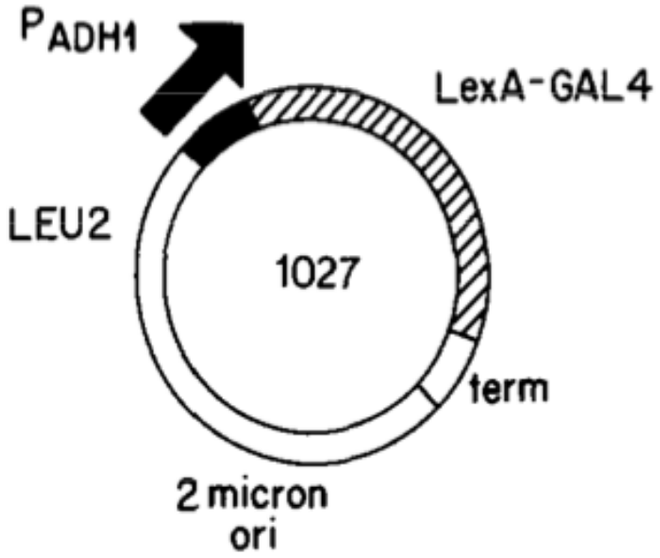
Synthetic Biology Open Language Visual

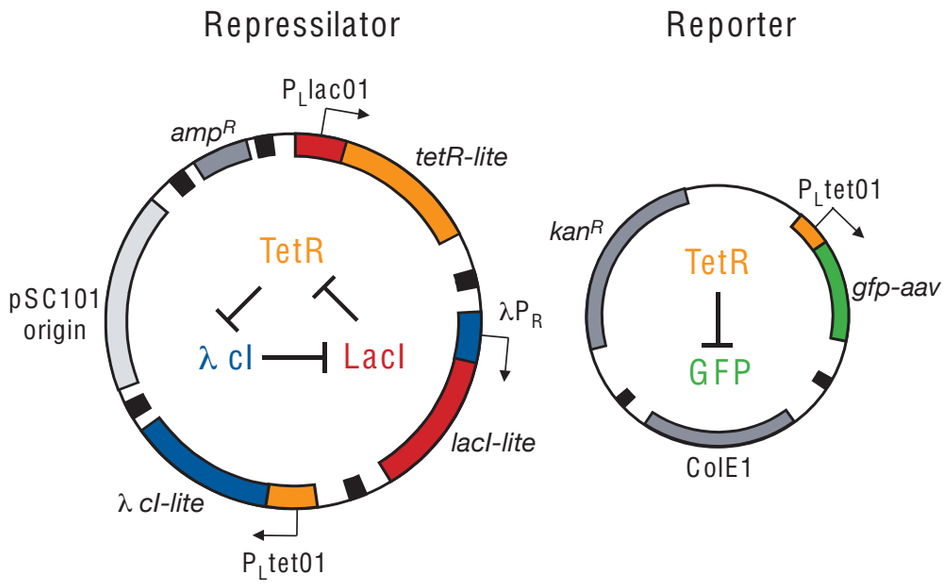
An open-source graphical standard for synthetic biology

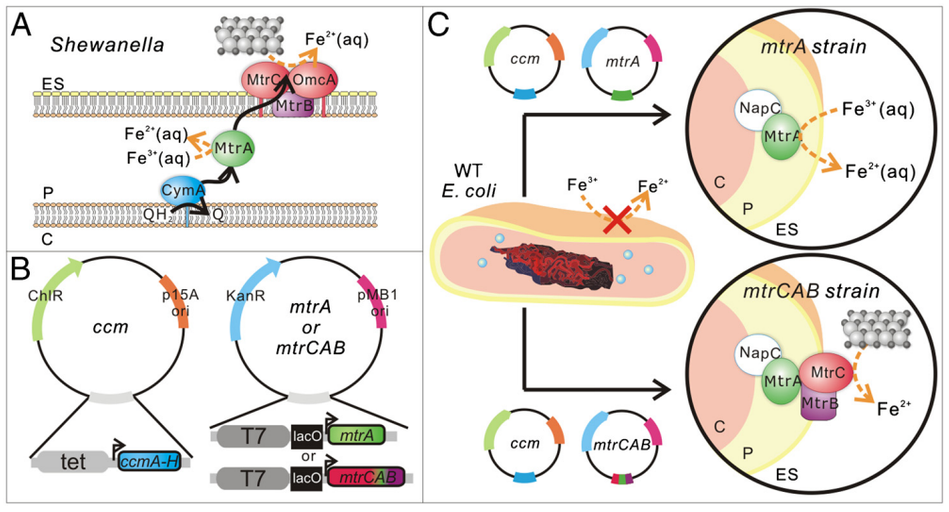
Jacqueline Quinn, Jacob Beal, Swapnil Bhatia, Patrick Cai, Joanna Chen, Kevin Clancy, Robert Sidney Cox III, Michal Galdzicki, Nathan Hillson, Akshay Maheshwari, Chris Myers, Umesh P, Matthew Pocock, Cesar Rodriguez, Herbert M Sauro, Larisa Soldatova, Guy-Bart Stan, Mandy Wilson and Drew Endy

