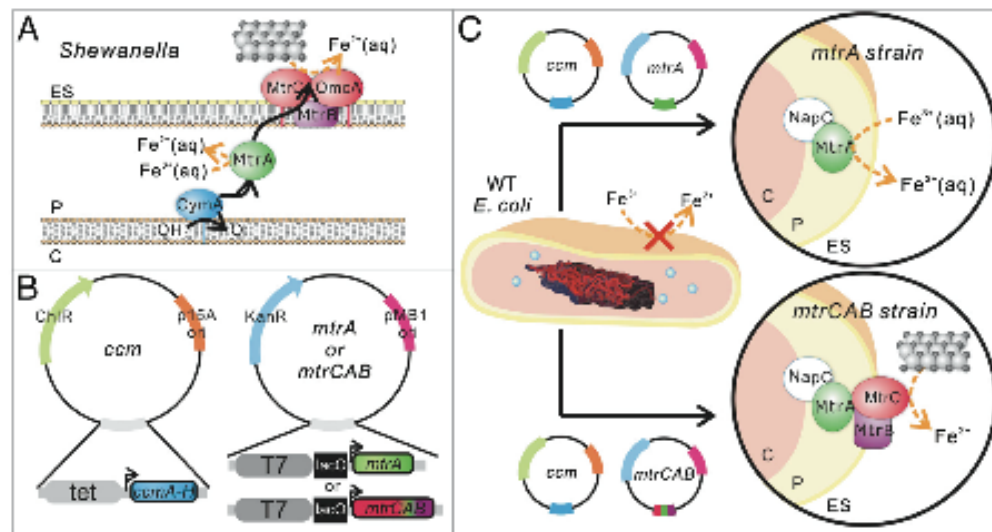
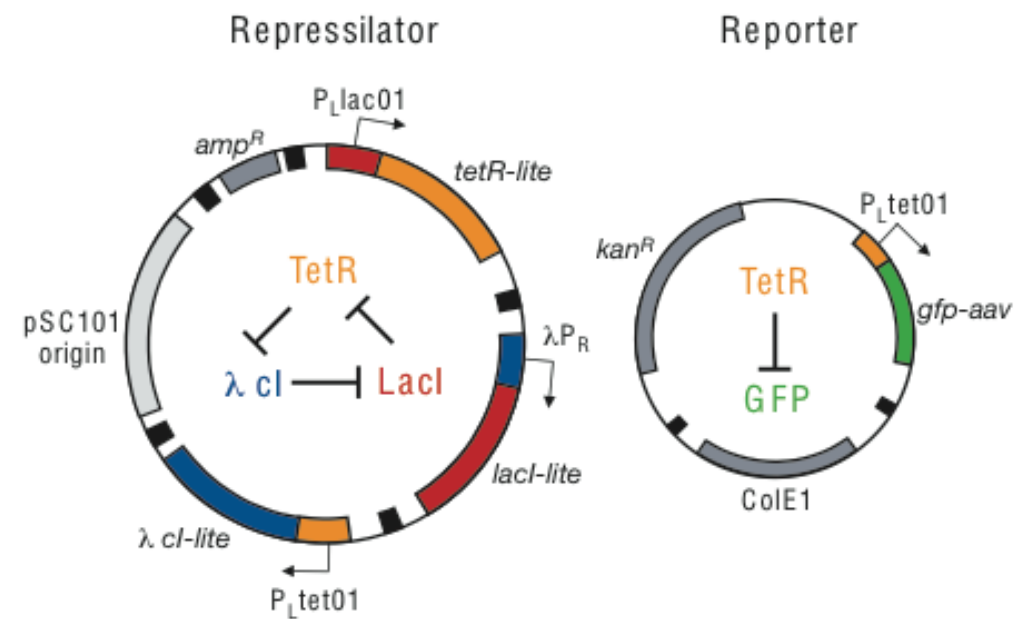
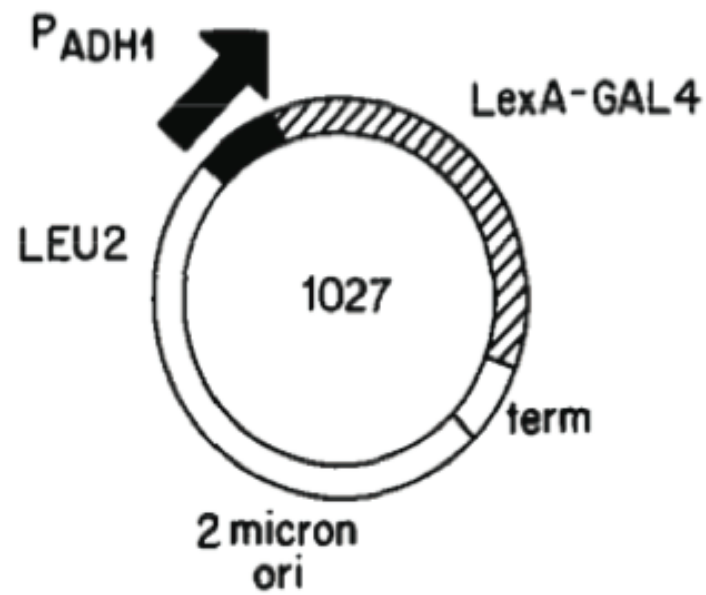


