

MIT

Bio Bricks

Data Book



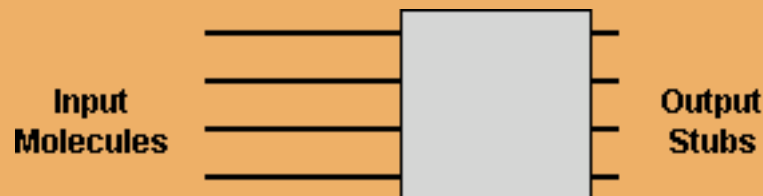
TIPS - Transcription Initiations Per Second

Implied TIPS (ITIPS)

the number of times the RNA Polymerase binds to the regulatory region and begins transcription of the protein



Definition
Value (TIPS)



Standard Waveform

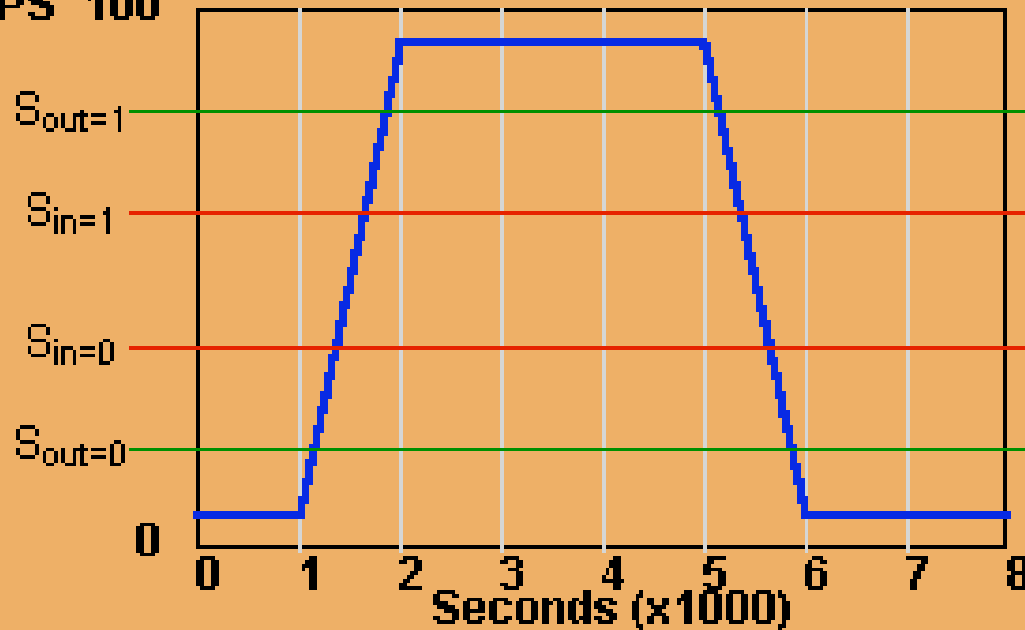
$S_{out}=0$
Output Maximum Zero
20

$S_{out}=1$
Output Minimum One
80

$S_{in}=0$
Input Min Zero Threshold
40

$S_{in}=1$
Input Max One Threshold
60

TIPS 100





BioBricks Design Elements

Ribosome Binding Site

BBa RBS-1

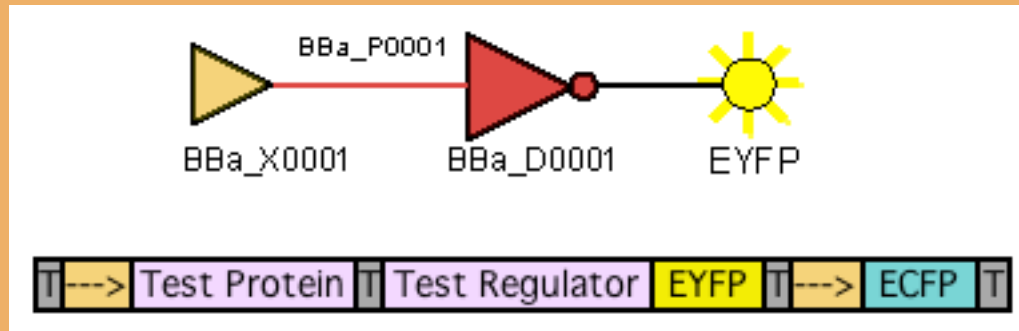
attaaagaggagaaaggtacc

Protein Degradation Tail

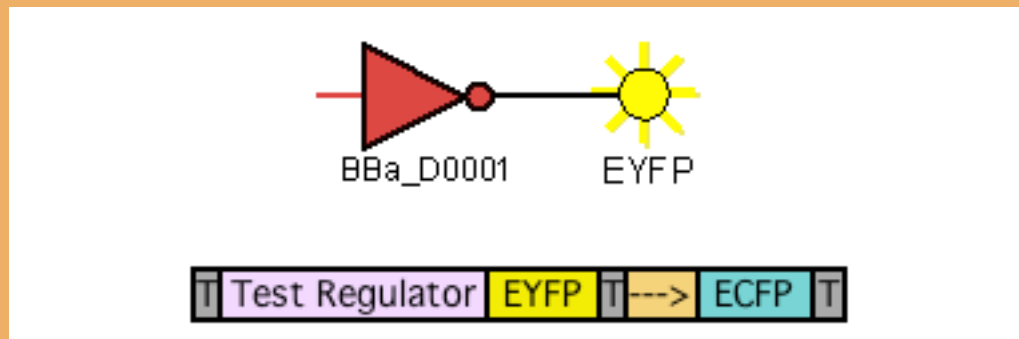


the transfer curve

low output measurement

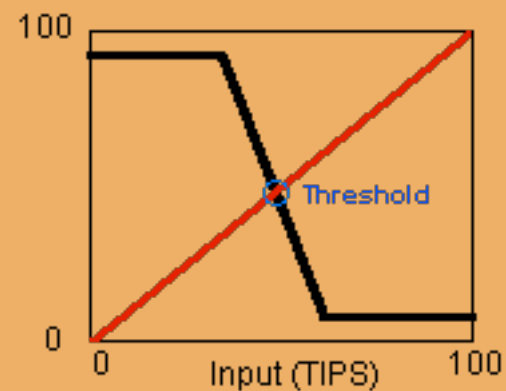
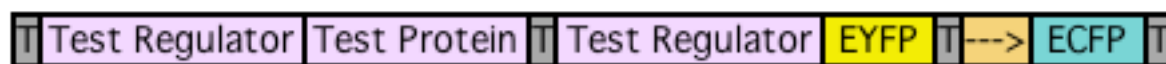
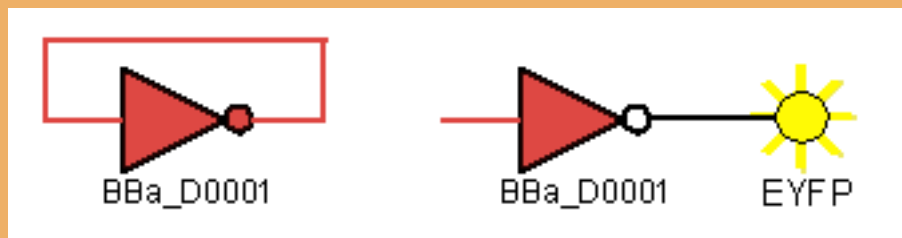


high output measurement

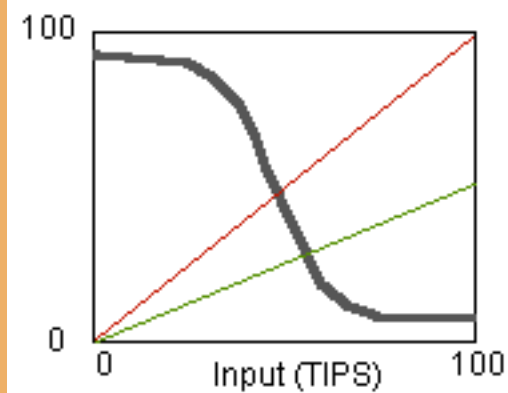
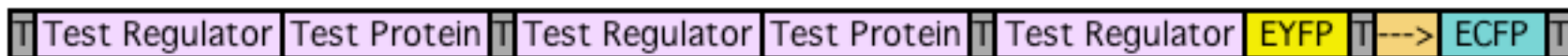
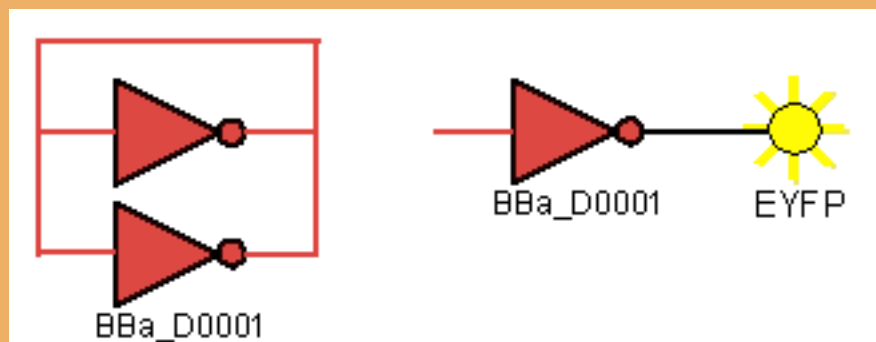