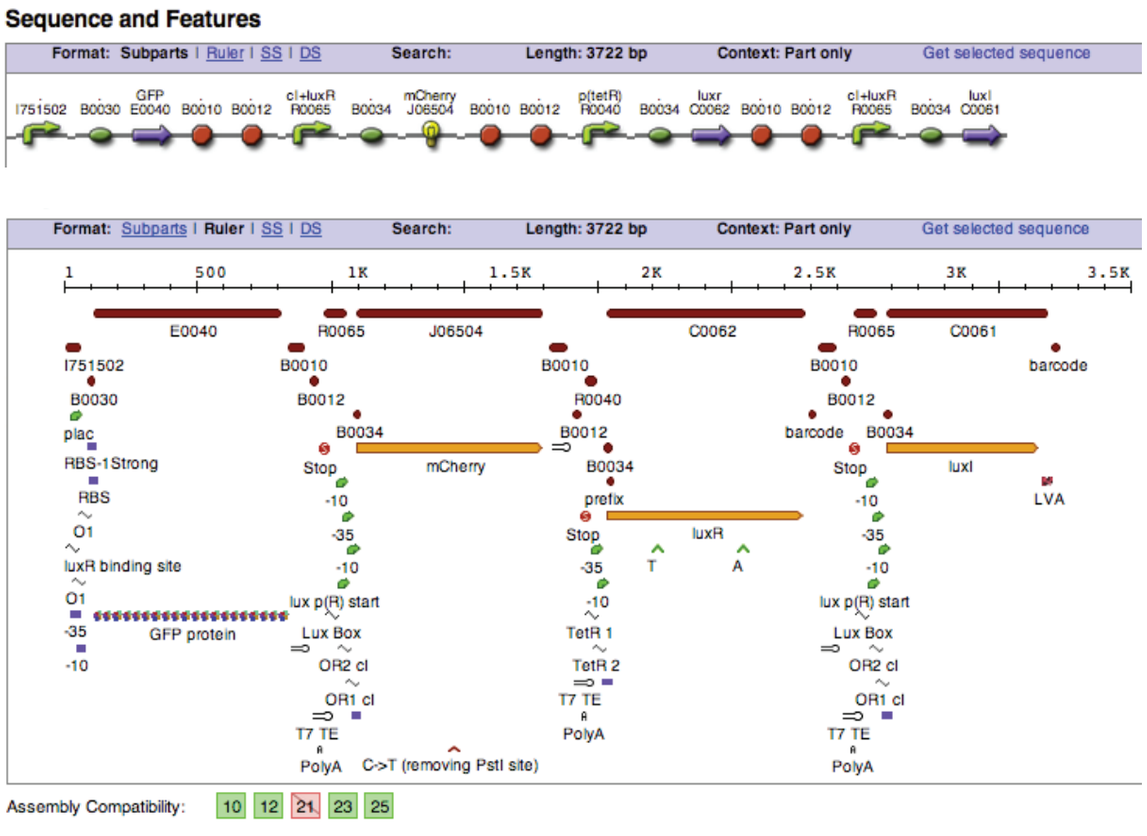
The Fifth International Workshop on Bio-Design Automation
July 12, 2013

sbol visual (the basics)









visual representation of genetic design

promoter	origin of replication
cds	primer binding site
ribosome entry site	blunt restriction site
terminator	sticky restriction site
operator	5’ overhang
insulator	3’ overhang
ribonuclease site	assembly scar
rna stability element	signature
protease site	user defined
protein stability element	

standardized symbol set

SBOL Visual Symbol

Represents

DNAComponent (SBOL Object)

Display Name: Promoter
Definition: SO:0000167

-uri : http://partsregistry.org/part/BBa_J23100
-displayId : BBa_J23100
-name : J23100
-description : constitutive promoter family member
-type[0..*] : http://purl.obolibrary.org/obo/SO_0000167

Sequence Ontology Term

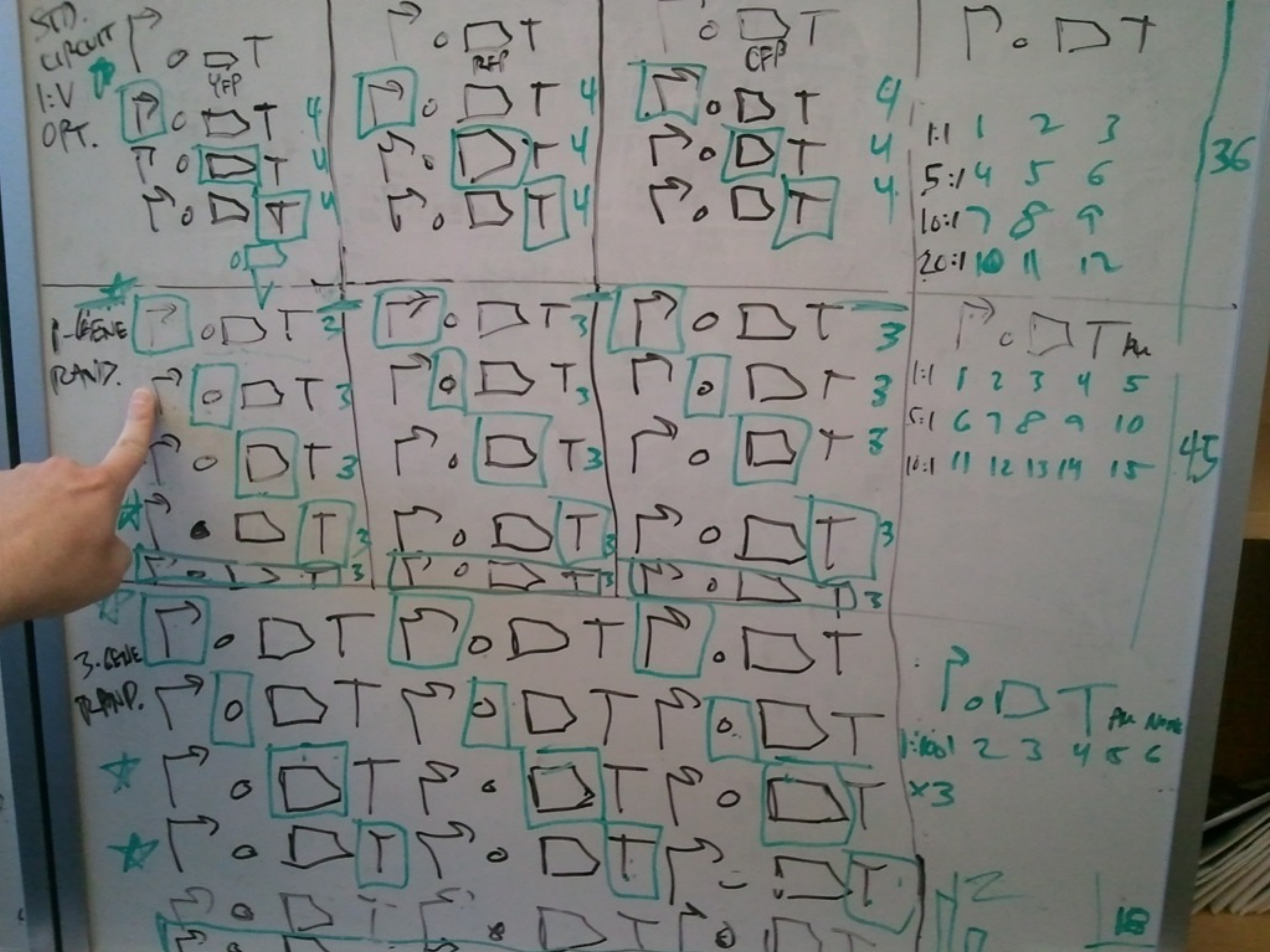
SO:0000167 ! promoter
definition...

