




Sep 06, 2022

CRISPResso analysis

 In 1 collectionHanqin Li¹, Yogendra Verma¹, Dirk Hockemeyer¹, Frank Soldner²¹University of California, Berkeley; ²Albert Einstein College of Medicine1 *Works for me* Sharedx.doi.org/10.17504/protocols.io.b4nxqvfn

Devin E Snyder

ABSTRACT

This protocol describes the process of using CRISPResso to analyze Next Generation Sequencing (NGS) data from CRISPR-targeted, genome-edited samples.

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PROTOCOL CITATION

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COLLECTIONS

**Genotyping by next generation sequencing**

KEYWORDS

ASAPCRN

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PARENT PROTOCOLS

Part of collection

[Genotyping by next generation sequencing](#)

- 1 Install CRISPResso2
- 2 In linux, use the following command:


```
CRISPResso --fastq_r1 R1_reads.fastq.gz --fastq_r2 R2_reads.fastq.gz --amplicon_seq  
amplicon_sequence_here -g sgRNA_sequence_here
```
- 3 Use CRISPRessoBatch command if having many samples
- 4 For more details, <https://github.com/pinellolab/CRISPResso2>

Clement K, Rees H, Canver MC, Gehrke JM, Farouni R, Hsu JY, Cole MA, Liu DR, Joung JK, Bauer DE, Pinello L (2019). CRISPResso2 provides accurate and rapid genome editing sequence analysis.. Nature biotechnology.
<https://doi.org/10.1038/s41587-019-0032-3>