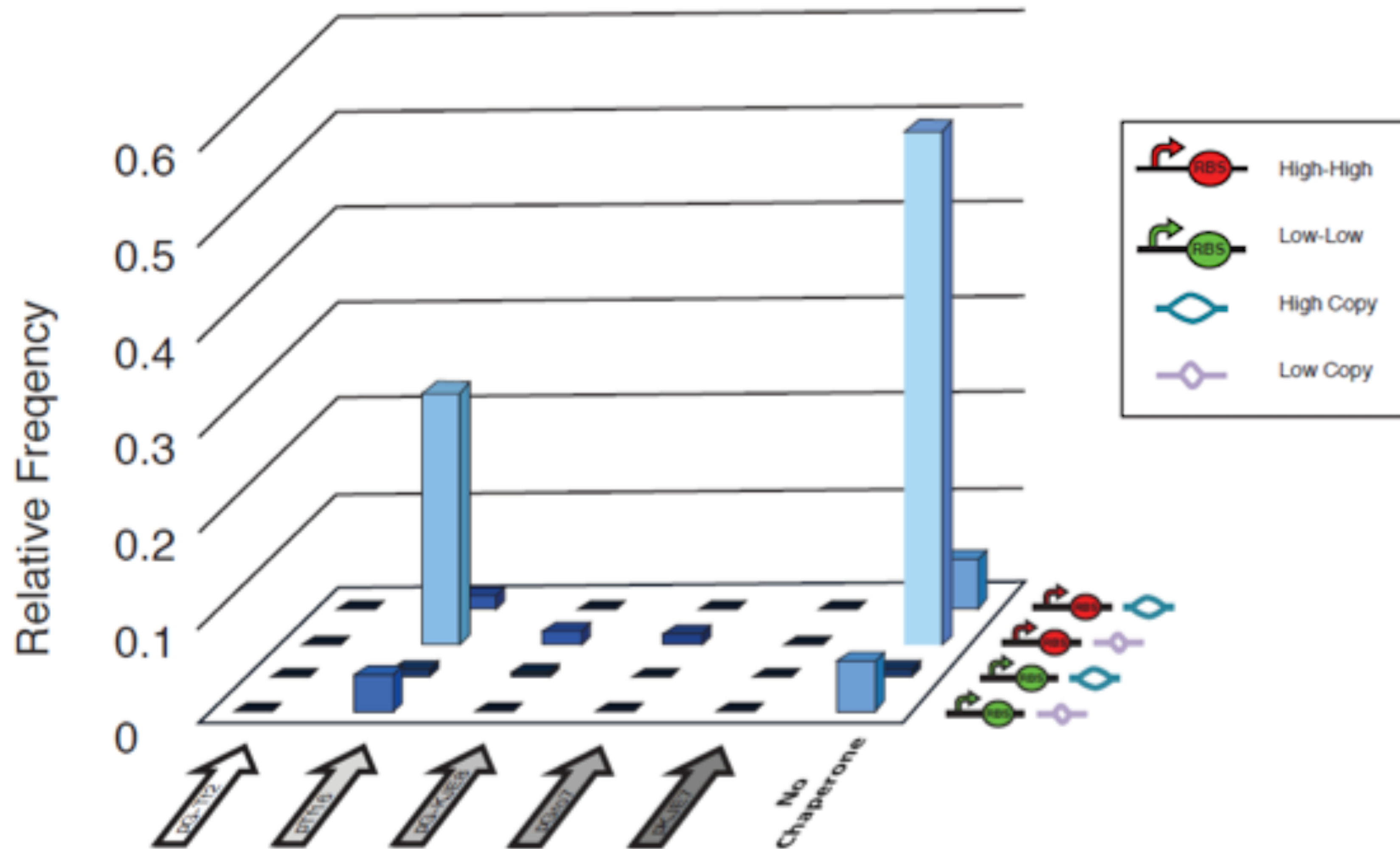


First Programmed Evolution Results






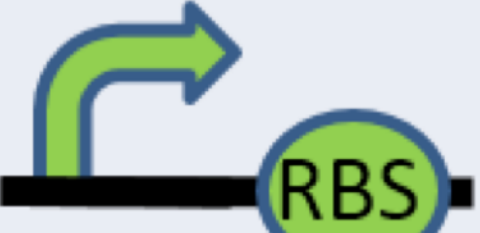

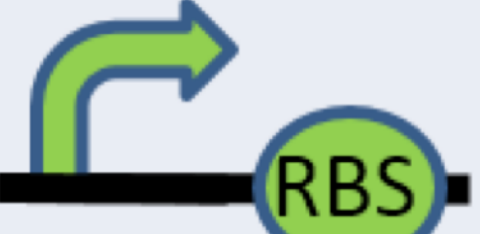




output genotypes, optimized theophylline production



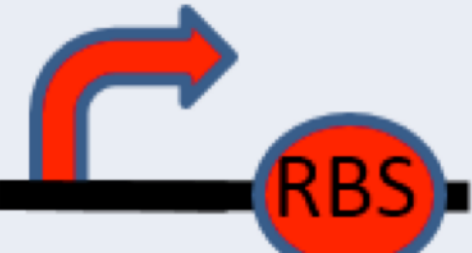

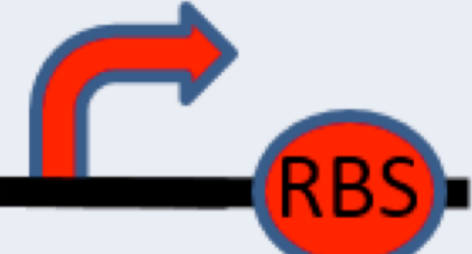








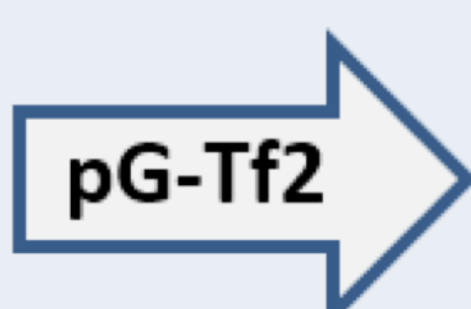
E. coli Programmed to Optimize output genotypes, optimized theophylline production



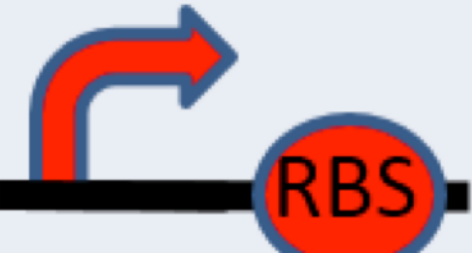

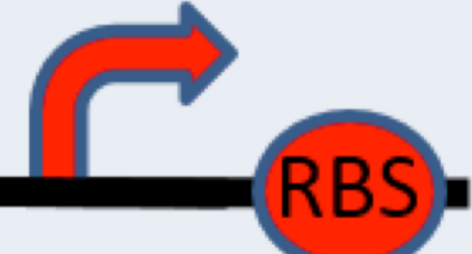








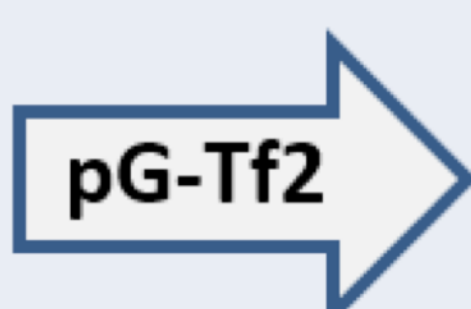
E. coli Programmed to Optimize

Promoter-RBS	Origin	Chaperone	Theophylline Production	Relative Fitness
 High-High	 Low Copy	No Chaperone	0.44	1.00
 High-High	 Low Copy	 pTf16	0.35	0.49
 Low-Low	 Low Copy	No Chaperone	0.43	0.10
 Low-Low	 High Copy	No Chaperone	0.14	0.01
 High-High	 Low Copy	 pG-Tf2	0.19	0.00

E. coli Programmed to Optimize

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Programmed Evolution of *E.coli* for Optimization of Drug Production

(in press, PLOS ONE)



Collaborative 2012 Research Team



Collaborative 2013 Research Team



What is the secret to success?

“Would you like me to give you a formula for success? It's quite simple, really. **Double your rate of failure.** You are thinking of failure as the enemy of success. But it isn't at all. You can be discouraged by failure or you can learn from it, so go ahead and make mistakes. Make all you can. Because remember, that's where you will find success.”

Thomas J. Watson
Founder of IBM

The scenery only changes for the lead dog.



The scenery only changes for the lead dog.



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Research should be fun!