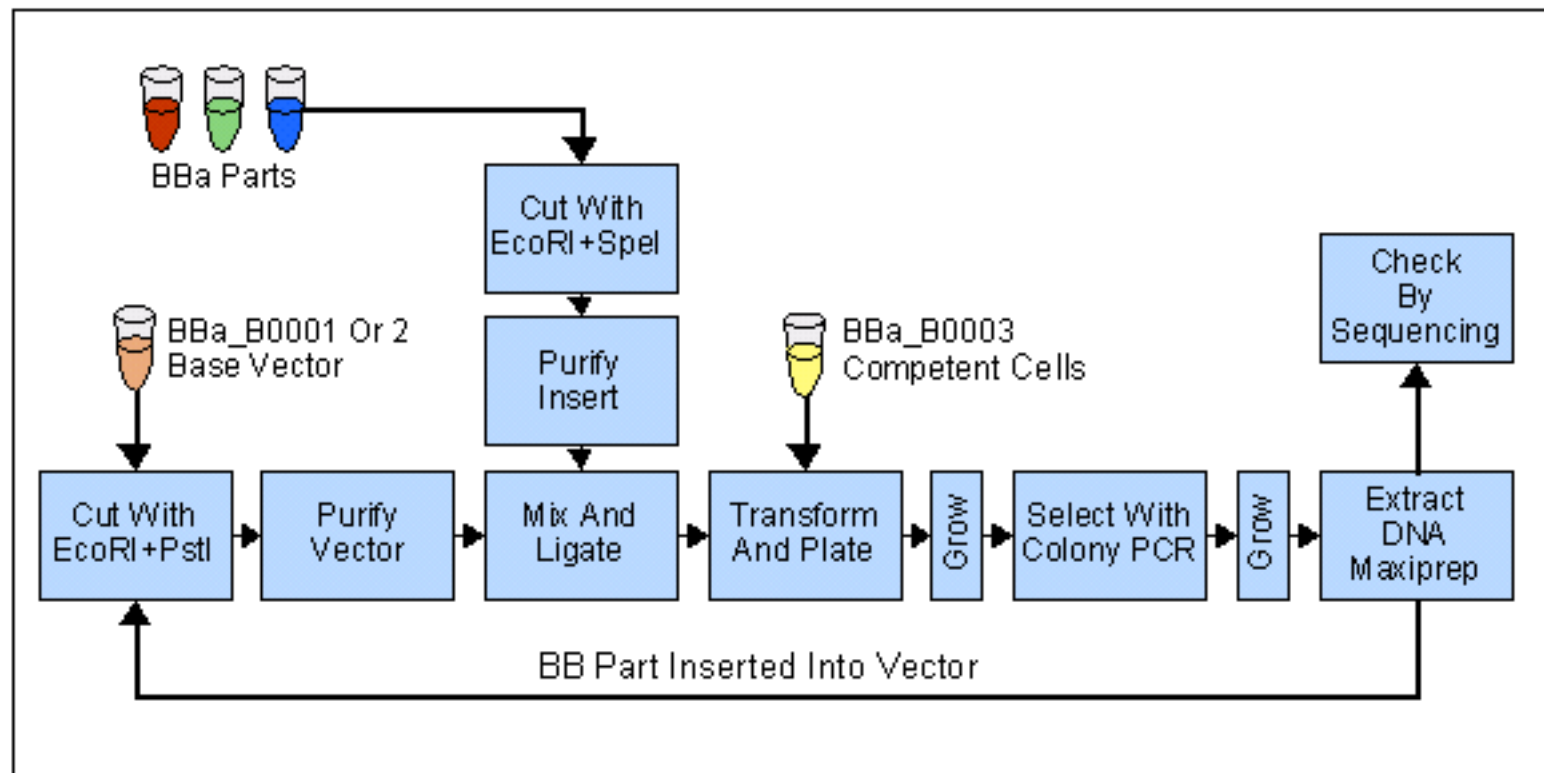
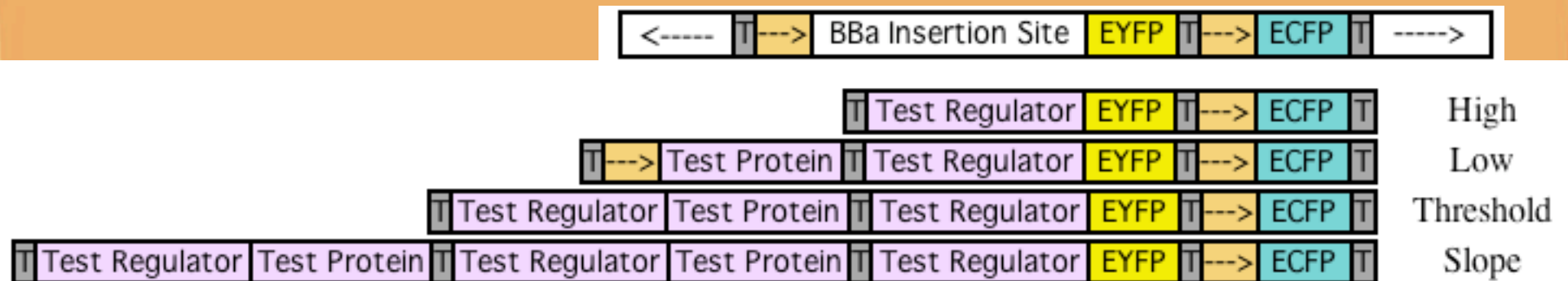
threshold measurement



slope measurement



BioBrick Standard Assembly



Verison 0.

BioBrick Enzymes

EcoRI
G AATTC
CTTAA G
PstI
CTGCA G
G ACGTC
SpeI
A CTAGT
TGATC A
XbaI
T CTAGA
AGATC T
NotI
GC GGCCGC
CGCCGG CG
SpeI / XbaI
ACTAGA
TGATCT