Defines Meaning

Defines Type

relationship to SBOL

use in various contexts

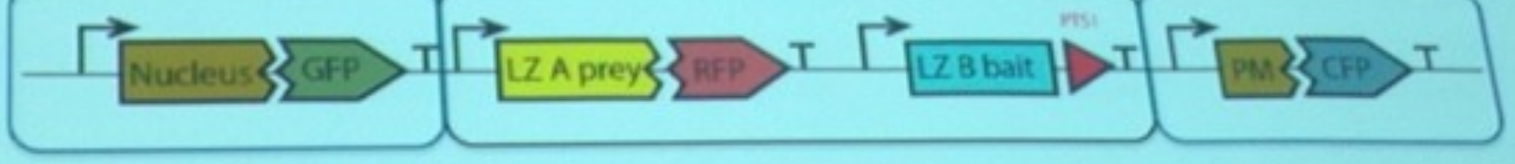

STD. CIRCUIT
1:V
OPT.
YFP
RFP
CFP
1:1 1 2 3
5:1 4 5 6
10:1 7 8 9
20:1 10 11 12
36
1-GENE
RAND.
1:1 1 2 3 4 5
5:1 6 7 8 9 10
10:1 11 12 13 14 15
45
3-GENE
RAND.
1:100 1 2 3 4 5 6
×3
18

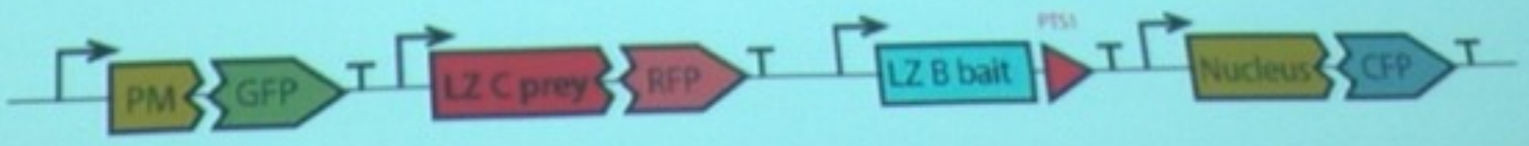
Using MiCodes in a zipper assay

When you see this MiCode...

