# CRISPR-BETS

*Release 1.0.0*

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ONE

# INTRODUCTION

CRISPR-BETS (CRISPR-Base Editing To Stop codon) is developed for designing gRNA to knockout gene by CRISPR base editing system. CRISPR-BETS has both online and desktop version, which are integrated into a user-friendly graphic user interface (GUI) and compatible with major operating systems (Windows, MacOS, Linux). Guide RNAs can be designed easily without any environment installation. Users can complete the analysis with a simple mouse click. Results will display with detailed information and fancy images, which are able to be downloaded. Moreover, CRISPR-BETS allows instant check the gRNA specificity.

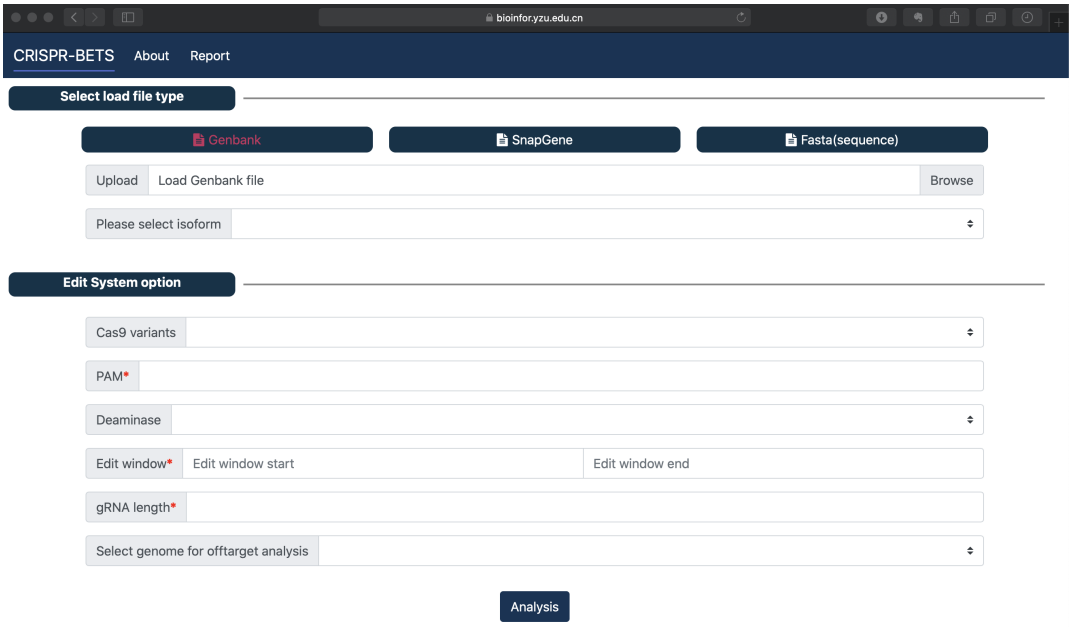
CHAPTER

TWO

# DOWNLOAD AND INSTALLATION

## 2.1 CRISPR-BETS Web online version

- Please visit http://bioinfor.yzu.edu.cn/crisprbets/




## 2.2 CRISPR-BETS Desktop version

- **Install via precompiled file(recommend)**
  - **1. Download CRISPR-BETS precompiled file**

    Download Win Version.

    Download macOS Version.

Download Linux Version.

### – 2. Installation

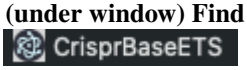
CRISPR-BETS Desktop version was written in javascript on the Electron framework, so there is no need to install other dependencies and complicated installation process, just unzip it!

**1. Unzip the downloaded compressed file.**

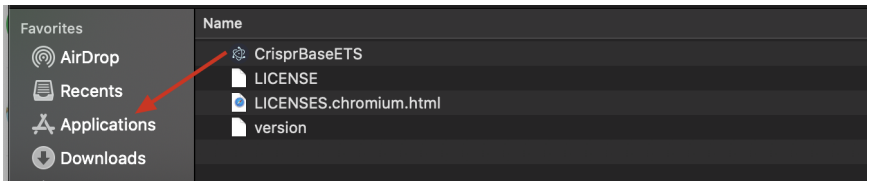
**2. Enter the Unziped file directory.**

> **Attention:** Step 3 is different for different operating systems.

