Resource Summary Report

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CRISPResso

RRID:SCR_021538
Type: Tool

Proper Citation

CRISPResso (RRID:SCR_021538)

Resource Information

URL: https://crispresso.pinellolab.partners.org/submission

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Description: Software suite of tools to qualitatively and quantitatively evaluate outcomes of genome editing experiments in which target loci are subject to deep sequencing and provides integrated, user friendly interface. Used for analysis of CRISPR-Cas9 genome editing outcomes from sequencing data. CRISPResso2 provides accurate and rapid genome editing sequence analysis.Used for analysis of deep sequencing data for rapid and intuitive interpretation of genome editing experiments.

Synonyms: CRISPResso2

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

Defining Citation: PMID:27404874, PMID:30809026

Keywords: Quantification, visualization, CRISPR-Cas9 outcomes, coding sequences evaluation, noncoding elements evaluation, selected off target sites evaluation, genome editing evaluation.

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NHLBI P01 HL32262;
NHLBI R01 HL119099;
NIBIB R01 EB022376;
NIDDK P30 DK049216;
NIDDK R03 DK109232;
NIGMS R35 GM118062;
NIGMS R35 GM118158

Availability: Free, Available for download, Freely available

Resource Name: CRISPResso

Resource ID: SCR_021538

Alternate URLs: https://github.com/pinellolab/CRISPResso2, https://github.com/pinellolab/CRISPResso

Record Creation Time: 20220129T080356+0000

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Ratings and Alerts

No rating or validation information has been found for CRISPResso.

No alerts have been found for CRISPResso.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Kabra M, et al. (2026) Synonymous editing alters ion channel function, favoring prime editing for retinal disease correction. International journal of biological sciences, 22(9), 4670.

Fenoglio S, et al. (2026) Temporal control of sgRNA library activation unlocks large-scale in vivo CRISPR screens. Cell reports methods, 6(7), 101470.

Wang Q, et al. (2025) PAM-readID is a rapid, simple, and accurate PAM determination method for CRISPR-Cas enzymes in mammalian cells. Communications biology, 8(1), 1601.

De Angeli P, et al. (2025) Single-guide RNA Cas9 and enhanced-deletion Cas9 rescue a recurrent USH2A-related splicing defect. Molecular therapy. Nucleic acids, 36(2), 102523.

Regan SB, et al. (2025) Megabase-scale loss of heterozygosity provoked by CRISPR-Cas9 DNA double-strand breaks. Molecular cell, 85(22), 4119.

Fregona V, et al. (2024) Stem cell-like reprogramming is required for leukemia-initiating activity in B-ALL. The Journal of experimental medicine, 221(1).

Wu Y, et al. (2024) Robust and inducible genome editing via an all-in-one prime editor in human pluripotent stem cells. Nature communications, 15(1), 10824.

Green AC, et al. (2023) Formate overflow drives toxic folate trapping in MTHFD1 inhibited cancer cells. Nature metabolism, 5(4), 642.

Li C, et al. (2023) Computational Tools and Resources for CRISPR/Cas Genome Editing. Genomics, proteomics & bioinformatics, 21(1), 108.

González-Romero E, et al. (2023) PCR-Based Strategy for Introducing CRISPR/Cas9 Machinery into Hematopoietic Cell Lines. Cancers, 15(17).

Ronson GE, et al. (2023) Mechanisms of synthetic lethality between BRCA1/2 and 53BP1 deficiencies and DNA polymerase theta targeting. Nature communications, 14(1), 7834.

Cervia LD, et al. (2023) A Ubiquitination Cascade Regulating the Integrated Stress Response and Survival in Carcinomas. Cancer discovery, 13(3), 766.

Zou K, et al. (2023) Optimized CRISPR/Cas9 system for gene knockout in chicken DF1 cells. Poultry science, 102(10), 102970.

Wu Y, et al. (2023) Protocol for the design, conduct, and evaluation of prime editing in human pluripotent stem cells. STAR protocols, 4(4), 102583.

Nitschke NJ, et al. (2023) Frequency and Functional Characterization of RUNX1 Germline Variants in Myeloid Neoplasms. Human mutation, 2023, 4738660.

Niu Y, et al. (2022) Multiparametric and accurate functional analysis of genetic sequence variants using CRISPR-Select. Nature genetics, 54(12), 1983.

Bernard BE, et al. (2022) CRISPR/Cas-based Human T cell Engineering: Basic Research and Clinical Application. Immunology letters, 245, 18.

Tsuchida CA, et al. (2022) Chimeric CRISPR-CasX enzymes and guide RNAs for improved genome editing activity. Molecular cell, 82(6), 1199.

Salonia F, et al. (2022) A dual sgRNA-directed CRISPR/Cas9 construct for editing the fruit-specific ?-cyclase 2 gene in pigmented citrus fruits. Frontiers in plant science, 13, 975917.

Barneda D, et al. (2022) Acyl chain selection couples the consumption and synthesis of phosphoinositides. The EMBO journal, 41(18), e110038.