Step 1 - Designing the Contents



Step 2 - Adding the Prefix and Suffix



PREFIX Primer

cctttctagag

11 bp

SUFFIX Primer

tactagtagcggccgctgcagcctt

25 bp

Step 3 - The BioBrick Base Vector



or direct synthesis

Complete PREFIX

gaattcgccggccgcttctagag

22 bp

Complete SUFFIX

tactagtagcggccgctgcag

21 bp





Ribosome Binding Sites

Part Number
Binding
Efficiency
Sequence

BBa

1.0

ggg aaa agg agg tgt-tactag-atg

BBa

0.84

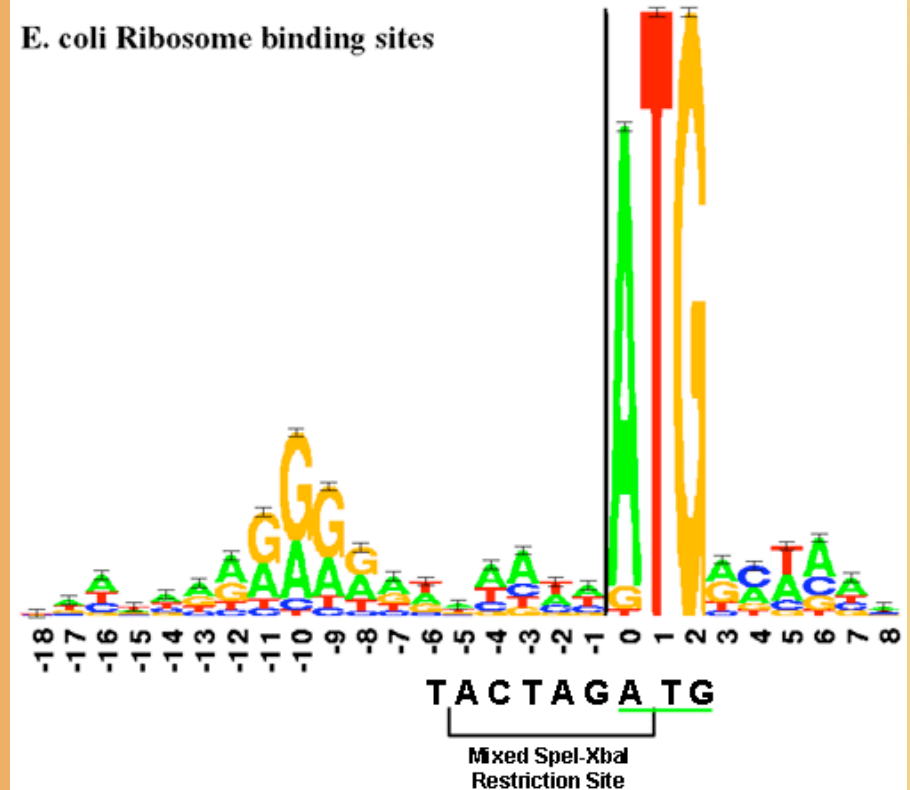
ggg aaa agg tgg tgt-tactag-atg

BBa

0.73

ggg aaa agg

E. coli Ribosome binding sites



RBS

AGGAGGTGT ACTAGT
TCCTCCACA TGATCA

SpeI

CDS

TCTAGA TG111222333
AGATCT AC111222333

XbaI

RBS+CDS

AGGAGGTGT ACTAGA TG111222333
TCCTCCACA TGATCT AC111222333

Mixed



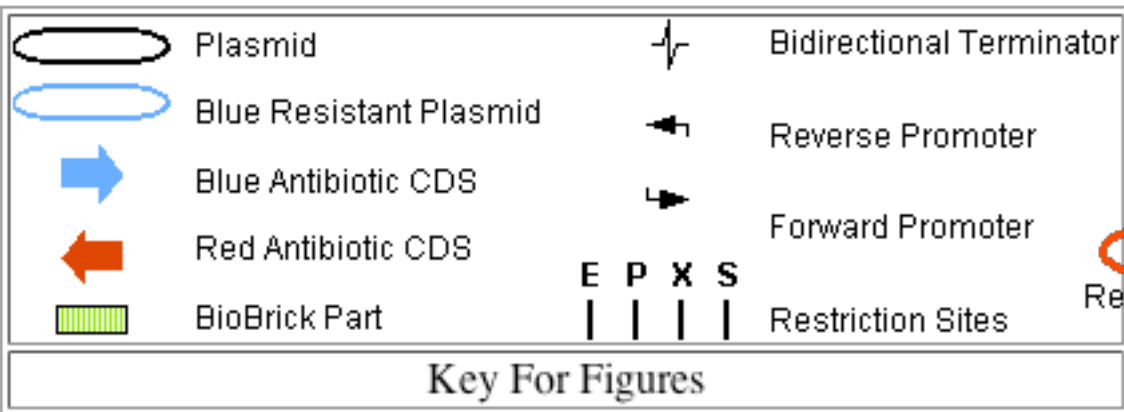
Version 1. Antibiotic Assembly

. The total time required for a single stage of standard assembly is likely to be about 4 days.
We estimate that a single stage of assembly based on selection could be performed in one day.

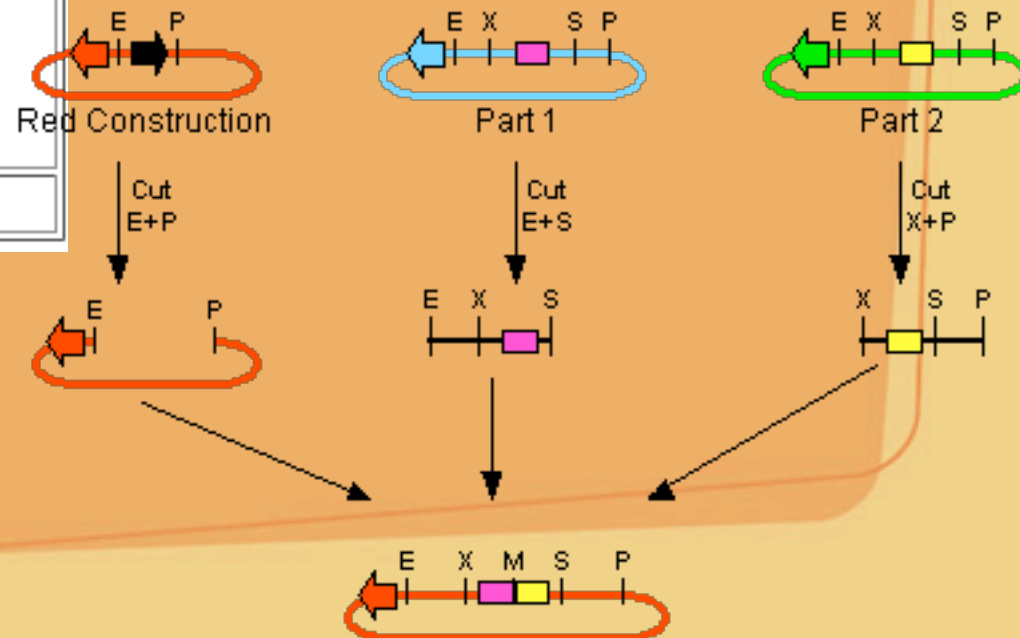


Red, Green, or Blue
Construction Plasmid

Part In Red, Green,
or Blue Plasmid



Spectinomycin, Kanamycin, and Chloramphenicol





Part Index

Brick	Type	Description	Status	Length
B0010	Terminator	Terminator, Transcription (T1)	Available	80
B0011	Terminator	Terminator, Transcription (luxICDABEG bidirectional)	Available	46
B0012	Terminator	Terminator, Transcription (T7 TE)	Available	41
B0013	Terminator	Terminator, Transcription (T7 TE bidirectional)	Available	47
B0014	Terminator	Terminator, Transcription (B0012, B0011)	Available	95
B0015	Terminator	Terminator, Transcription (B0010, B0012)	Available	130
B0016	Terminator	Terminator, Transcription (T7 RNAP specific, T_Phi)	Available	92
B0017	Terminator	Terminator, Transcription (B0010, B0010)	Available	168
B0020	Terminator	Terminator, Transcription (Reverse T1)	Building	
B0021	Terminator	Terminator, Transcription (LuxICDABEG bidirectional)	Available	46
B0022	Terminator	Terminator, Transcription (Reverse TE)	Available	84
B0023	Terminator	Terminator, Transcription (Reverse T7 Bidirectional)	Available	90
B0024	Terminator	Reverse double Terminator (from B0014)	Available	
B0025	Terminator	Reverse double Terminator (from B0015)	Available	
B0030	RBS	RBS.1 (strong)	Available	15
B0031	RBS	RBS.2 (medium)	Available	14
B0032	RBS	RBS.3 (weak)	Available	13
B0033	RBS	RBS.4 (weaker -- test)	Available	11
B0034	RBS	RBS.5 (Elowitz RBS)	Available	12
B0035	RBS	RBS (non-standard SD sequence)	Planning	8
B0040		Spacer.1 (generic)	Available	70



RBS.1 (strong)

Available

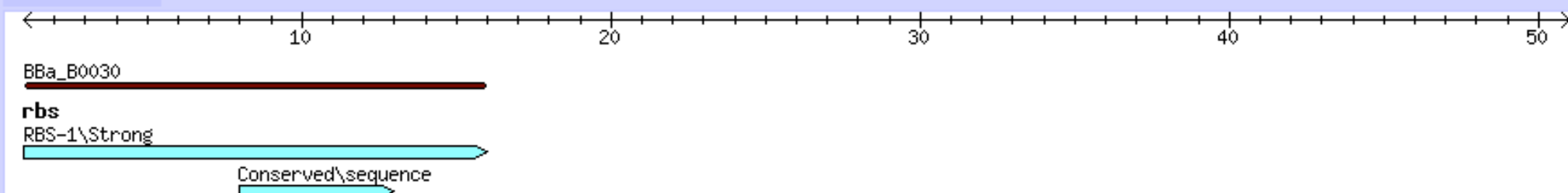
Description Strong RBS based on Ron Weiss thesis. Strength is considered relative to BBa_B0031, BBa_B0032, BBa_B0033.

Sequence

Get Sequence

Redraw With:

Part Only



1 11 21 31 41 51 61 71 81 91
| attaaagagg agaaa
taatttctcc tcttt

Crosslinks & Compatibility

Other Part Linked Compatible Notes

Lengths

Part Only 15 Vf-Vr

Source

Biology

Properties

Chassis Property Typical Min Max Units

Notes

Varies from -6 to +1 region from original sequence to accomodate BioBricks suffix ("orig" in figure 4-14 of Ron Weiss thesis).

No secondary structures are formed in the given RBS region. Users should check for secondary structures induced in the RBS by upstream and downstream elements in the +50 to -50 region, as such structures will greatly affect the strength of the RBS.

Inventory

Location Amount Units Form Prod. Date Notes

Files

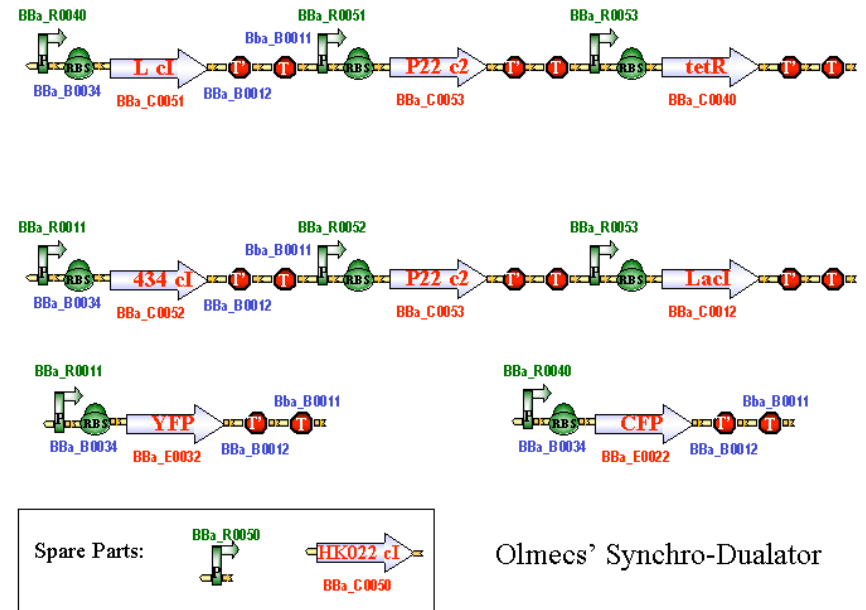
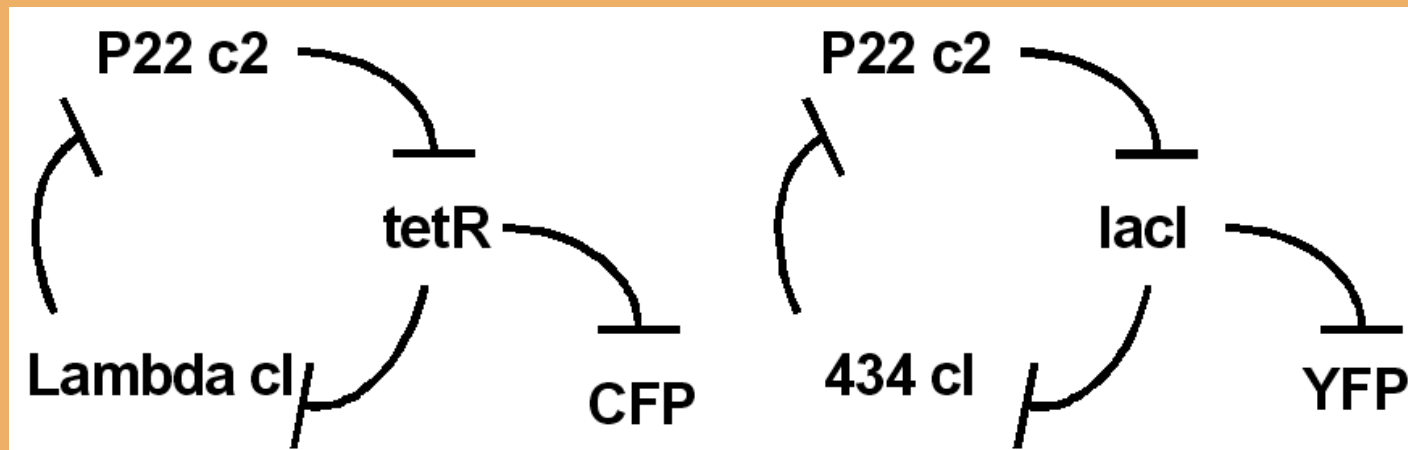
Designer(s) Constructed by Vinay S Mahajan, Voichita D. Marinescu, Brian Chow, Alexander D Wissner-Gross and Peter Carr IAP, 2003. Contact info [Brian Chow](#)