**3. (under window) Find the CRISPR-BETS icon and double-click it.**




**3 (under macOS) Find the CRISPR-BETS icon and drag it to Applications folder, Open the terminal and enter the following command.**

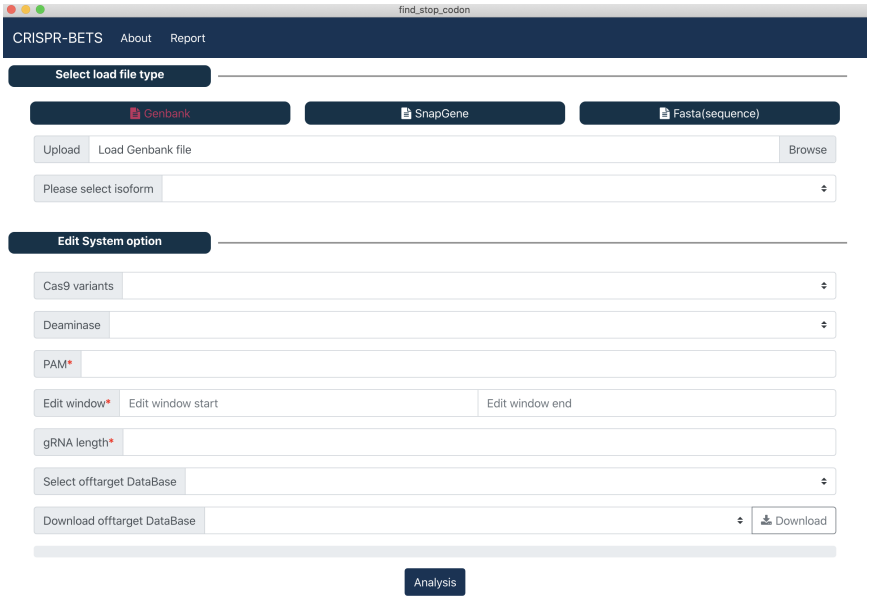



```
sudo xattr -d com.apple.quarantine  /Applications/
↪CrisprBaseETS.app
```

**3 (under Linux) Open the terminal and enter the following command.**

```
THE CRISPR-BETS unzipped directory/CRISPR-BETS
```

**4. Show main window, Done**




- **Install via source code**

```
git clone https://github.com/zhangtaolab/CRISPR-BETS_desktop.git
cd CRISPR-BETS_desktop
npm install electron@11.2.0 -g
npm install
electron .
```

CHAPTER

THREE

# TUTORIAL TO DESIGN GRNA FOR CRISPR BASE EDITING KNOCKOUT SYSTEM.

## 3.1 Step 1: Prepare input file

CRISPR-BETS allows **Genbank**, **Snapgene**, **Fasta** file formats as input.

1. **Genbank** The GenBank format for most genes can be downloaded from NCBI(https://www.ncbi.nlm.nih.gov/).

   Download `Genbank example file`.

2. **Snapgene** For Snapgene file(.dna), CRISRP-BETS uses a continuous CDS feature to determine the coding sequence of the gene, and different continuous CDS features serve as different isoforms. Snapgene file(.dna) could be generated by SnapGene software (from Insightful Science; available at https://www.snapgene.com/).

   Download `Snapgene example file`.

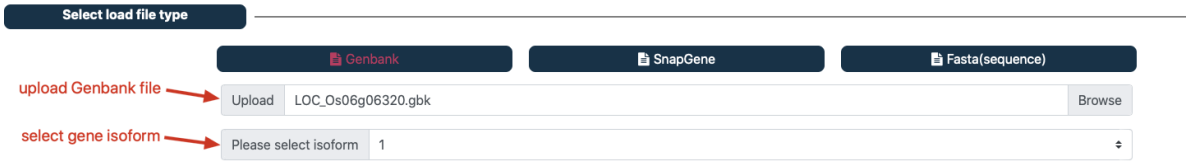
3. **Fasta** The CRISPR-BETS will use exonerate(https://www.ebi.ac.uk/about/vertebrate-genomics/software/exonerate) align CDS sequence to DNA sequence to found Splicing site.