# Synthetic Biology Open Language Visual

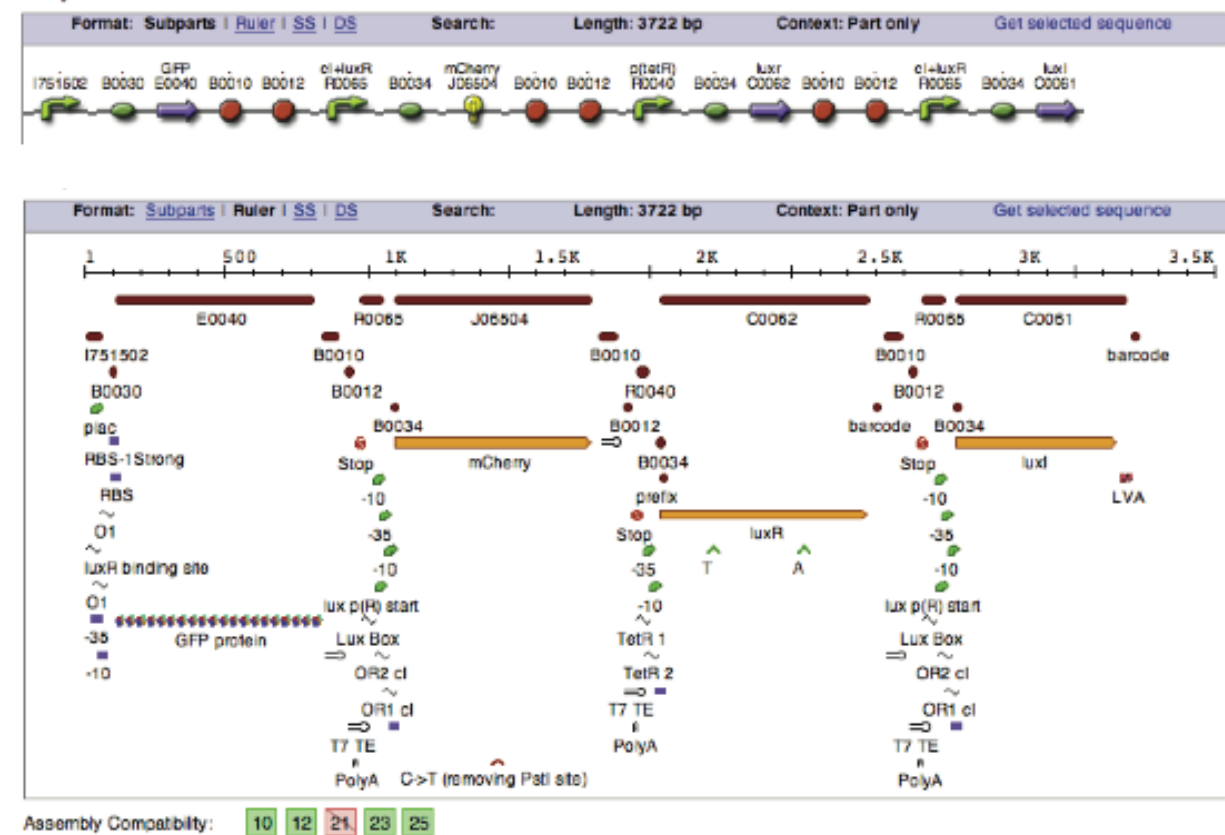
An open-source graphical standard for synthetic biology

Jackie Quinn  
SBGN 10 - August 17, 2014

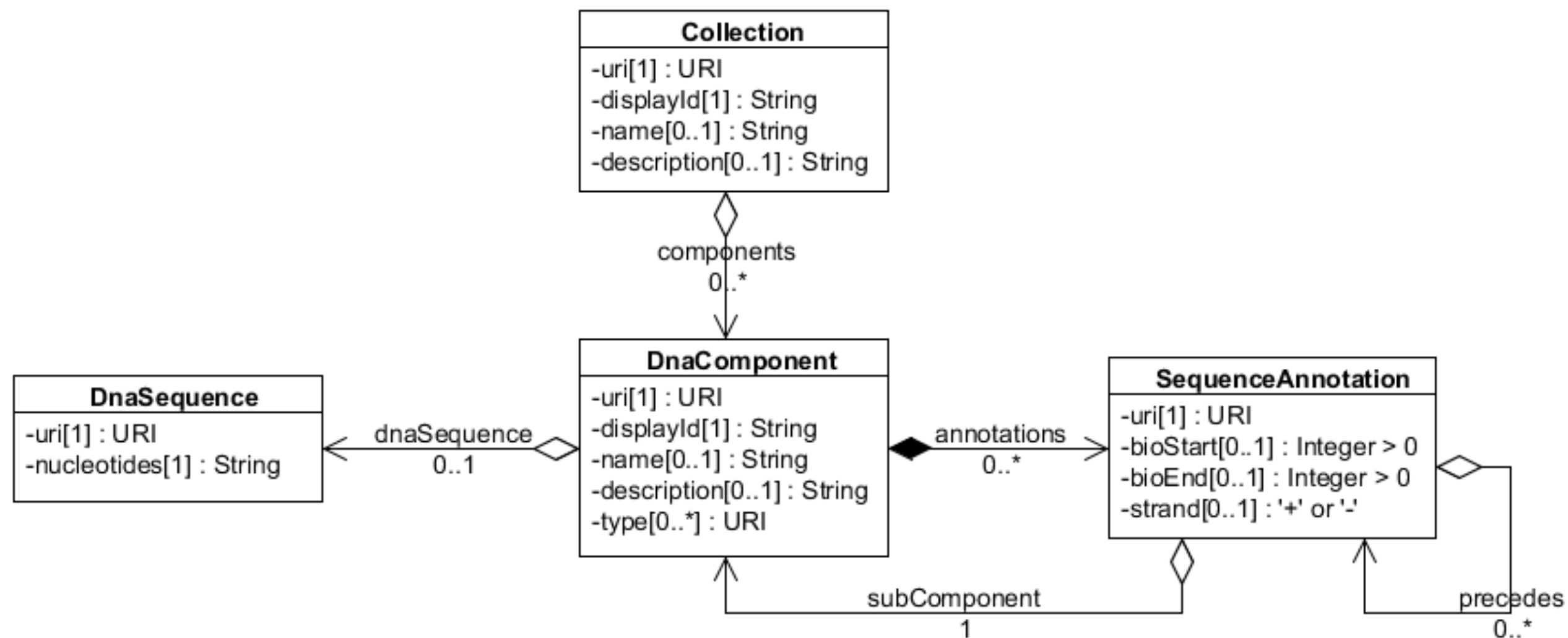
# SBOL and SBOL Visual (the basics)