...you know you're assaying this zipper pair

Strong zipper pair





UC Berkeley

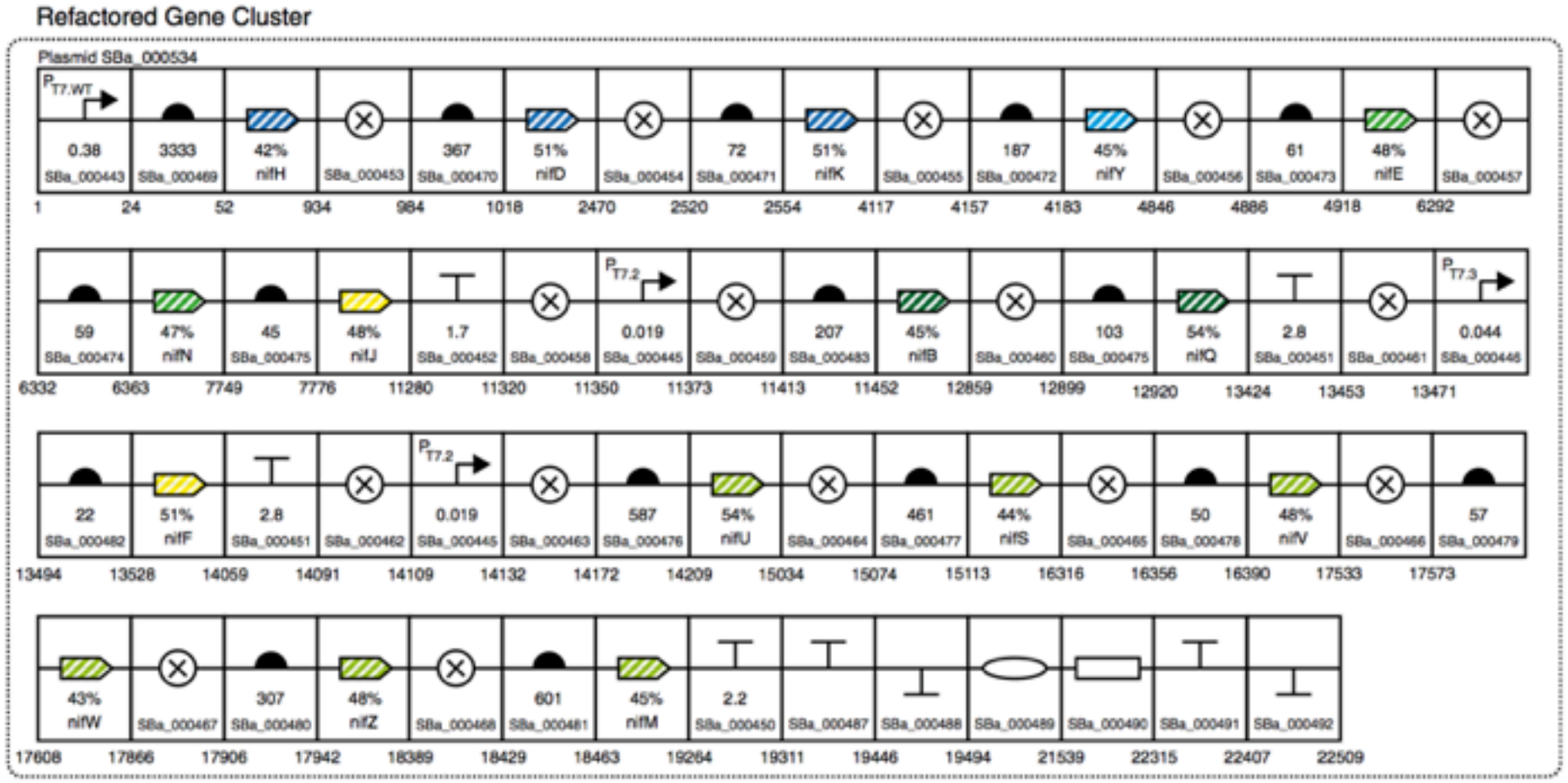
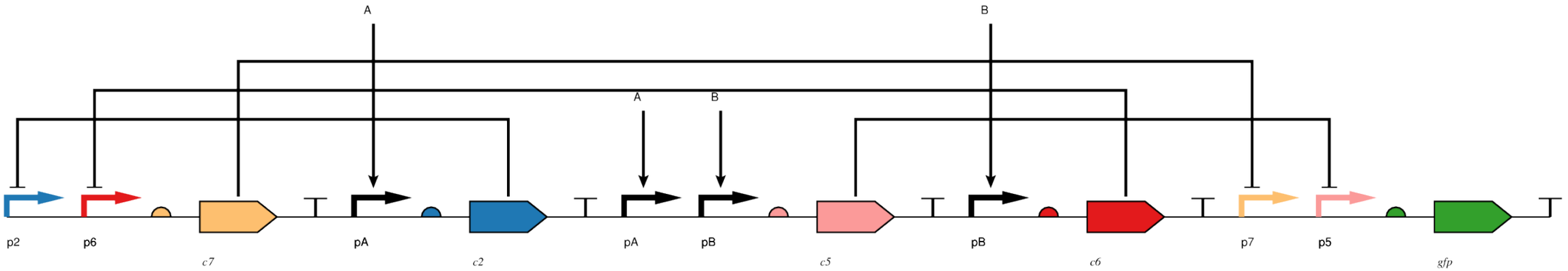


Fig. 4. Comprehensive schematic illustration for the complete refactored gene cluster and controller. Each of the 89 parts is represented according to the Synthetic Biology Open Language visual standard (www.sbolstandard.org), and the SynBERC Registry part number (registry.synberc.org) and part activity are shown. The full sequences of each plasmid have been deposited in GenBank (SBa_000534, JQ903614; SBa_000559, JQ903615; SBa_000560, JQ903616). The T7 promoter strengths are measured with monomeric red fluorescent protein and reported in REUs (*Materials and Methods*). Terminator strengths are measured in a reporter plasmid and reported as the fold reduction in monomeric red fluorescent protein (RFP) expression compared with a reporter without a terminator. The RBS strength is reported in as arbitrary units of expression from the induced P_{tac} promoter (1 mM IPTG) and a fusion gene between the first 90 nt of the gene and RFP. The nucleotide numbers for the plasmids containing the refactored cluster and controller are shown. The codon identity of each recoded gene compared with WT is shown as a percentage.

software




```
p p2 2
p p6 6
r r 7 nl
c c7 7
t
```

```
p pA
r r 2 nl
c c2 2
t
```

```
p pA
p pB
r r 5 nl
c c5 5
t
```

```
p pB
r r 6 nl
c c6 6
t
```

