## 1 Introduction

A mechanistic model of CRISPR/Cas9 gene isertion is presented.

### 1.1 System of reaction diagrams

Lets denote our plasmid CRISPeasy, then the replication rate of our vector is expressed as

$$
\stackrel{k}{\rightharpoonup} \text { CRISPeasy } \stackrel{\delta}{\rightharpoonup}
$$

where $k$ is the vector replication rate and $\delta$ its degradation rate. The degradation of Arabinose and IPTG as well as the production of Cas9 protein controled by Arabinose, Recombinase A protein controled by IPTG and sgRNA is expressed as

$$
\begin{aligned}
& \text { Arabinose } \xrightarrow{\delta_{\text {Arabinose }}} \\
& I P T G \xrightarrow{\delta_{I P T G}} \\
& \text { Cas } 9^{\prime}+\text { Arabinose } \xrightarrow{k_{\text {Cas } 9}} \operatorname{Cas} 9 \xrightarrow{\delta_{\text {Cas } 9}} \\
& \operatorname{Rec} A^{\prime}+I P T G \xrightarrow{k_{\text {RecA }}} \operatorname{Rec} A \xrightarrow{\delta_{\text {RecA }}} \\
& \operatorname{sgRN} A^{\prime} \xrightarrow{k_{s g R N A}} \operatorname{sgRNA} \xrightarrow{\delta_{s g R N A}}
\end{aligned}
$$

where $\operatorname{Cas} 9^{\prime}, \operatorname{Rec} A^{\prime}$ and $\operatorname{sgRN} A^{\prime}$ are DNA concentration of the respective proteins, $k_{C a s 9}, k_{\text {RecA }}$ are the translation plus the transcription rates and $k_{s g R N A}$ is the transcription rate. Also, we denote $\delta_{\text {Arabinose }}, \delta_{I P T G}, \delta_{C a s 9}, \delta_{\text {RecA }}$ and $\delta_{s g R N A}$ as the rates of degradation of each one of the organisms.

The protein Cas9 binds with $\operatorname{sgRNA}$ to form the complex $C_{1}$.

$$
C a s 9+s g R N A \xrightarrow{k_{1}} C_{1}
$$

The complex $C_{1}$ diffuses to the target site for the cleavage. Denote the complex formed by $C_{1}$ with the $g D N A$ as $C_{2}$, and $g D N A^{*}$ as the cleaved $g D N A$.

$$
C_{1}+g D N A \underset{k_{-2}}{\stackrel{k_{2}}{\rightleftharpoons}} C_{2} \stackrel{k_{*}}{\rightleftharpoons} g D N A^{*}
$$

Denote $g D N A^{* *}$ as the $g D N A$ cleaved and partially digested forming sticky ends due to RecBCD. Where $C_{3}$ is the intermediate complex formed by RecBCD and $g D N A^{*}$.

$$
g D N A^{*}+\operatorname{Rec} B C D \xrightarrow{k_{3}} C_{3} \xrightarrow{k_{* *}} g D N A^{* *}+\operatorname{Rec} B C D
$$

Recombinase A protein joins the sticky ends of $g D N A$ to form the complex $C_{4}$.

$$
g D N A^{* *}+\operatorname{Rec} A \xrightarrow{k_{4}} C_{4}
$$

The complex $C_{4}$ joins the CRISPeasy vector to form the complex $C_{5}$ and seeks for homology. When homology is found, DNA Polymerase joins $C_{5}$ and
fills the empty space. We will note $g D N A_{\#}$ as the genomic DNA repaired with the rfp gene inserted.

$$
C_{4}+C R I S P e a s y \stackrel{k_{5}}{\longrightarrow} C_{5} \xrightarrow{k_{\#}} g D N A_{\#}+\operatorname{Rec} A+C R I S P_{\text {easy }}
$$

### 1.2 Differential equations

We want to model the variation of modified genomic DNA, ie. with rfp gene inserted, which we denoted as $g D N A_{\#}$. Using the Law of mass action we can deduce from the reaction diagrams the following systems of differential equations govering the system.

- $\frac{d[\operatorname{Cas} 9]}{d t}=k_{C a s 9}\left[\right.$ Cas $\left.9^{\prime}\right][$ Arabinose $]-\delta_{\text {Cas9 }}[$ Cas 9$]-k_{1}[$ Cas 9$][\operatorname{sgR} N A]$
- $\frac{d[\text { Arabinose }]}{d t}=-\delta_{\text {Arabinose }}[$ Arabinose $]-k_{\text {Cas } 9}\left[\right.$ Cas $\left.9^{\prime}\right][$ Arabinose $]$
- $\frac{d[s g R N A]}{d t}=k_{s g R N A}\left[s g R N A^{\prime}\right]-\delta_{s g R N A}[s g R N A]-k_{1}[C a s 9][s g R N A]$
- $\frac{d[\operatorname{Rec} A]}{d t}=k_{\operatorname{Rec} A}\left[\operatorname{Rec} A^{\prime}\right][I P T G]-\delta_{\operatorname{Rec} A}[\operatorname{Rec} A]-k_{4}[\operatorname{Rec} A]\left[g D N A^{* *}\right]+$
- $\frac{d[I P T G]}{d t}=-k_{R e c A}[I P T G]\left[\operatorname{Rec} A^{\prime}\right]-\delta_{I P T G}[I P T G]$
- $\frac{d\left[C_{1}\right]}{d t}=k_{1}[\operatorname{Cas} 9][\operatorname{sgRNA}]+k_{-2}\left[C_{2}\right]-k_{2}\left[C_{1}\right][g D N A]$
- $\frac{d\left[C_{2}\right]}{d t}=k_{2}\left[C_{1}\right][g D N A]-k_{-2}\left[C_{2}\right]-k_{*}\left[C_{2}\right]$
- $\frac{d\left[g D N A^{*}\right]}{d t}=k_{*}\left[C_{2}\right]-k_{3}\left[g D N A^{*}\right][\operatorname{Rec} B C D]$
- $\frac{d\left[C_{3}\right]}{d t}=k_{3}\left[g D N A^{*}\right][\operatorname{Rec} B C D]-k_{* *}\left[C_{3}\right]$
- $\frac{d\left[g D N A^{* *}\right]}{d t}=k_{* *}\left[C_{3}\right]-k_{4}\left[g D N A^{* *}\right][\operatorname{Rec} A]$
- $\frac{d\left[C_{4}\right]}{d t}=k_{4}\left[g D N A^{* *}\right][\operatorname{Rec} A]-k_{5}\left[C_{4}\right][$ CRISPeasy $]$
- $\frac{d\left[C_{5}\right]}{d t}=k_{5}\left[C_{4}\right][$ CRISPeasy $]-k_{\#}\left[C_{5}\right]$
- $\frac{d\left[g D N A_{\#}\right]}{d t}=k_{\#}\left[C_{5}\right]$