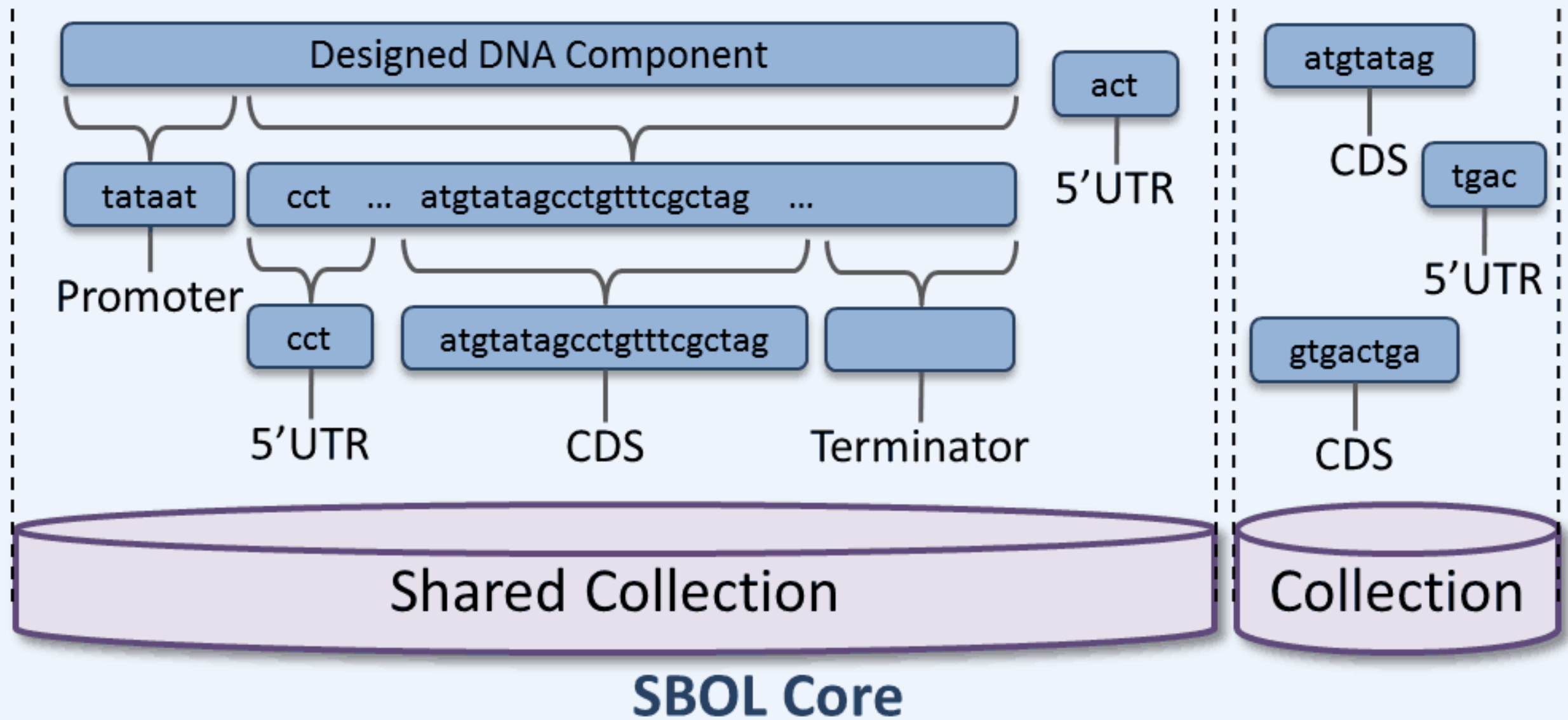
### Sequence and Features


















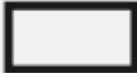



visual representation of genetic design

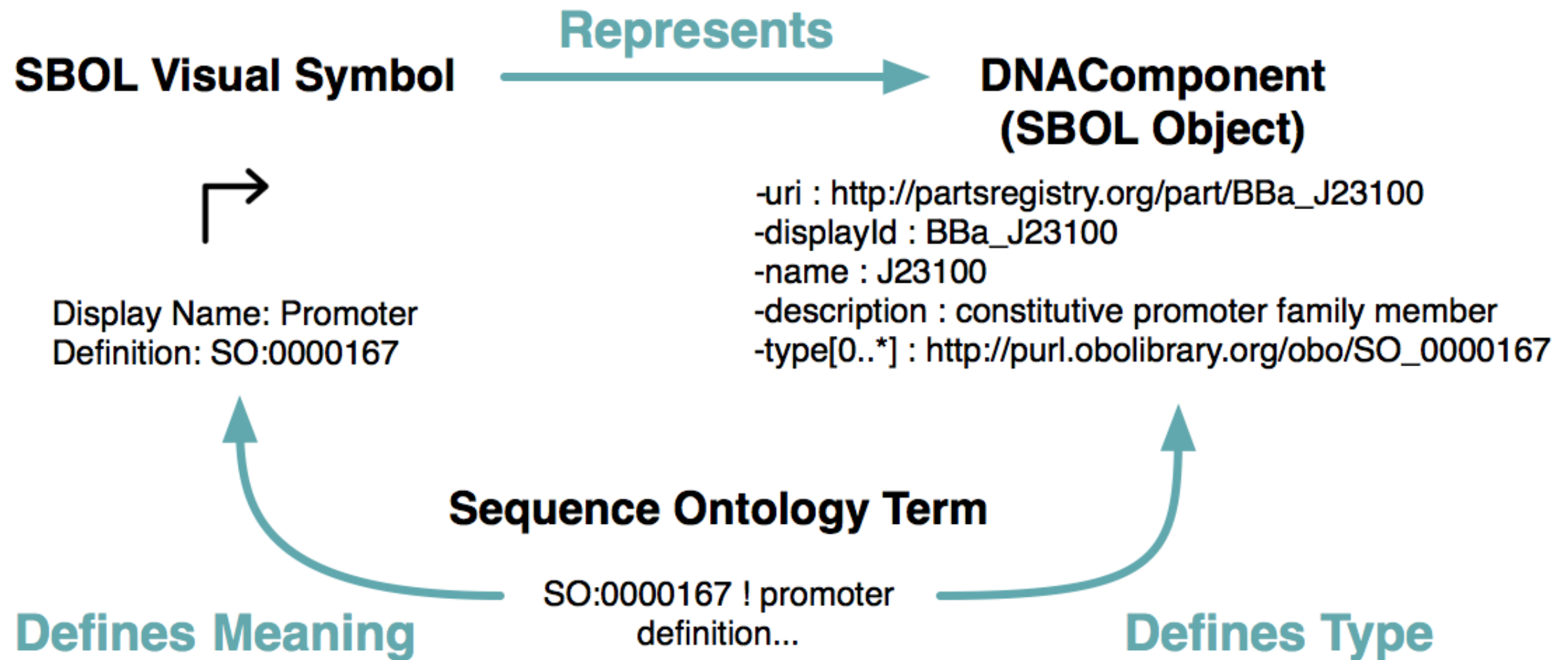


## SBOL Visual



 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

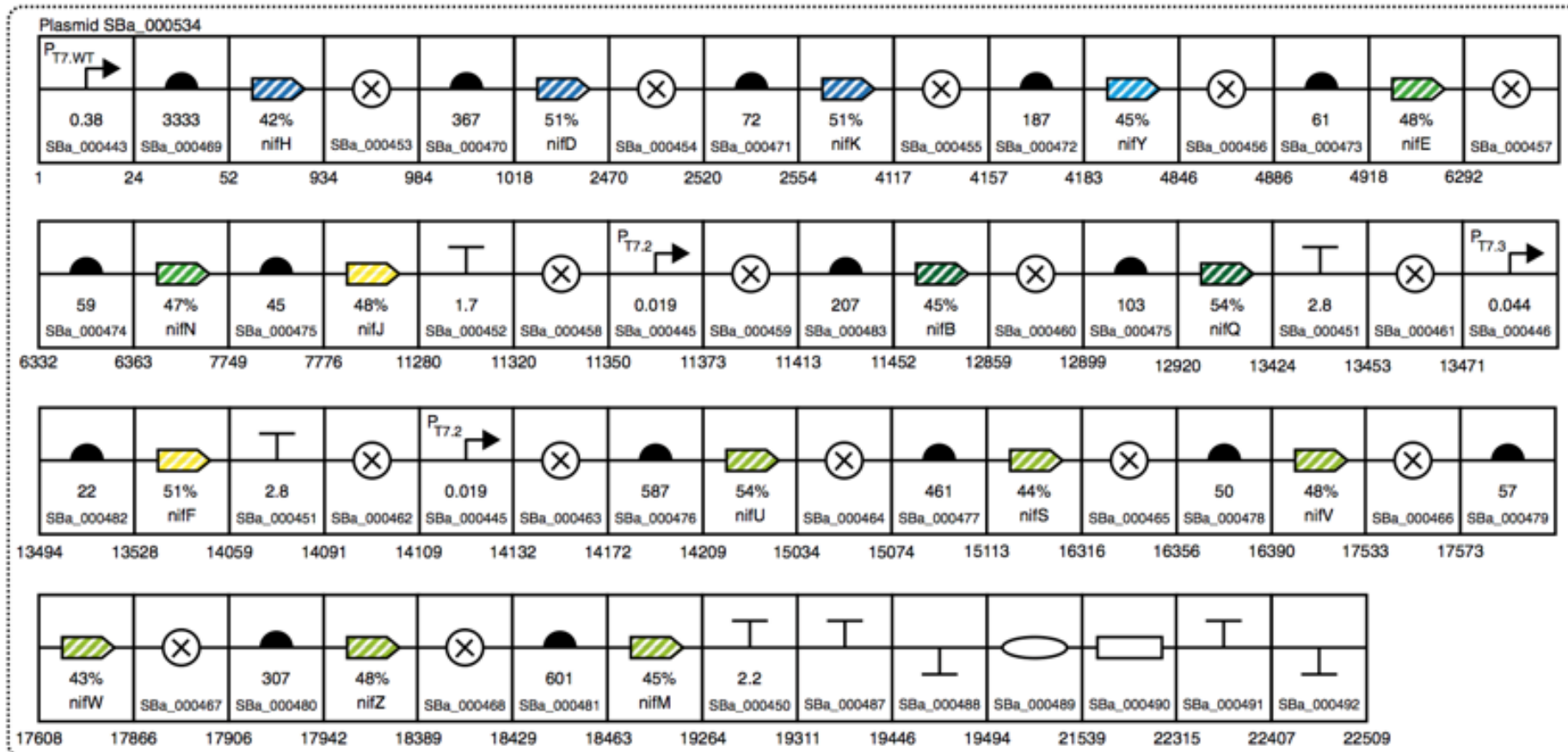