Check Log

Add

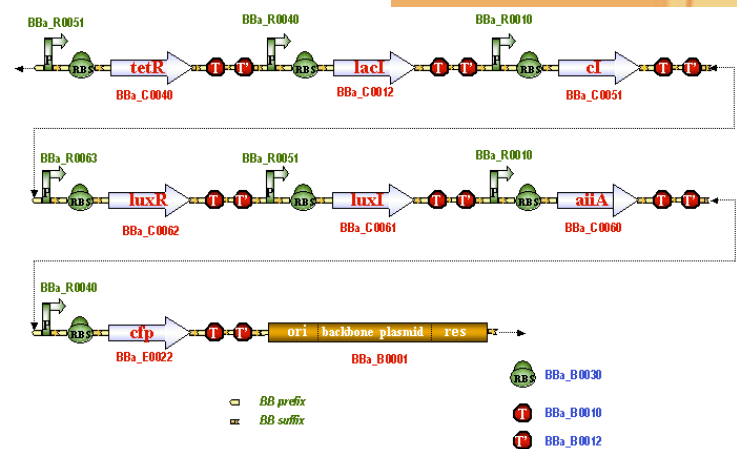
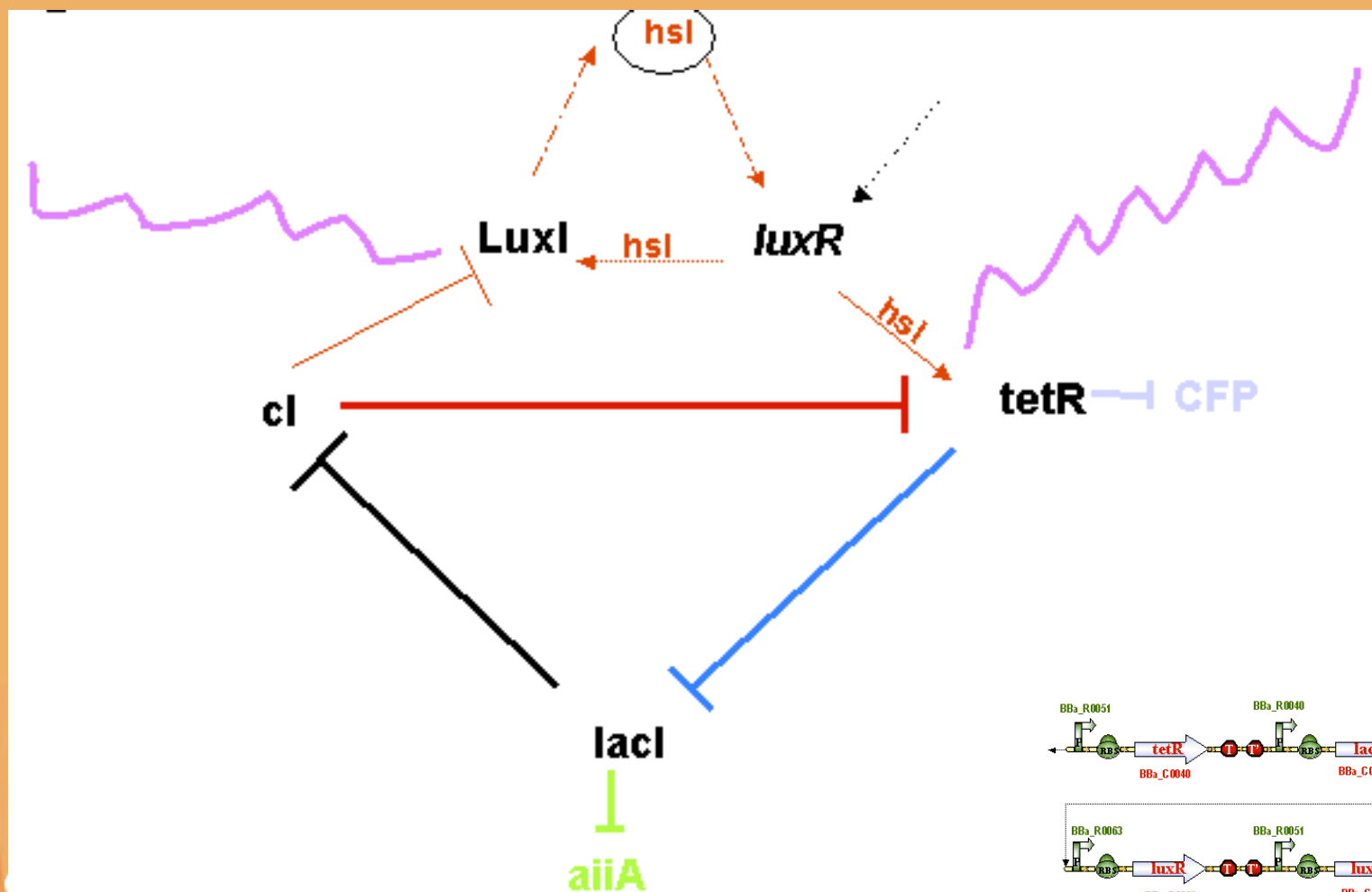


