

Resource Summary Report

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REDIttools

RRID:SCR_012133

Type: Tool

Proper Citation

REDIttools (RRID:SCR_012133)

Resource Information

URL: <https://code.google.com/p/reditools/>

Proper Citation: REDIttools (RRID:SCR_012133)

Description: A suite of python scripts to perform high-throughput investigation of RNA editing using next-generation sequencing data.

Resource Type: software resource

Defining Citation: [PMID:23742983](#)

Keywords: standalone software, illumina, roche, pacific biosciences, life technologies, python, bio.tools

Availability: MIT License

Resource Name: REDIttools

Resource ID: SCR_012133

Alternate IDs: biotools:reditools, OMICS_05860

Alternate URLs: <https://bio.tools/reditools>

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260815T182446+0000

Ratings and Alerts

No rating or validation information has been found for REDIttools.

No alerts have been found for REDIttools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 152 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Yang M, et al. (2026) KnockRBP: an integrated multi-omics database of functional perturbation profiles for RNA-binding proteins. *Nucleic acids research*, 54(D1), D1174.

Cao Q, et al. (2026) Dynamic and extensive A-to-I RNA recoding in immunoglobulin shapes myeloid neoplasm transcriptome. *The Journal of biological chemistry*, 302(2), 111066.

Yi Y, et al. (2026) A dual role of EZH2 in regulating A-to-I RNA editing and mRNA stability through ADAR. *Nature communications*, 17(1).

Kockler ZW, et al. (2026) APOBEC3A is the predominant global editor of cytosines in human mRNAs and in single-strand RNA viruses. *bioRxiv : the preprint server for biology*.

Wang J, et al. (2026) Sensitive monitoring of enhancer and noncoding RNA transcription via ribozyme-assisted RNA editing. *Nature communications*, 17(1).

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(17), e18238.

Nepal C, et al. (2026) Epigenomic, transcriptomic, and proteomic characterization of breast cancer cell line reference samples. *Cell reports methods*, 6(1), 101276.

Fonzino A, et al. (2026) Ab initio detection of multiple epitranscriptomic modifications from Oxford nanopore technology direct RNA sequencing data. *Briefings in bioinformatics*, 27(1).

Liu C, et al. (2026) Exogenous Epstein-Barr virus nuclear antigen 1 induces ADAR1-driven tumor resistance against immunotherapy. *Signal transduction and targeted therapy*, 11(1), 63.

Mitchell L, et al. (2026) Differential A-to-I editing of SINE B2 RNAs unveils an epitranscriptome response to A?? neurotoxicity. *Life science alliance*, 9(9).

Joore IP, et al. (2025) Correction of pathogenic mitochondrial DNA in patient-derived disease models using mitochondrial base editors. *PLoS biology*, 23(6), e3003207.

Mustfa SA, et al. (2025) Porous Silicon Nanoneedles Efficiently Deliver Adenine Base Editor to Correct a Recurrent Pathogenic COL7A1 Variant in Recessive Dystrophic Epidermolysis Bullosa. *Advanced materials* (Deerfield Beach, Fla.), 37(17), e2414728.

Hao C, et al. (2025) An ADAR2-mimic base editor for efficient C-to-U RNA editing in vivo. *Proceedings of the National Academy of Sciences of the United States of America*, 122(45), e2505269122.

Cui J, et al. (2025) Mitochondrial Genome Insights into Evolution and Gene Regulation in *Phragmites australis*. *International journal of molecular sciences*, 26(2).

Cai W, et al. (2025) Mammary gland multi-omics data reveals new genetic insights into milk production traits in dairy cattle. *PLoS genetics*, 21(4), e1011675.

Qin W, et al. (2025) Rationally Designed TadA-Derived Cytosine Editors Enable Context-Independent Zebrafish Genome Editing. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(39), e09800.

Cheng AS, et al. (2025) In vivo base editing rescues ADPKD in a humanized mouse model. *Nature communications*, 16(1), 11212.

Duan Y, et al. (2025) Abundant A-to-I RNA editing in spermatocytes may suppress transposons to compensate for piRNA downregulation in male germlines. *RNA biology*, 22(1), 1.

Wang Y, et al. (2025) CircAI: a comprehensive database of CircRNA associated with A-to-I RNA editing. *Database : the journal of biological databases and curation*, 2025.

Xie Q, et al. (2025) Trans-generational maintenance of mitochondrial DNA integrity in oocytes during early folliculogenesis. *PLoS genetics*, 21(12), e1011562.