relationship to SBOL

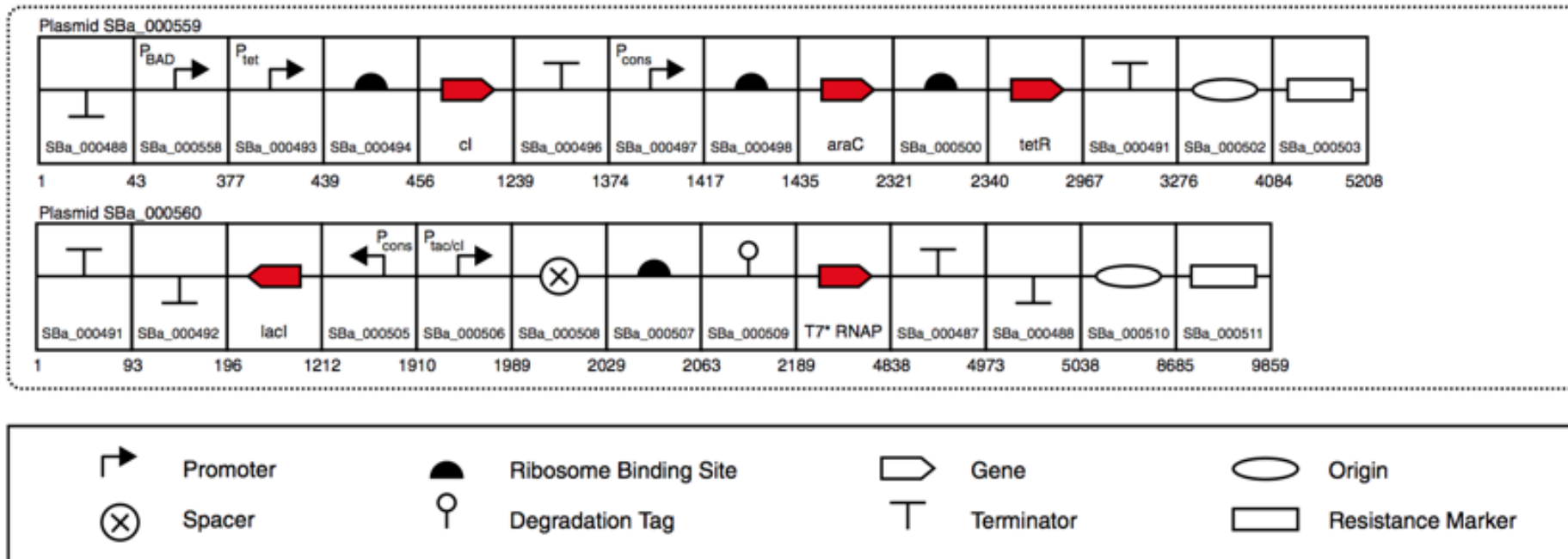
**use in various contexts**



## Refactored Gene Cluster



## Controller



**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](http://www.sbolstandard.org)), and the SynBERC Registry part number ([registry.synberc.org](http://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.



## Using MiCodes in a zipper assay

When you see this  
MiCode...

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



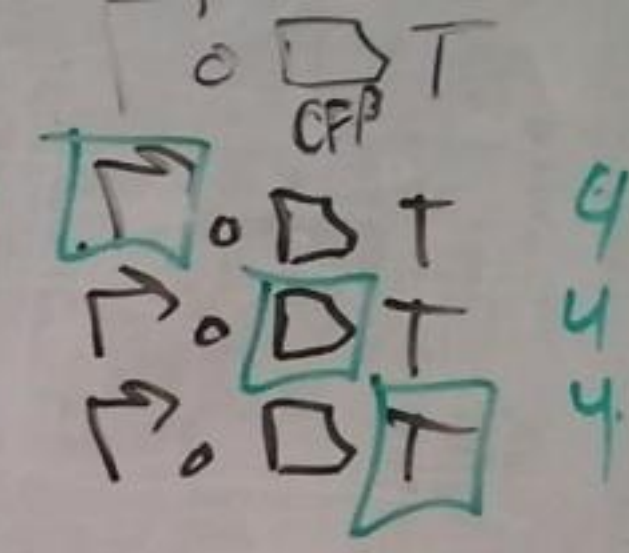
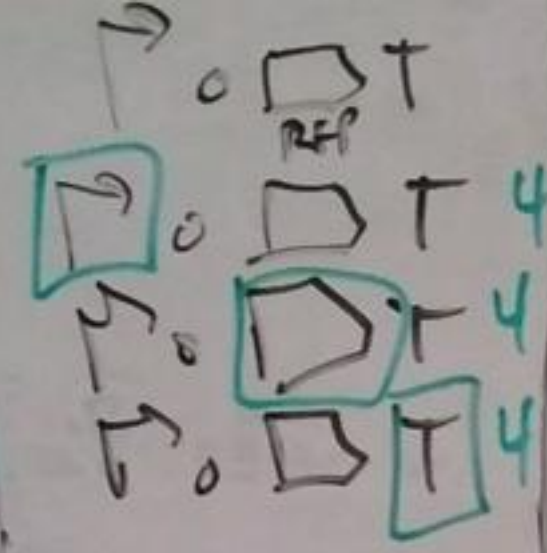
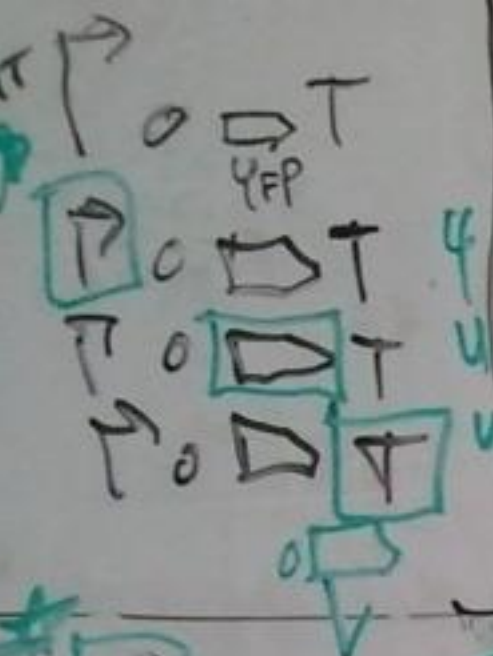
Strong zipper pair