   Download `DNA Fasta example file`. Download `CDS Fasta example file`

## 3.2 Step 2: Select and upload file

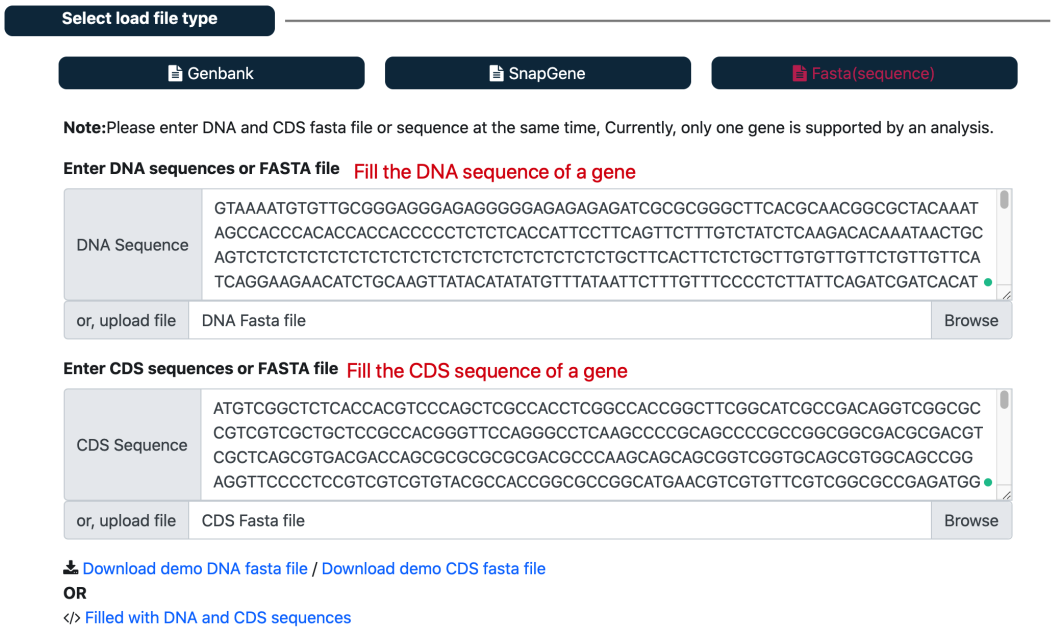
### 3.2.1 upload GenBank or Snapgene file

1. Navigate to the **'Select load file type'** panel. click 'GenBank' button (GenBank is the default input file).
2. Upload the GenBank files.
3. Select gene isoform (support for Genbank and Snapgene file).



### 3.2.2 upload fasta file or sequences

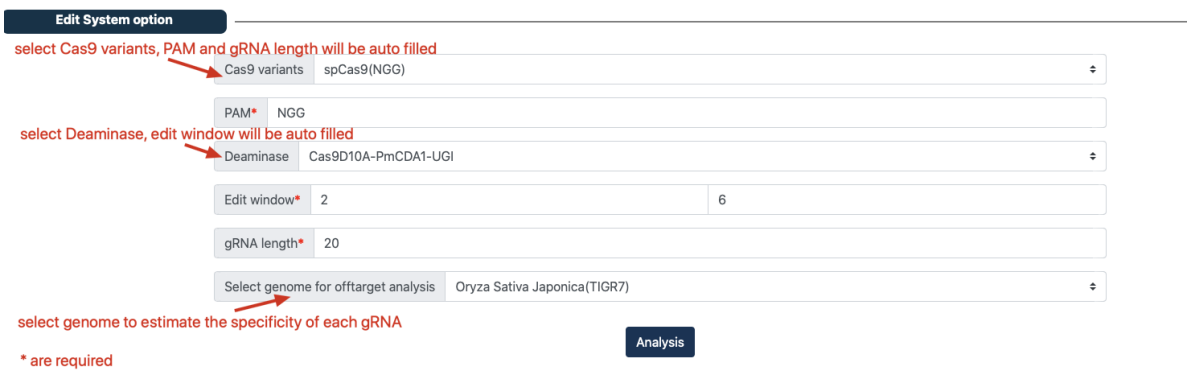
1. Navigate to the **'Select load file type'** panel. click 'Fasta(sequence)' button
2. Fill the text box with both the DNA and CDS sequences of a gene.




**NOTE:In order to design cross-CDS gRNA, enter both DNA and CDS FASTA files or sequences. Currently, only one gene is supported by an analysis.**

## 3.3 Step 3: Select edit system option

1. Navigate to the **'Edit system option'** panel.
2. (optional) Select **'Cas9 variants'**, **'PAM'** and **'gRNA length'** will be automatically filled.
3. (optional) Select **'Deaminase'**, **'Edit window'** will be automatically filled.
4. The user fill **'PAM'**, **'gRNA length'** and **'Edit window'**.
5. (optional) The user select genome to estimate the specificity of each gRNA.
6. Click the **'Analysis'** button and wait for the analysis to complete.



### 3.3.1 Parameter description

**1. Cas9 variants:** Select the appropriate Cas9 variant. Once selected, the parameters **PAM** and **gRNA length** will be filled in automatically, not required.