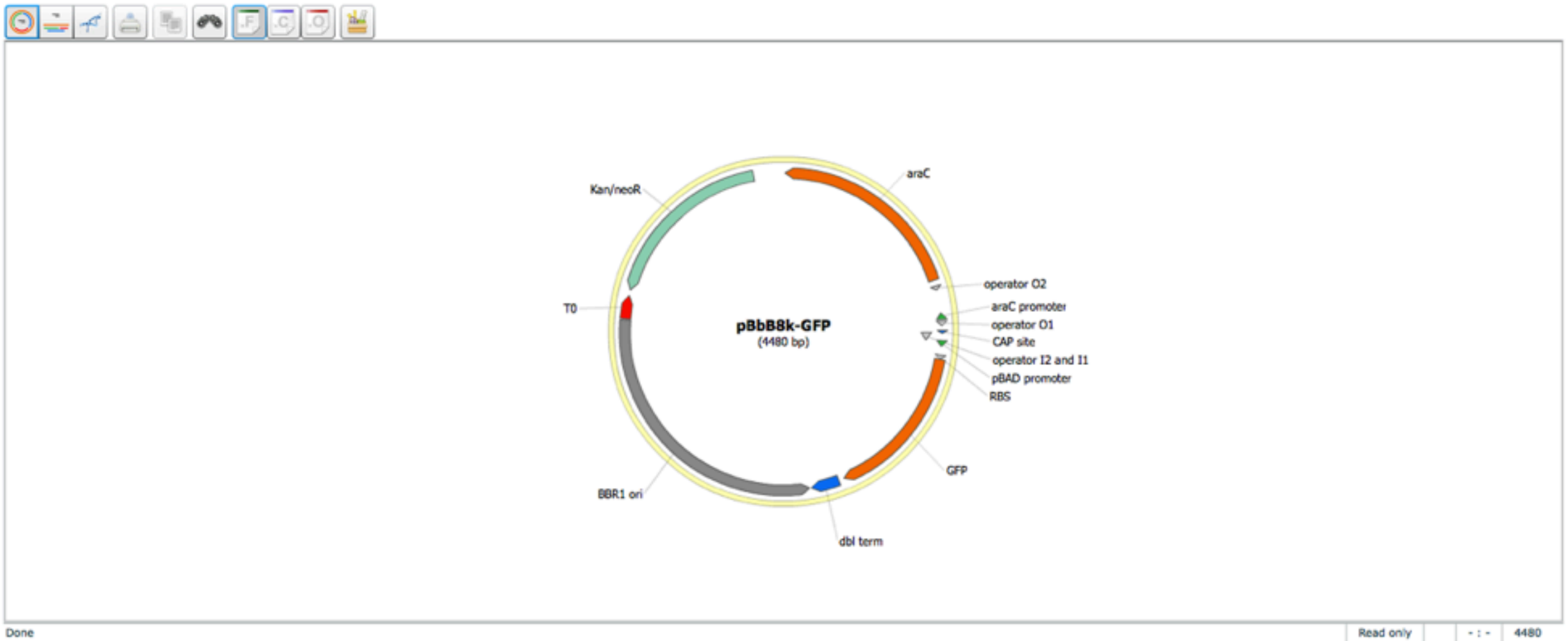
```
p p7 7
p p5 5
r r 4 nl
c gfp 4
t
```

```
# Arcs
c2 rep p2
c5 rep p5
c6 rep p6
c7 rep p7
A ind pA
B ind pB
```

PigeonCAD
pigeoncad.org

SEQUENCE

Delete | Open | Download | Hide Pigeon Image



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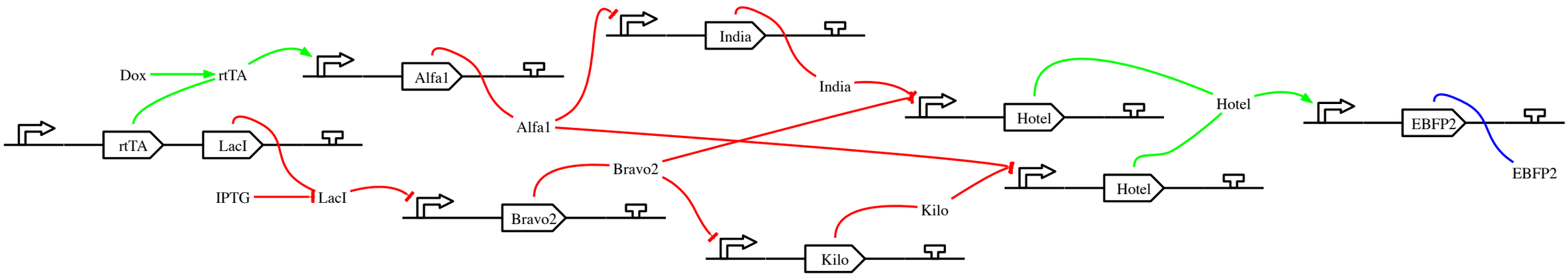
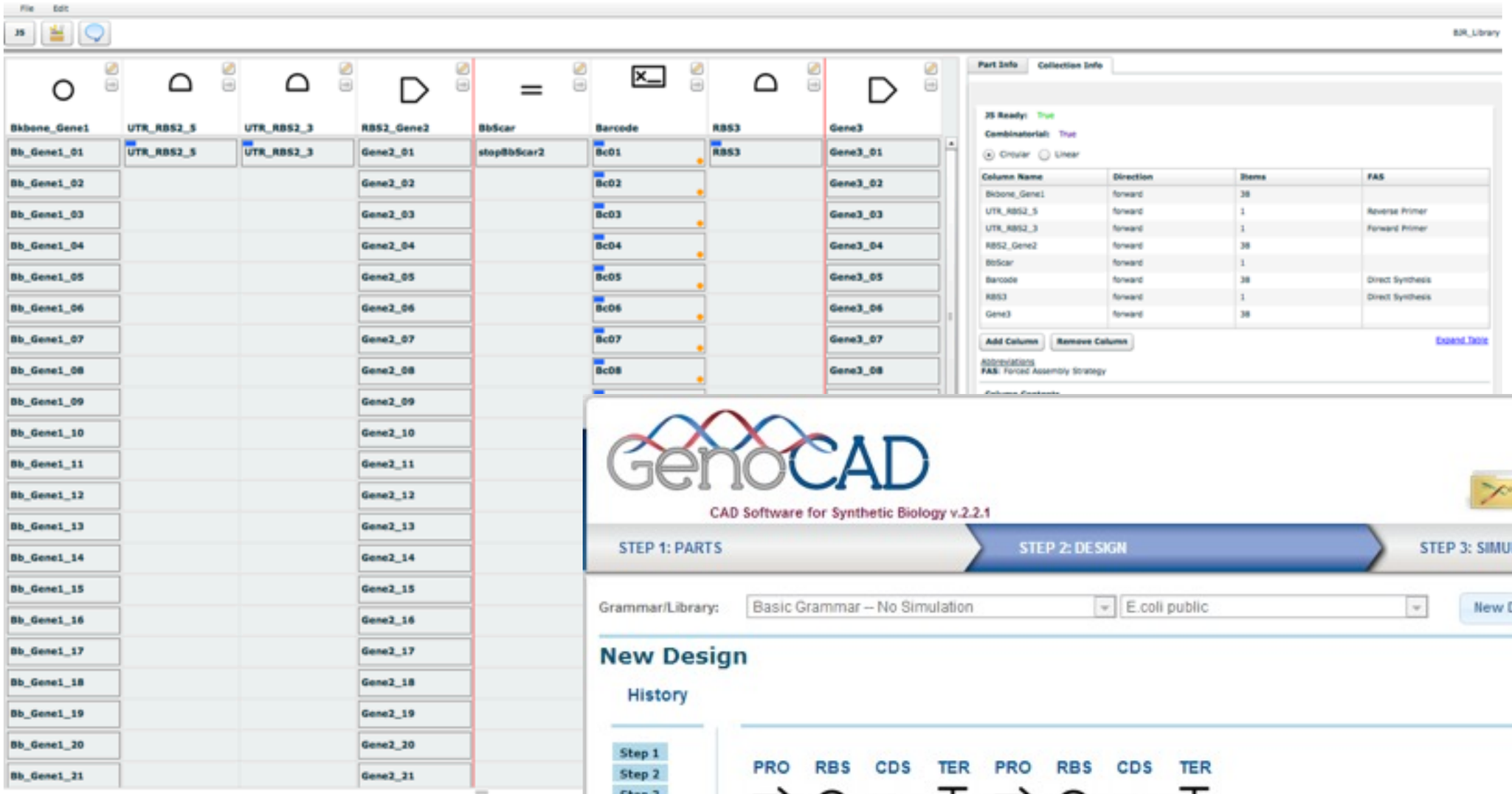
JBEI-ICE