MiCodes



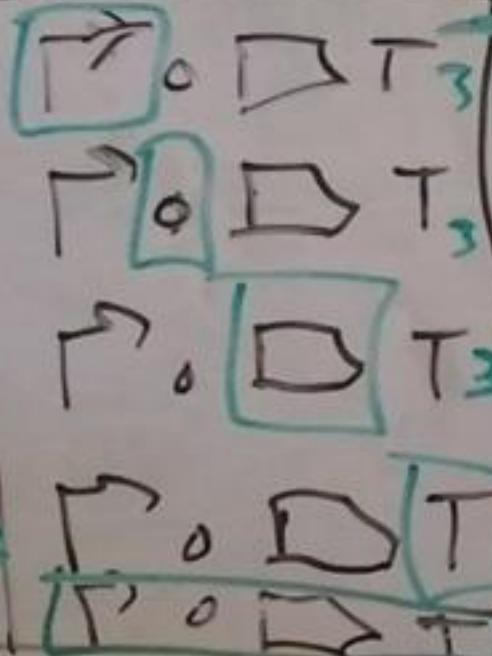
5th.  
Circuit  
1:V  
OPT.



	1	2	3
1:1	4	5	6
5:1	7	8	9
10:1	10	11	12

36

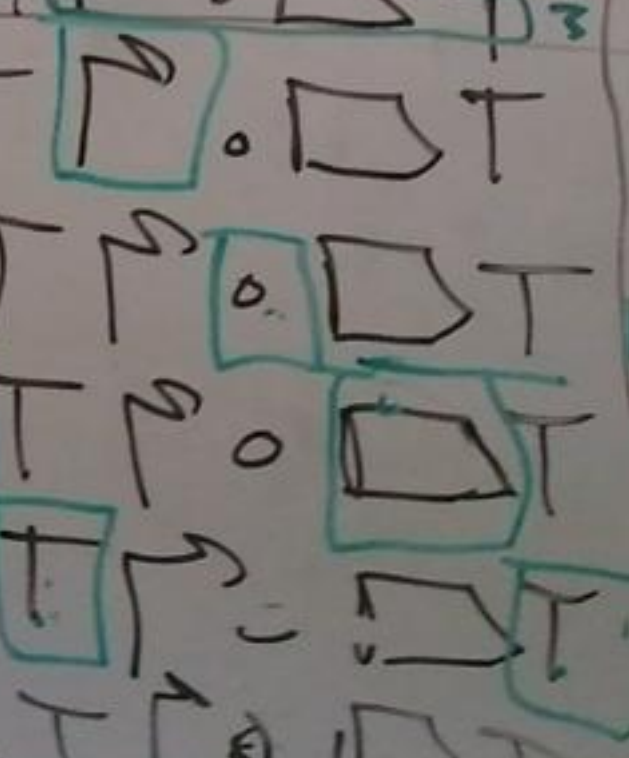
1-GENE  
RAND.



	1	2	3	4	5
1:1	6	7	8	9	10
5:1	11	12	13	14	15

45

3-GENE  
RAND.



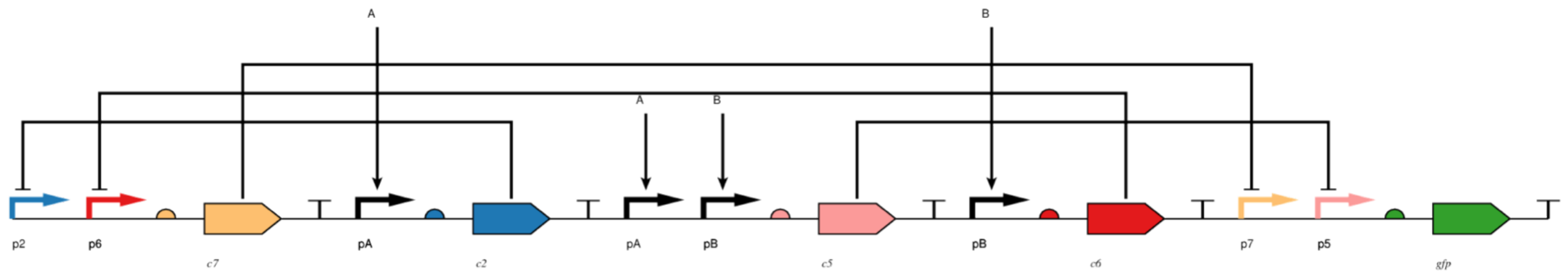
	1	2	3	4	5	6
1:1	7	8	9	10	11	12
5:1	13	14	15	16	17	18