**2. PAM:** The default value is NGG, which can be customized, required.

**3. Edit window:** The default values are 1 and 20 (The farthest first base of PAM is represented as a 1), which can be customized, required.

**4. gRNA length:** The default value is 20, which can be customized, required.

**5. Select genome for offtarget analysis:** Select species genome for off-target analysis, this step will increase the running time of CRISPR-BETS, not required.

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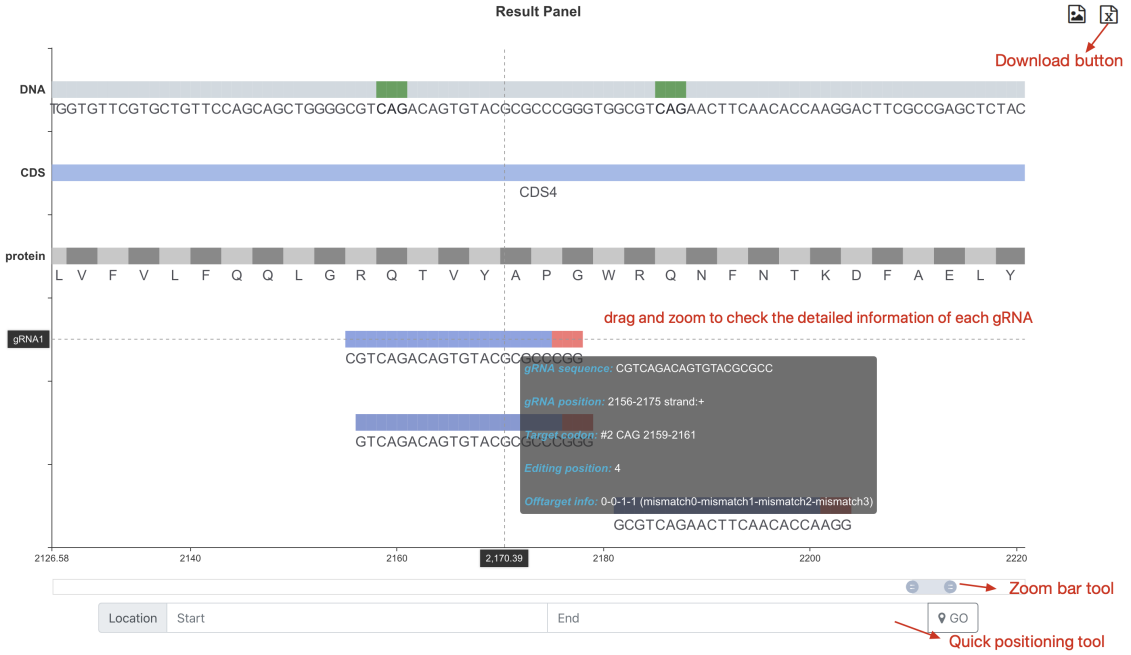
## 3.4 Step 4: Scanning result panel and download result information

1. Navigate to the 'result panel', the user can drag and zoom to check the detailed information of each gRNA.
2. Click 'save result as txt' button to download result.




### 3.4.1 The following two functional buttons exist in the upper right corner of the results panel

**Screenshot:** Take a screenshot of the current page.

**save result as file:** Take a screenshot of the current page.

### 3.4.2 Output result description

**The first row:** Target gene name, determined according to the uploaded file name.

| | | |
|---|---|---|
| 1 | target gene | OsCenh3-1.gb |

**The second row:** Edit system option.

| | | |
|---|---|---|
| 2 | Edit System option | Cas9 variants:SpCas9-NGG |

**The third row:** Gene DNA sequences.

| | | |
|---|---|---|
| 3 | gene DNA sequence | CAAAACCAAGGGCCTAACCGCAAA |

**The fourth row:** The position of CDS in DNA.

| | | |
|---|---|---|
| 4 | gene CDS position | CDS1:141-246 |

**Row five to the last:** Each target codon and its corresponding gRNA, different information is separated by ';'.

| target codon info | gRNA info |
|---|---|
| target codon:CAG;<br>target codon ID:#1;<br>position in DNA:200-203 | position in DNA:198-218;<br>sequence:TCCAGTTCGAACGCTCCCCT;<br>PAM:CGG;<br>strand:+;<br>target_codon:#1;<br>Cytosine to be edited in gRNA position:3;<br>offtarget_info:0-0-0-0(mismatch0-mismatch1-mismatch2-mismatch3) |

## 3.5 Video tutorials

YouTube (EN).

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CHAPTER

FOUR

# INDICES AND TABLES

- genindex
- modindex
- search