public-registry.jbei.org



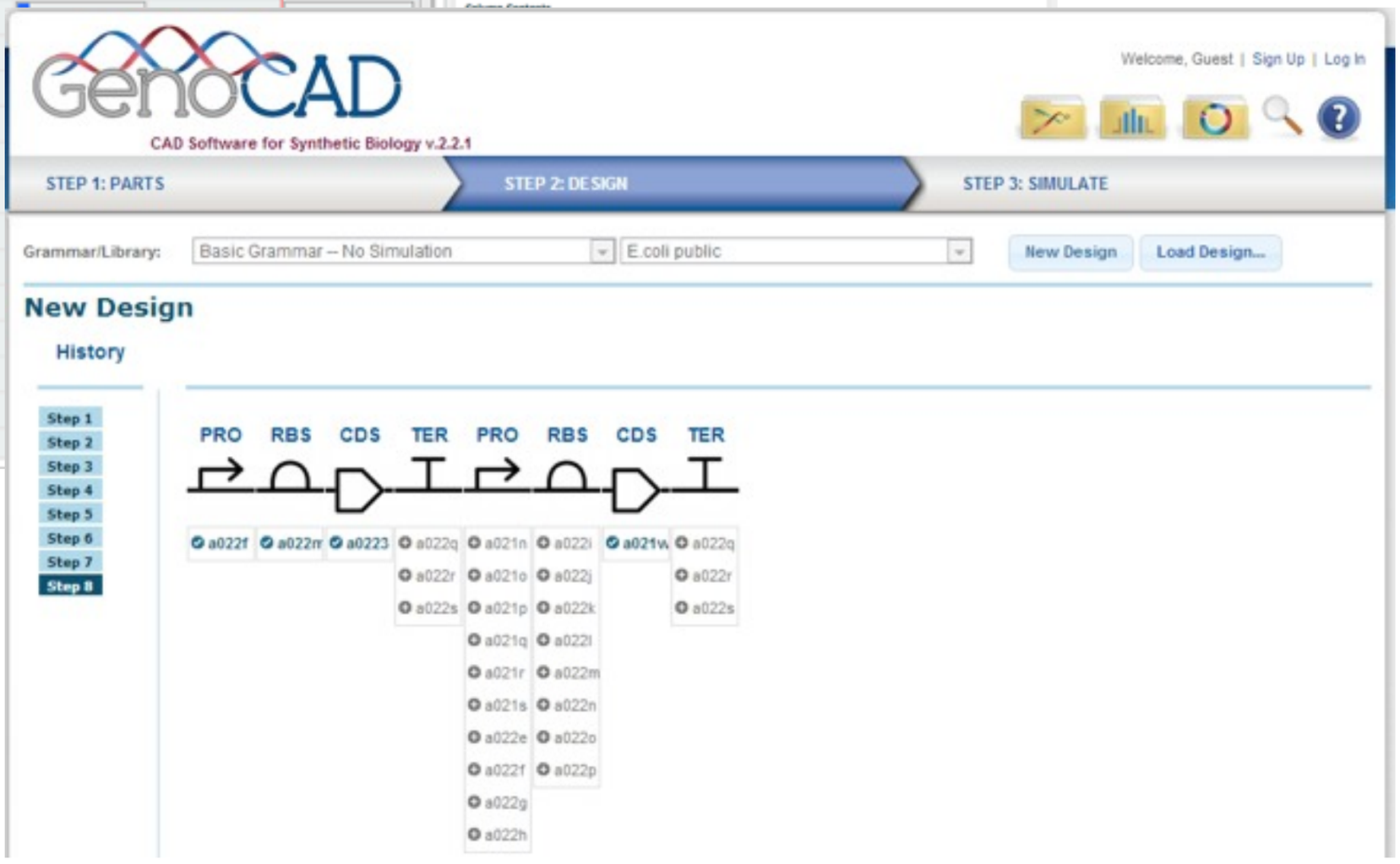
BioCompiler

synbiotools.bbn.com



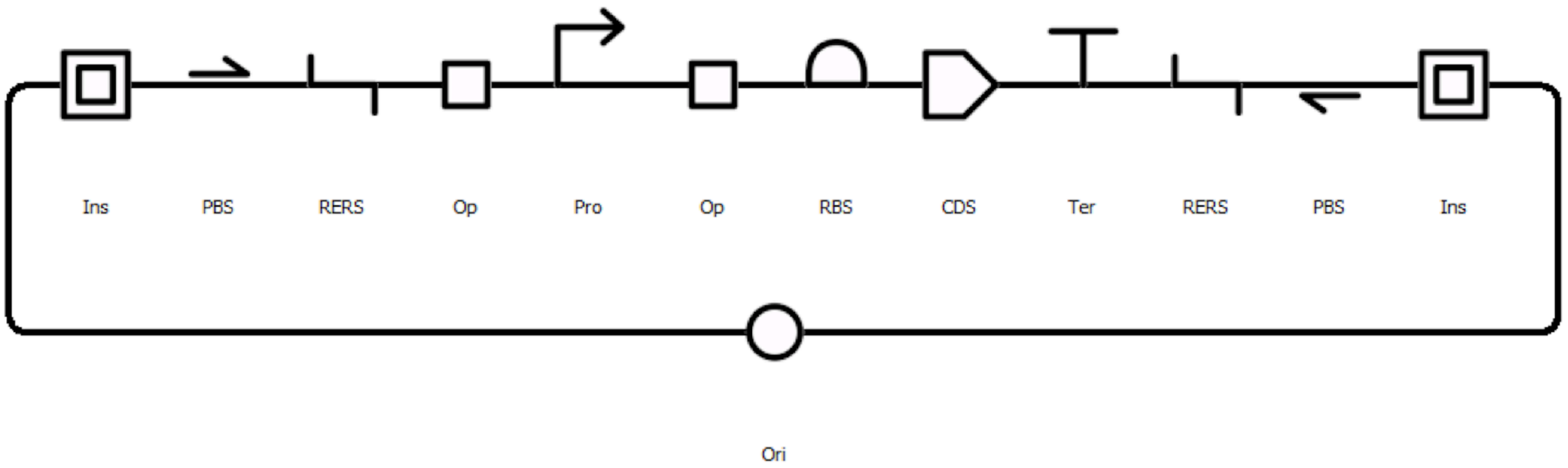
DeviceEditor

j5.jbei.org

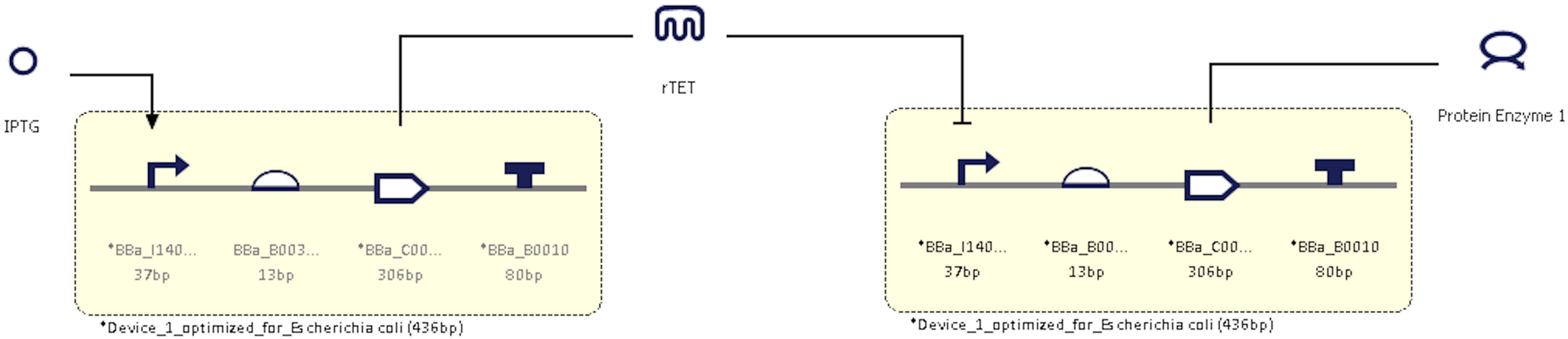


GenoCAD

genocad.org



SBOL Designer



VectorNTI Express Designer

next steps

SO:0000684 ! nuclease sensitive site
SO:0000059 ! nuclease binding site
SO:0000179 ! clone insert start
SO:0000103 ! clone insert end

SO:0000004 ! interior coding exon
SO:0000104 ! polypeptide
SO:0000120 ! protein coding primary transcript
SO:0000147 ! exon
SO:0000195 ! coding exon
SO:0000196 ! five prime coding exon coding region
SO:0000196 ! five prime exon coding region
SO:0000197 ! three prime coding exon coding region
SO:0000197 ! three prime exon coding region
SO:0000200 ! five prime coding exon
SO:0000236 ! ORF
SO:0000316 ! CDS
SO:0000332 ! coding conserved region
SO:0000717 ! reading frame
SO:0000839 ! polypeptide region
SO:0000851 ! CDS region
SO:0000852 ! exon region
SO:0001215 ! coding region of exon

SO:0000436 ! ARS
SO:0000296 ! origin of replication
SO:0000724 ! oriT
SO:0000340 ! chromosome
SO:0001235 ! replicon