x3

12

18

software



p p2 2  
 p p6 6  
 r r 7 n1  
 c c7 7  
 t

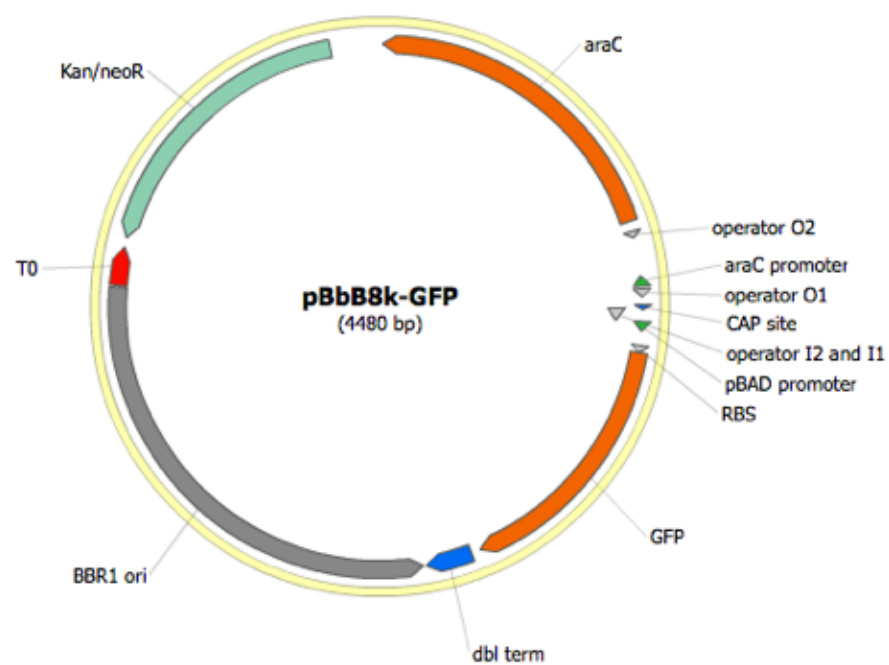
p pA  
 r r 2 n1  
 c c2 2  
 t

p pA  
 p pB  
 r r 5 n1  
 c c5 5  
 t

p pB  
 r r 6 n1  
 c c6 6  
 t

p p7 7  
 p p5 5  
 r r 4 n1  
 c gfp 4  
 t

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

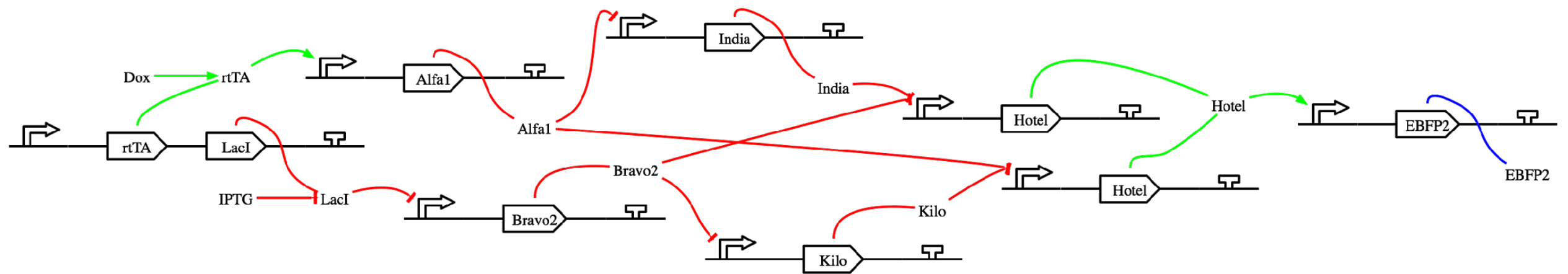


Done

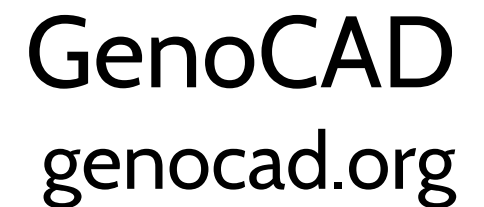