better autocorrelation than the repressilator

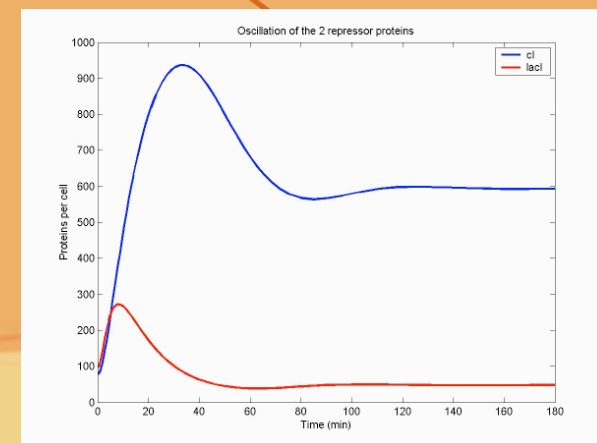
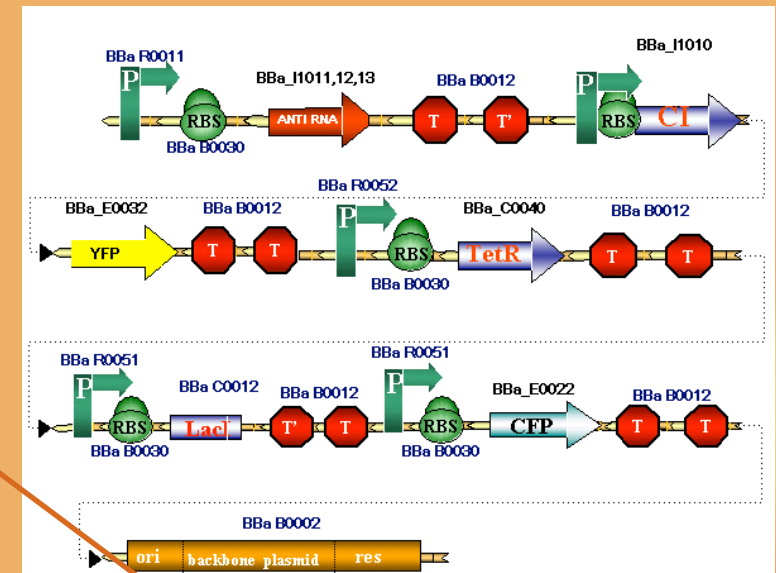
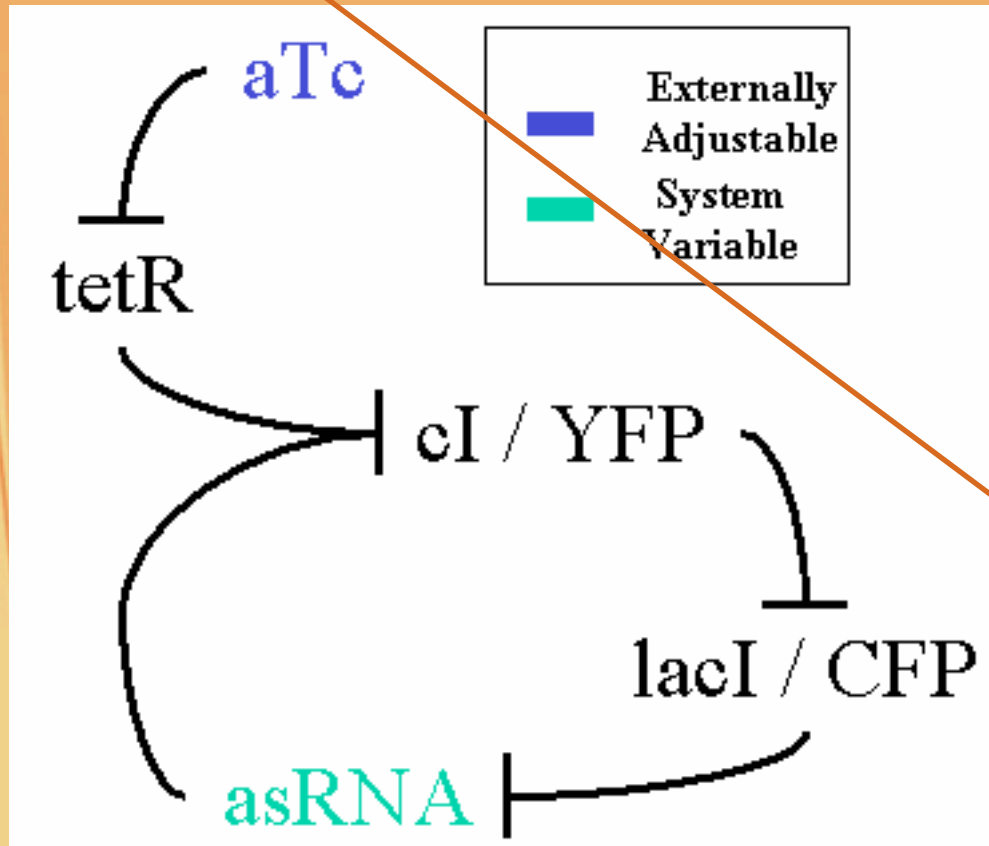




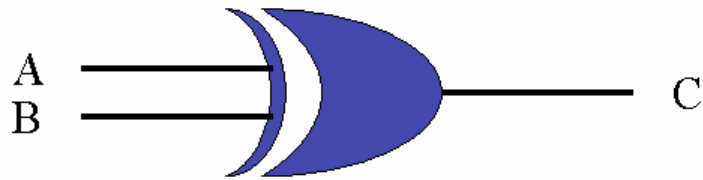
Synchronization of a repressilator



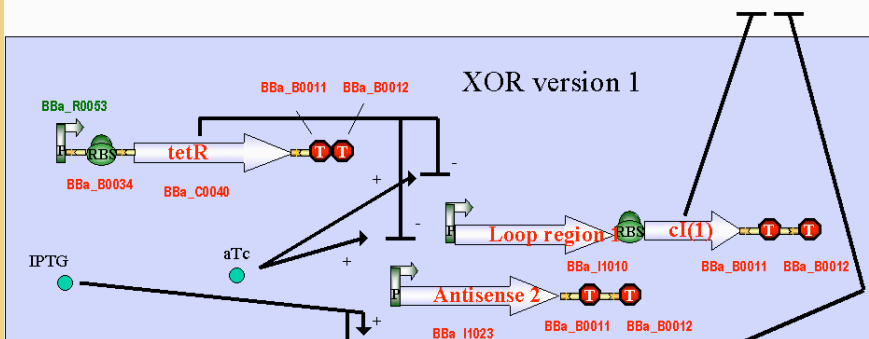
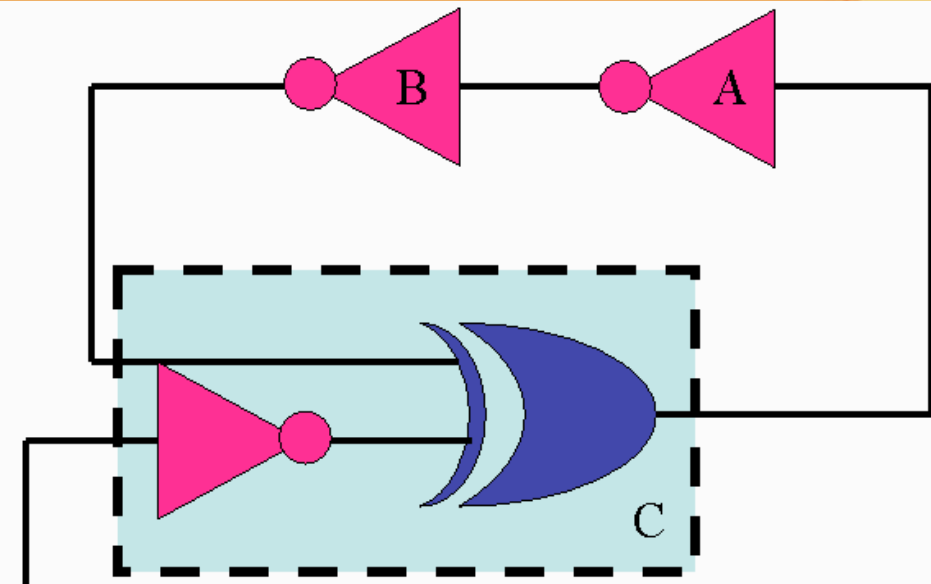
decreasing the period using an anti-sense RNA interference



XOR gate using antisense inhibition strategies



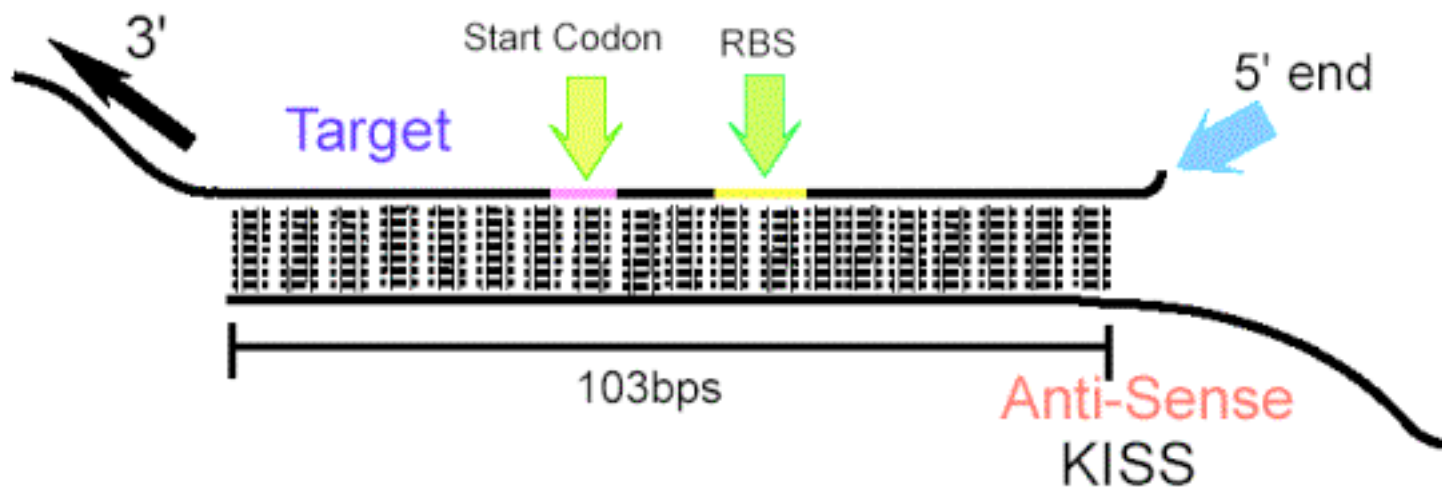
A	B	C
0	0	0
0	1	1
1	0	1
1	1	0



D: External input

0 Repressilator

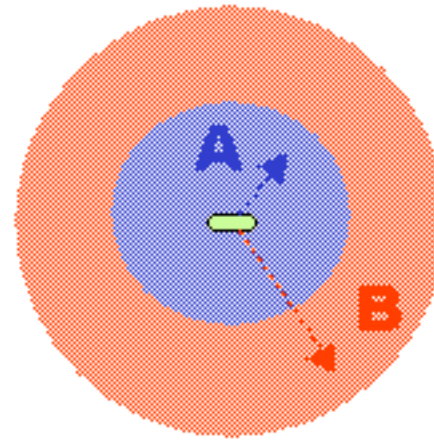
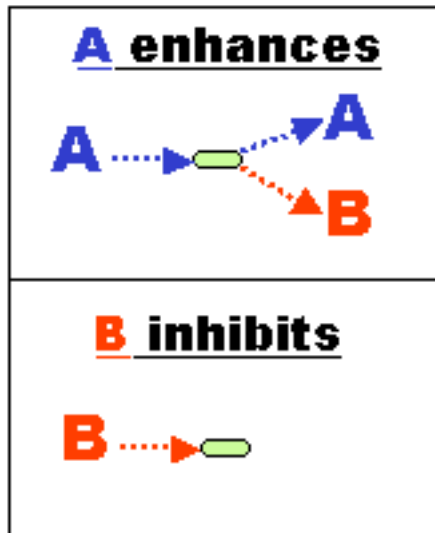
1 Latch