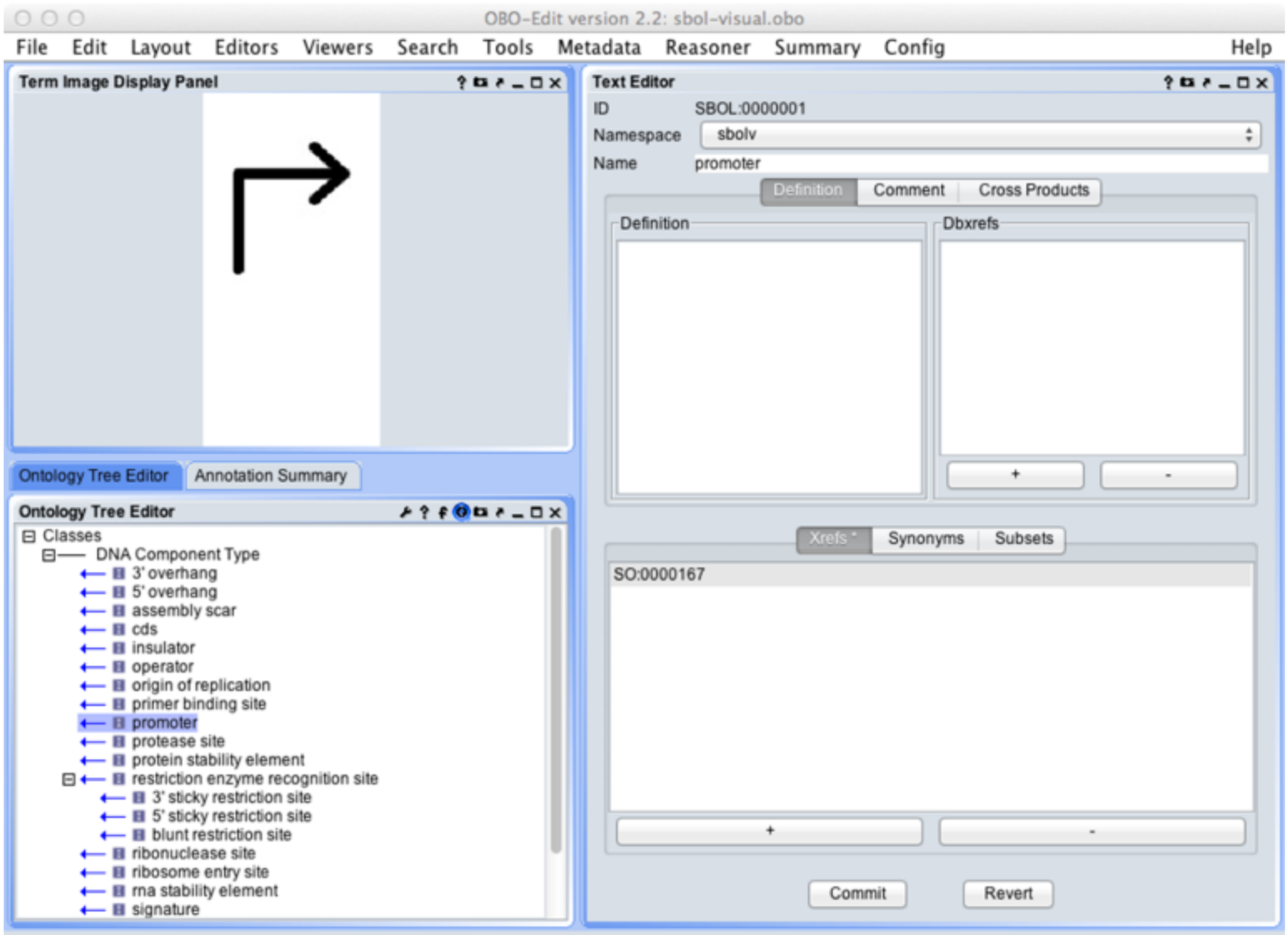
SO:0000057 ! operator
SO:0000165 ! enhancer
SO:0000235 ! TF binding site
SO:0000409 ! binding site
SO:0000410 ! protein binding site
SO:0000625 ! silencer
SO:0000727 ! CRM
SO:0001654 ! nucleotide to protein binding site

SO:0000167 ! promoter
SO:0000315 ! TSS
SO:0001055 ! transcriptional cis regulatory region

SO:0000139 ! ribosome entry site
SO:0000140 ! attenuator
SO:0000581 ! cap
SO:0001647 ! kozak sequence

SO:0000141 ! terminator
SO:0000616 ! transcription end site

further ontological mappings



serializations and versioning

Agilent Technologies

CLARK PARSIA

Stardog

Raytheon BBN Technologies

AUTODESK

life technologies™

DNA 2.0

GENOME COMPILER
TOOLS FOR DESIGNING LIFE

AMYRIS

TinkerCell
UNIVERSITY of WASHINGTON

GenoCAD
VIRGINIA BIOINFORMATICS INSTITUTE
AT VIRGINIA TECH

iBioSim
THE UNIVERSITY OF UTAH

j5
jbei
Joint BioEnergy Institute

CSynBI
Centre for Synthetic Biology and Innovation
Imperial College London

CLOTHO
BOSTON UNIVERSITY
Berkeley
UNIVERSITY OF CALIFORNIA

biofab

Newcastle University

community growth

Get Involved!

Get Involved!

- Use SBOL Visual!

Get Involved!

- Use SBOL Visual!
- Tell us how it goes

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- Tell us how it goes
- Submit new symbols

Get Involved!

- Use SBOL Visual!
- Tell us how it goes
- Submit new symbols
- Join the Working Group

SBOL Visual Working Group

Aaron Adler
Jacob Beal
Swapnil Bhatia
Patrick Cai
Joanna Chen
Kevin Clancy
Robert Sidney Cox III
Michal Galdzicki
Nathan Hillson
Chris Myers
Umesh P
Matthew Pocock
Cesar Rodriguez
Herbert Sauro
Larisa Soldatova
Guy-Bart Stan
Grimaldo Urena
Alan Villalobos
Mandy Wilson

Thank You!

www.sbolstandard.org/visual
visual@sbolstandard.org

promoter	origin of replication
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insulator	3’ overhang
ribonuclease site	assembly scar
rna stability element	signature
protease site	user defined
protein stability element	