

CRISPR Informatics Course

Design and in silico analysis of CRISPR Base Editors gRNAs

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We will go through:

- i. Brief repetition of Base Editors
- ii. Guide RNA and its components
- iii. Designing and annotating gRNAs with BEstimate
- iv. Practical session

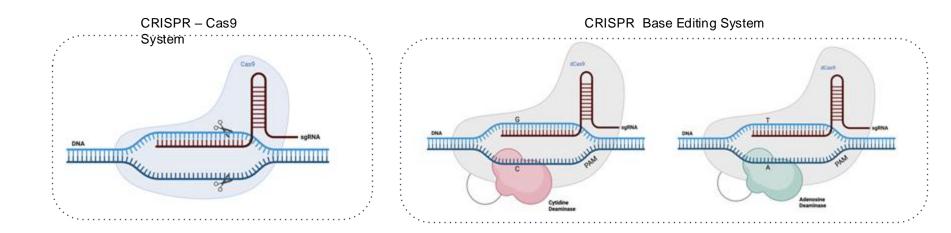
After this session, you can be able to:

→ Design and filter Base Editor gRNA for the experiments of interest





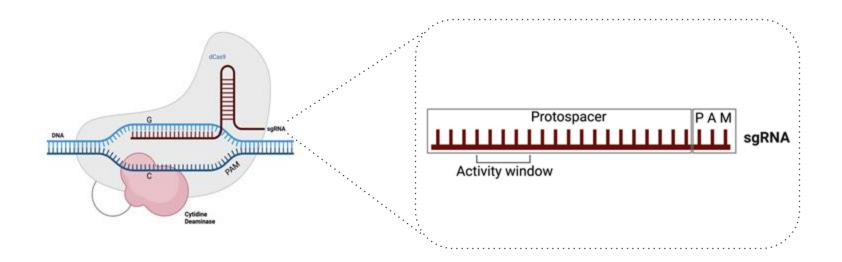
CRISPR Base Editors







CRISPR Base Editors and gRNA



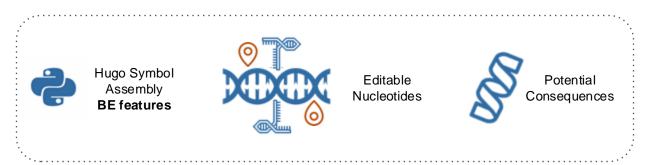




BEstimate

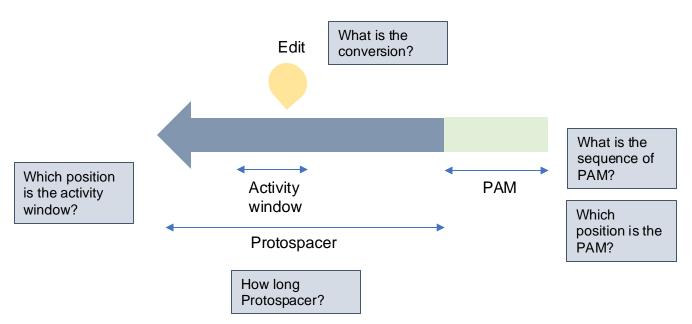
A python tool which systematically:

- Searches gRNA targetable sites across given genes for given Base Editors
- Analyses functional, structural and clinical effects of the potential edits





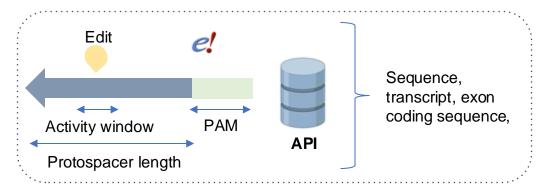








Step – 1 : Finding the gRNAs









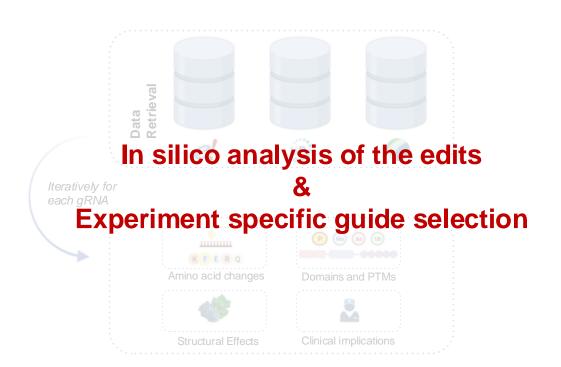
Step – 1 : Finding the gRNAs on <u>mutated genes</u>





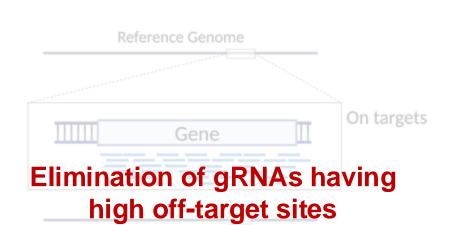


Step – 2 : gRNA Annotation





Step – 3 : Off-target Annotation











Other tools to discover

- > PnB Designer: gRNA design for DNA sequences and variants
- > beditor: gRNA design for variants
- > <u>BE-Designer</u>: gRNA design for sequences
- > <u>SNP-CRISPR</u>: gRNA design for variants
- > <u>BE-FF</u>: gRNA design for variants
- > <u>crisprVerse</u>: gRNA design for DNA sequences





Base Editor Efficiency

JOURNAL ARTICLE

Predicting base editing outcomes using positionspecific sequence determinants 8

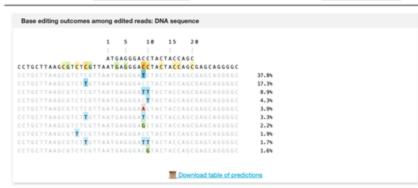
Ananth Pallaseni, Elin Madli Peets, Jonas Koeppel, Juliane Weller, Thomas Vanderstichele, Uyen Linh Ho, Luca Crepaldi, Jolanda van Leeuwen Felicity Allen, Leopold Parts

▲ Author Notes

FORECasT-BE for gRNA efficiency

BE-Hive for gRNA efficiency







- > Download and install BEstimate
- > Prepare the environment
- > How to run it
- > Examine the output files