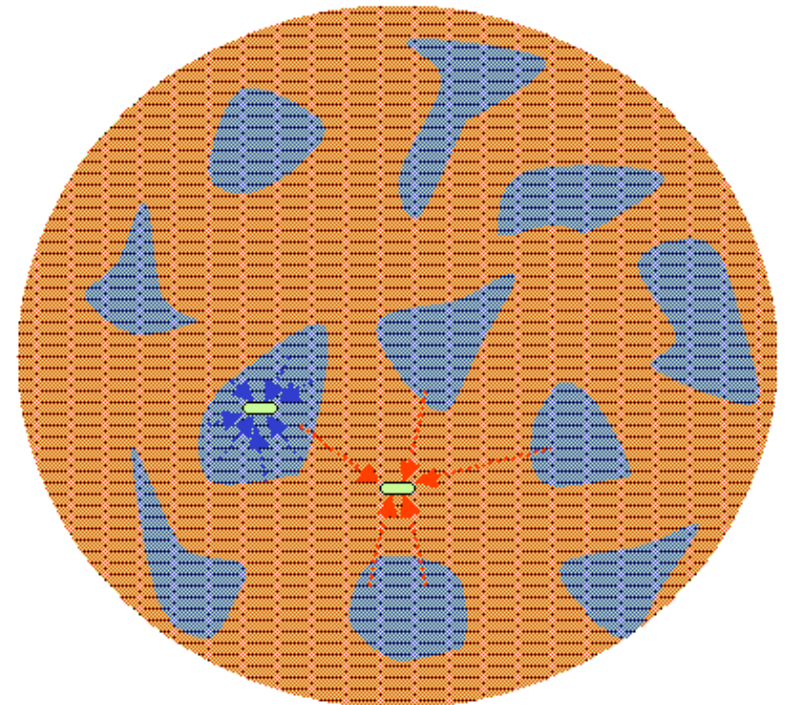
create polka dot patterns in colonies of bacteria cells

Two signals: **A** and **B**

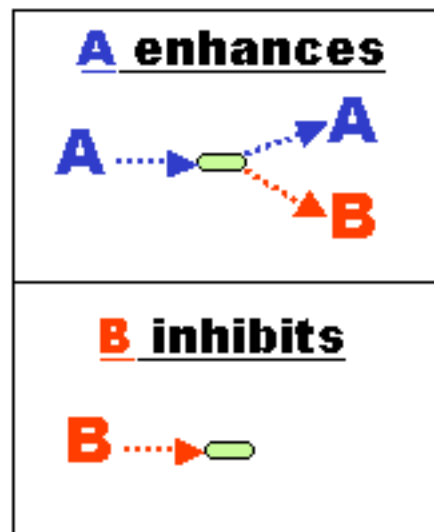


A is short-range

B is long-range



Cell truth table

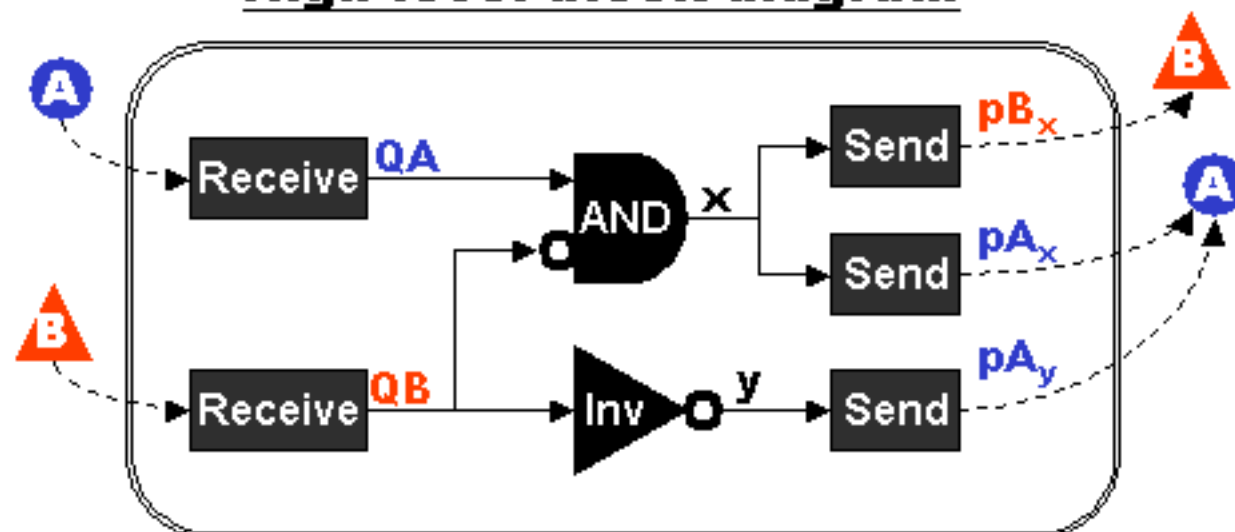


startup

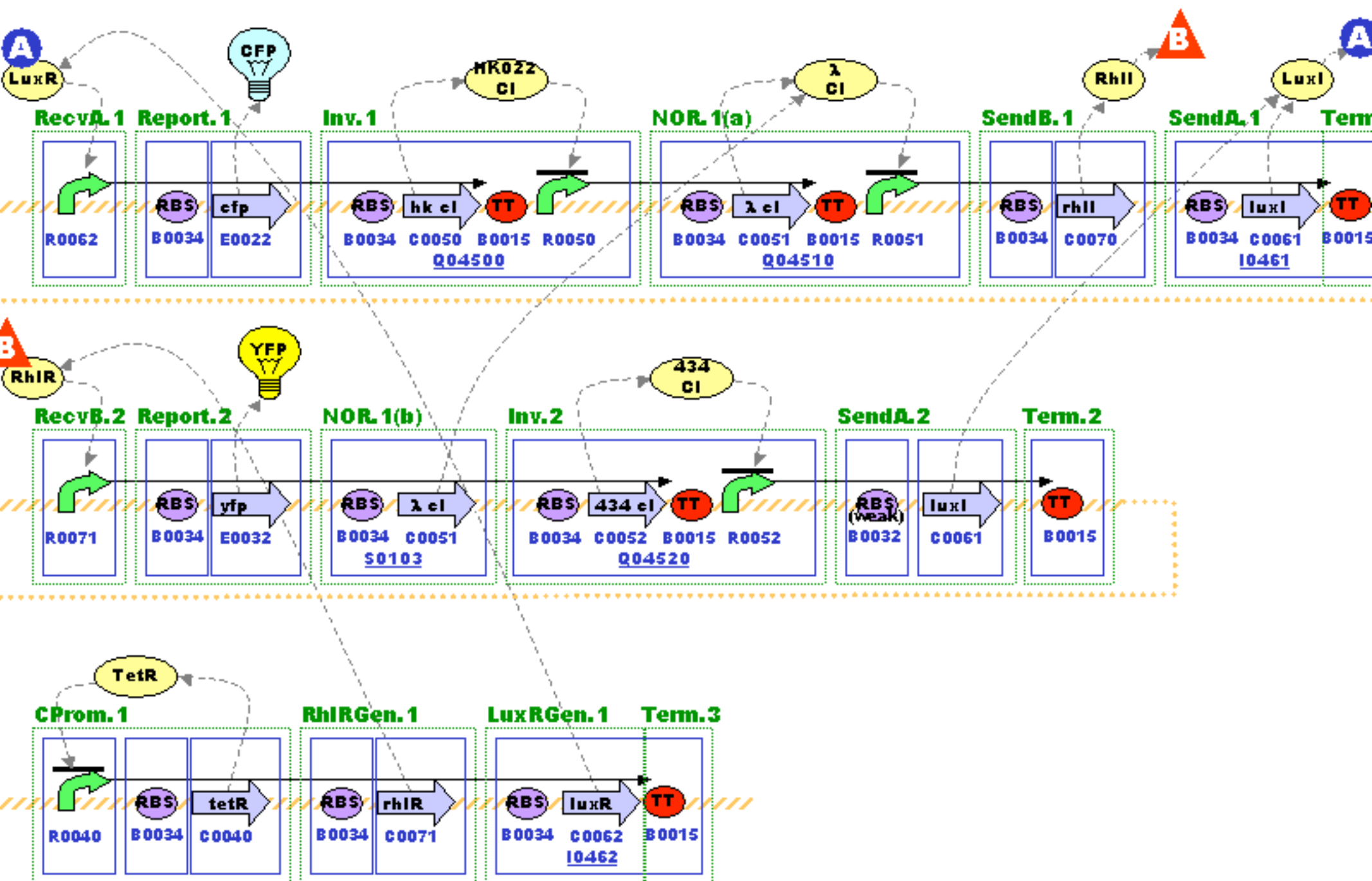
Inputs (quorum signals)		Outputs (production rates)	
QA	QB	pA	pB
0	0	pA_{00}	0
0	1	0	0
1	0	pA_{10}	pB_{10}
1	1	0	0