Read only

- : -

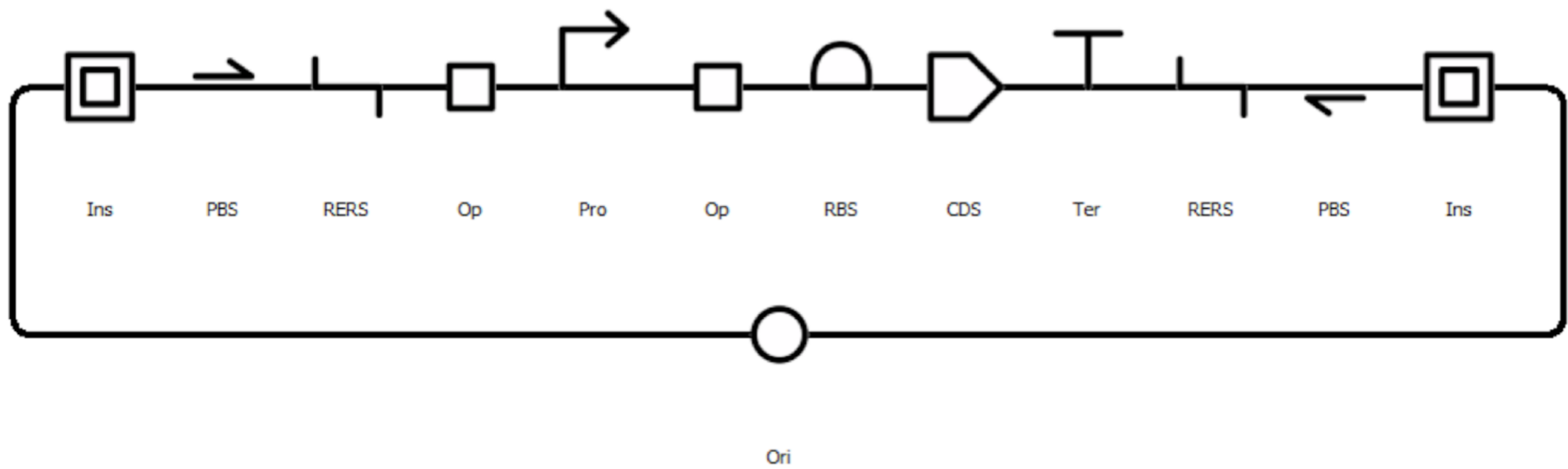
4480



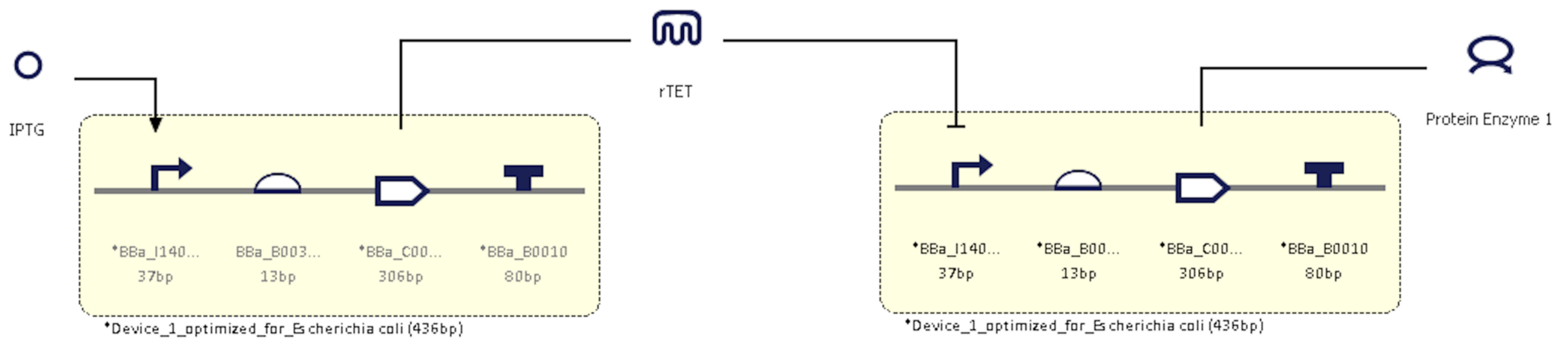




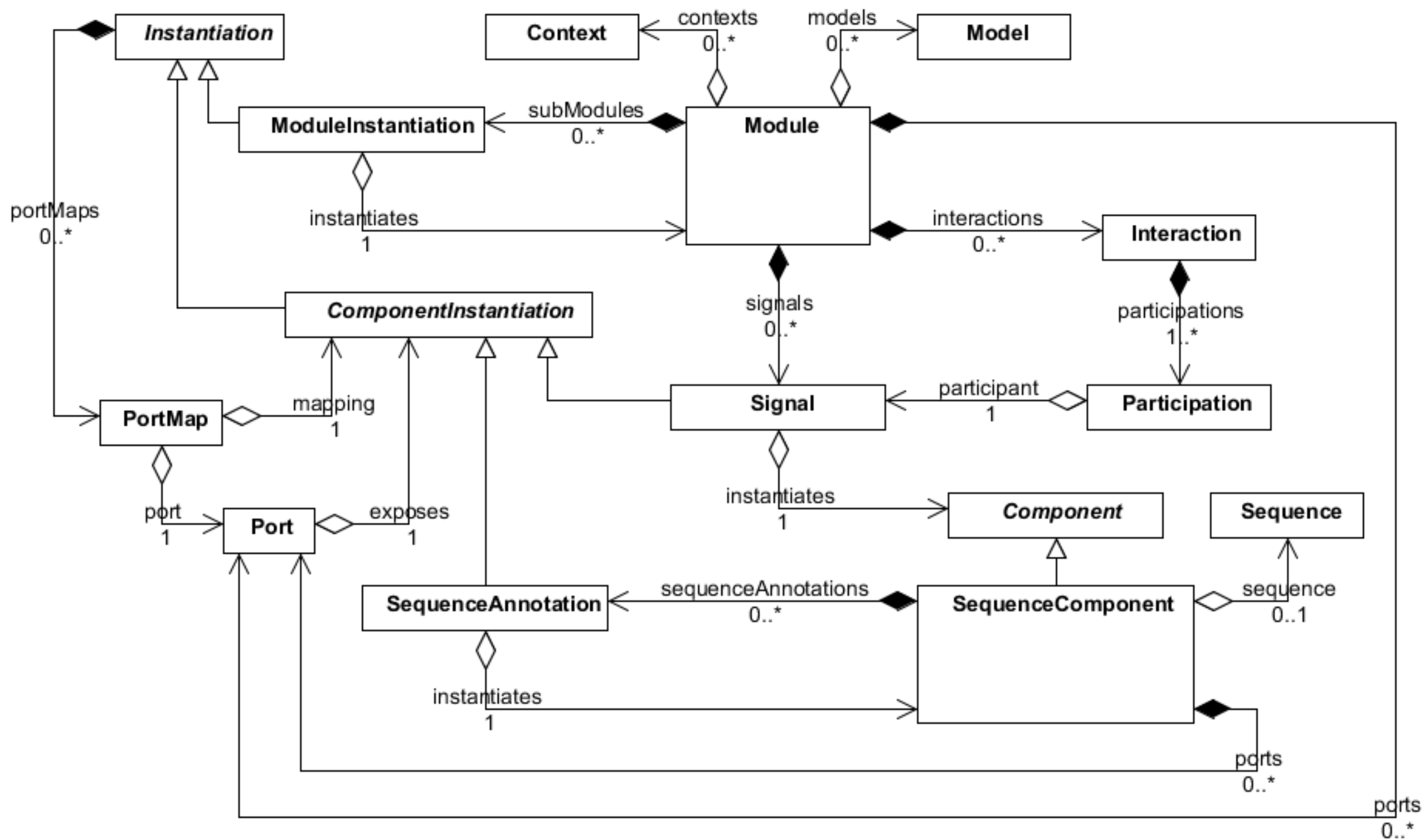




SBOL Designer



VectorNTI Express Designer



# SBOL Visual Working



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Herbert Sauro  
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# Thank You!

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