

Resource Summary Report

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CRISPResso2

RRID:SCR_024503

Type: Tool

Proper Citation

CRISPResso2 (RRID:SCR_024503)

Resource Information

URL: <https://github.com/pinellolab/CRISPResso2>

Proper Citation: CRISPResso2 (RRID:SCR_024503)

Description: Software pipeline designed to enable rapid and intuitive interpretation of genome editing experiments. Used for analysis of deep sequencing data for rapid and intuitive interpretation of genome editing experiments.

Resource Type: software application, software resource, data analysis software, data processing software

Keywords: sequencing data analysis, genome editing experiments interpretation,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CRISPResso2

Resource ID: SCR_024503

License URLs: <https://github.com/pinellolab/CRISPResso2/blob/master/LICENSE.txt>

Record Creation Time: 20231002T161336+0000

Record Last Update: 20250519T204440+0000

Ratings and Alerts

No rating or validation information has been found for CRISPResso2.

No alerts have been found for CRISPResso2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Sousa AA, et al. (2025) Systematic optimization of prime editing for the efficient functional correction of CFTR F508del in human airway epithelial cells. *Nature biomedical engineering*, 9(1), 7.

Pandey S, et al. (2025) Efficient site-specific integration of large genes in mammalian cells via continuously evolved recombinases and prime editing. *Nature biomedical engineering*, 9(1), 22.

Kato-Inui T, et al. (2024) Fusion of histone variants to Cas9 suppresses non-homologous end joining. *PloS one*, 19(5), e0288578.

Bick NR, et al. (2024) Engineered bacterial lipoyl transferase A (lplA) restores lipoylation in cell models of lipoylation deficiency. *The Journal of biological chemistry*, 300(12), 107995.

Davis JR, et al. (2024) Efficient prime editing in mouse brain, liver and heart with dual AAVs. *Nature biotechnology*, 42(2), 253.

Yang Q, et al. (2024) T4 DNA polymerase prevents deleterious on-target DNA damage and enhances precise CRISPR editing. *The EMBO journal*, 43(17), 3733.

An M, et al. (2024) Engineered virus-like particles for transient delivery of prime editor ribonucleoprotein complexes in vivo. *Nature biotechnology*, 42(10), 1526.

Husser MC, et al. (2024) Endogenous tagging using split mNeonGreen in human iPSCs for live imaging studies. *eLife*, 12.

Singh K, et al. (2024) Comprehensive analysis of off-target and on-target effects resulting from liver-directed CRISPR-Cas9-mediated gene targeting with AAV vectors. *Molecular therapy. Methods & clinical development*, 32(4), 101365.

Wei SC, et al. (2024) Evaluation of subretinally delivered Cas9 ribonucleoproteins in murine and porcine animal models highlights key considerations for therapeutic translation of genetic medicines. *bioRxiv : the preprint server for biology*.

Cheng P, et al. (2024) Zero-shot prediction of mutation effects with multimodal deep representation learning guides protein engineering. *Cell research*, 34(9), 630.

Chen K, et al. (2024) Engineering self-deliverable ribonucleoproteins for genome editing in the brain. *Nature communications*, 15(1), 1727.

Jang W, et al. (2024) Visualization of endogenous G proteins on endosomes and other organelles. *eLife*, 13.

Zhao L, et al. (2023) PAM-flexible genome editing with an engineered chimeric Cas9. *Nature communications*, 14(1), 6175.

Quan ZJ, et al. (2023) GREPore-seq: A Robust Workflow to Detect Changes After Gene Editing Through Long-range PCR and Nanopore Sequencing. *Genomics, proteomics & bioinformatics*, 21(6), 1221.

Doman JL, et al. (2023) Phage-assisted evolution and protein engineering yield compact, efficient prime editors. *Cell*, 186(18), 3983.

Kulhankova K, et al. (2023) Shuttle peptide delivers base editor RNPs to rhesus monkey airway epithelial cells in vivo. *Nature communications*, 14(1), 8051.

Liu Y, et al. (2023) Adenine base editor-mediated splicing remodeling activates noncanonical splice sites. *The Journal of biological chemistry*, 299(12), 105442.

Zhou X, et al. (2023) ProRefiner: an entropy-based refining strategy for inverse protein folding with global graph attention. *Nature communications*, 14(1), 7434.

Zeng H, et al. (2023) A split and inducible adenine base editor for precise in vivo base editing. *Nature communications*, 14(1), 5573.