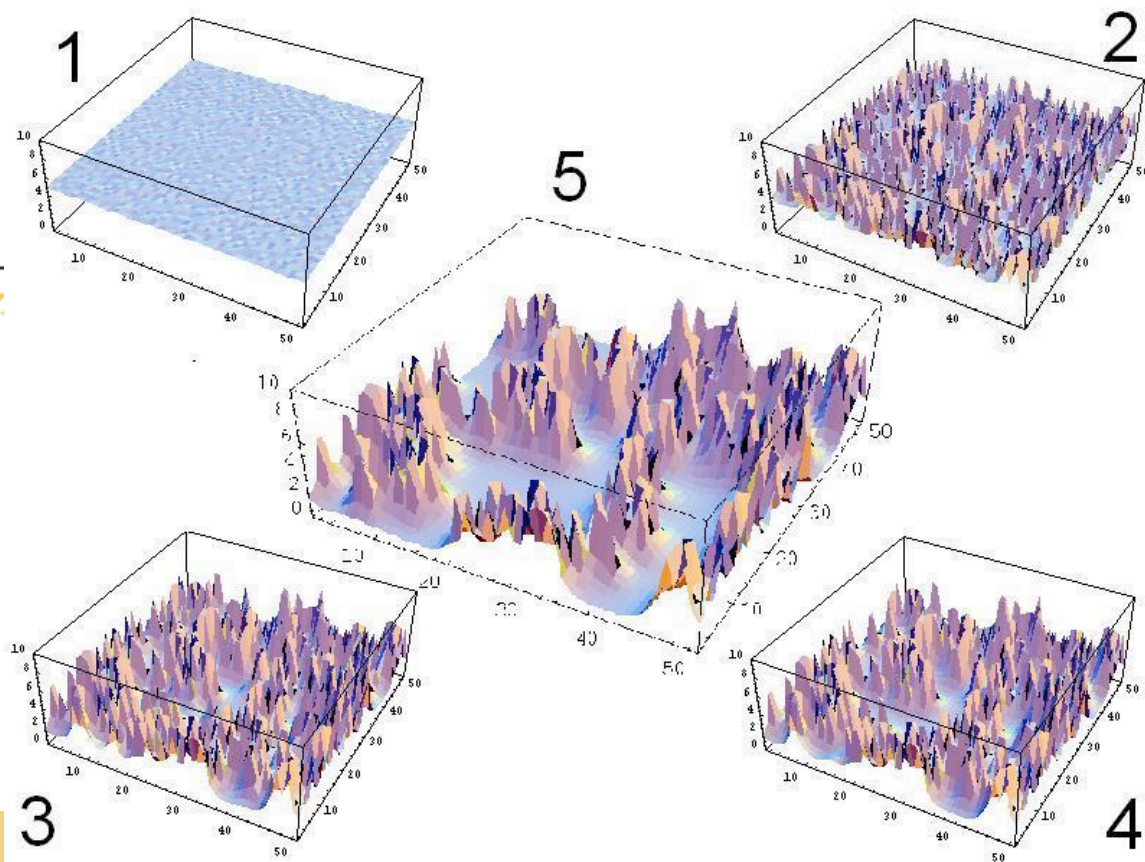
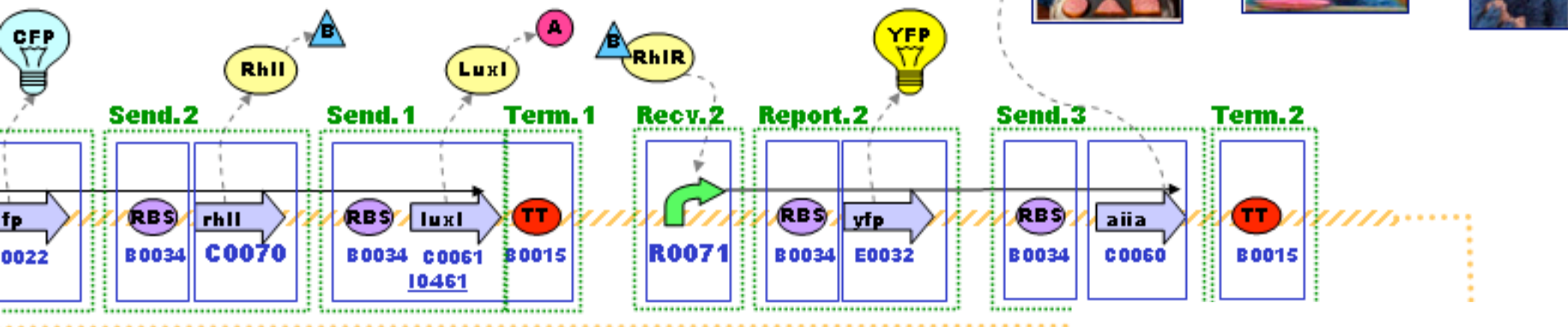
Gates (in block-diagram)	
0	1
0	0
1	1
0	0

High-level block diagram

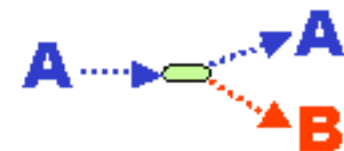


$$\begin{aligned}
 pA_{00} &= pA_y \\
 pA_{10} &= pA_x + pA_y \\
 pB_{10} &= pB_x
 \end{aligned}$$

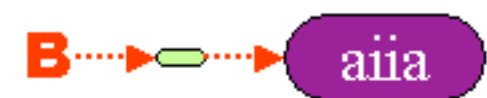




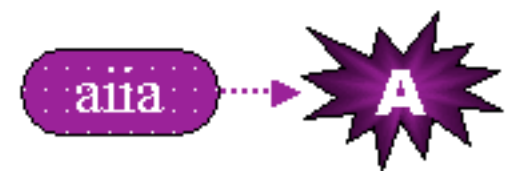
A enhances

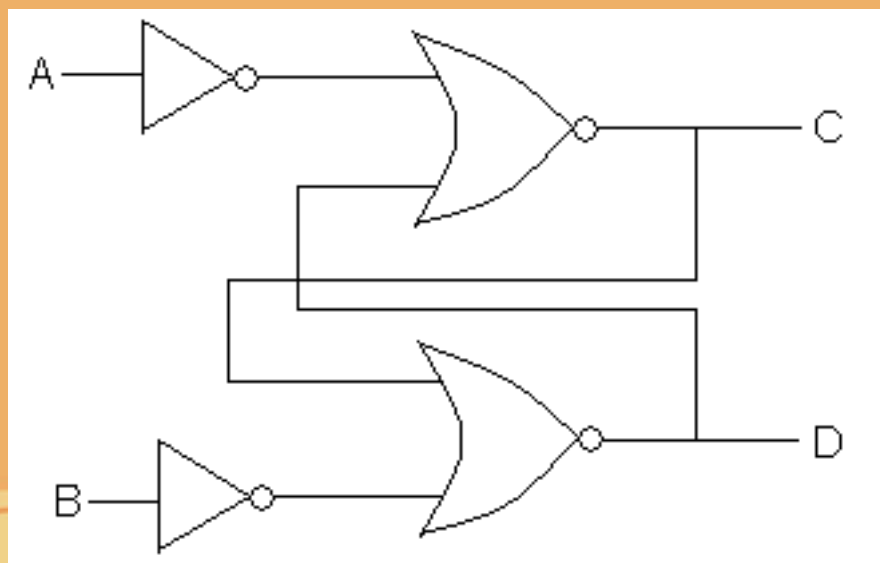
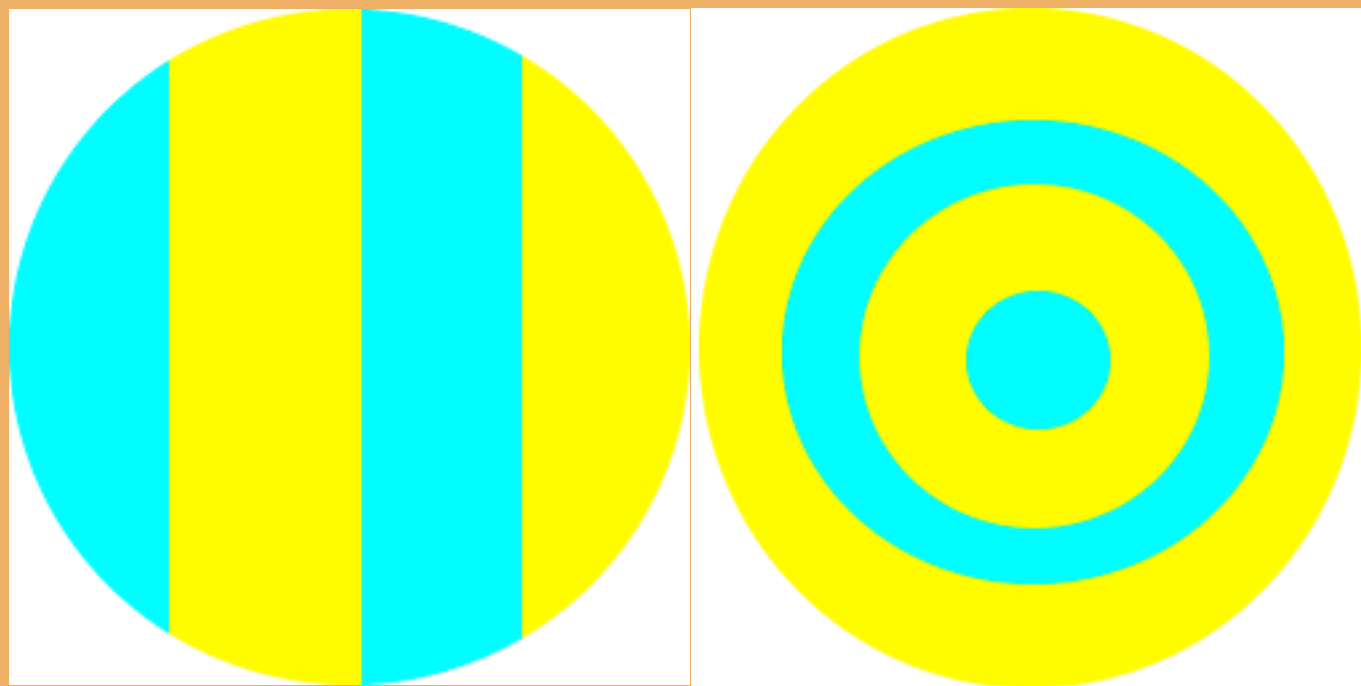


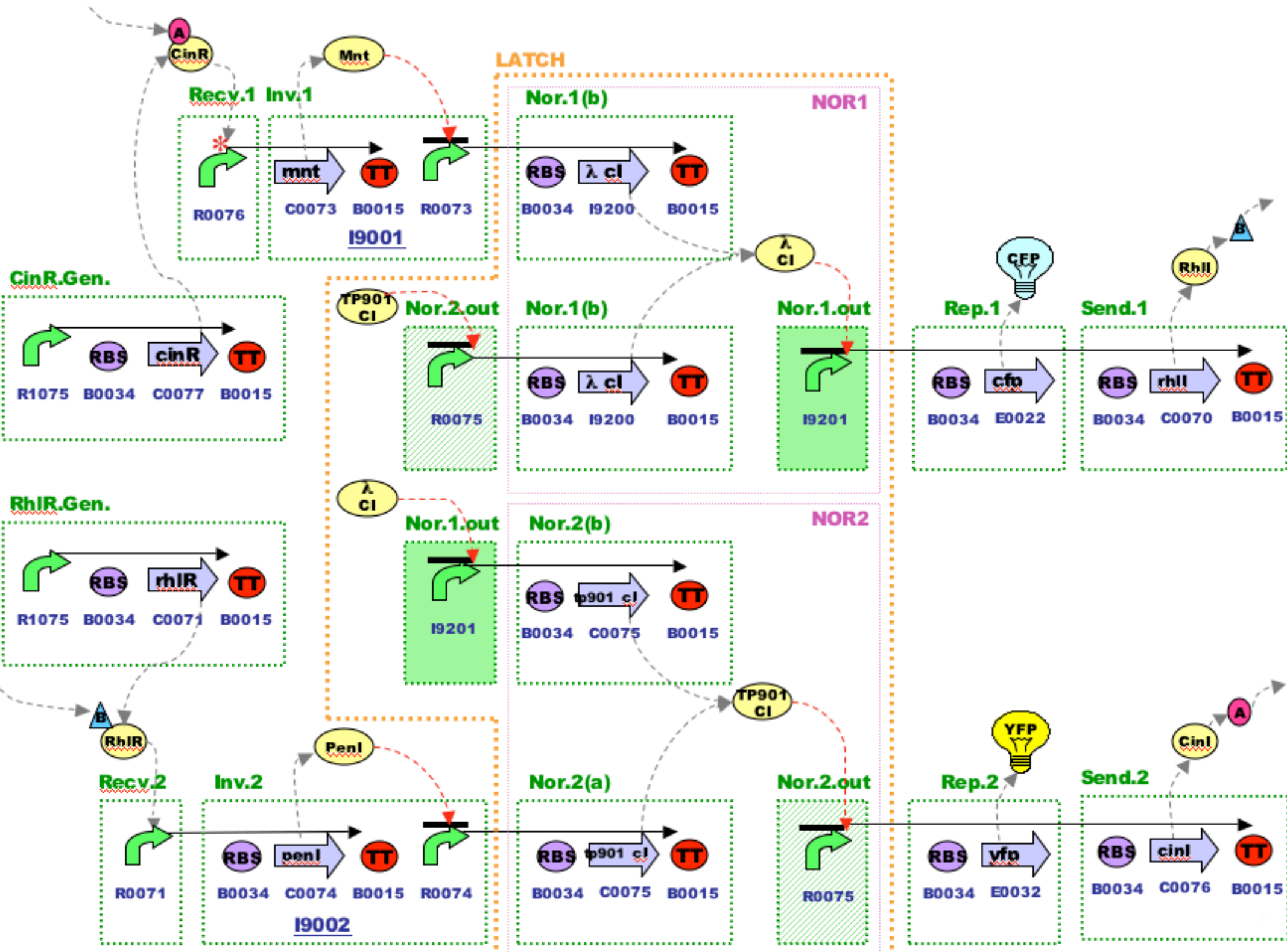
B produces aiia

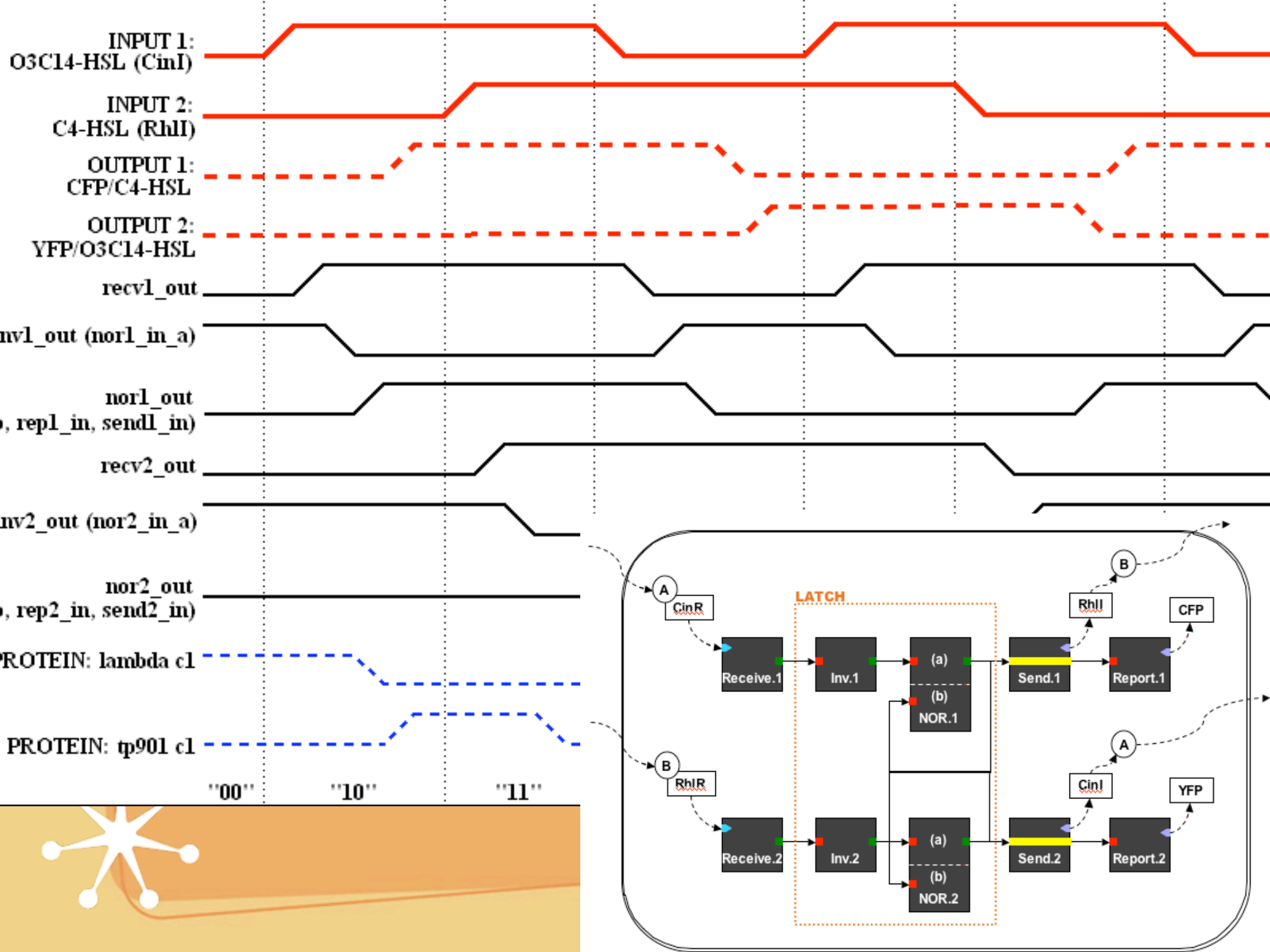


aiia destroys A











Team Fighting Darwins - The Unnatural Selector

Cell-to-Cell Signaling and *Pseudomonas aeruginosa* Infections

Fighting Darwins The Un-Natural Selector

