

Resource Summary Report

Generated by T1D on Aug 3, 2026

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: 20260801T190435+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 141 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

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.

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

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

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.

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

Xu P, et al. (2025) A loss-of-function human ADAR variant activates innate immune response and promotes bowel inflammation. *Nature communications*, 16(1), 8560.

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.

He Y, et al. (2025) RPS 2.0: an updated database of RNAs involved in liquid-liquid phase separation. *Nucleic acids research*, 53(D1), D299.

Zhu T, et al. (2025) Editome Disease Knowledgebase v2.0: an updated resource of editome-disease associations through literature curation and integrative analysis. *Bioinformatics advances*, 5(1), vbaf012.

Fonzino A, et al. (2025) REDInet: a temporal convolutional network-based classifier for A-to-I RNA editing detection harnessing million known events. *Briefings in bioinformatics*, 26(2).

Yang H, et al. (2025) Unveiling the mitochondrial genome of *Salvia splendens* insights into the evolutionary traits within the genus *Salvia*. *Scientific reports*, 15(1), 13344.

Lattuca R, et al. (2025) Systematic analysis of A-to-I RNA editing upon release of ADAR from the nucleolus. *RNA biology*, 22(1), 1.

Zhang Y, et al. (2025) DirectRM: integrated detection of landscape and crosstalk between multiple RNA modifications using direct RNA sequencing. *Nature communications*, 16(1), 9450.

Zhang S, et al. (2025) Comparative genomics uncovers organellar genome structural divergence in Caryophyllales and reveals widespread non-coding transcription in *Bougainvillea glabra* organellar. *BMC genomics*, 26(1), 722.

Yabuki A, et al. (2025) Massive RNA Editing in Ascetosporean Mitochondria. *Microbes and environments*, 40(1).

Qin PP, et al. (2025) Programming ADAR-recruiting hairpin RNA sensor to detect endogenous molecules. *Nucleic acids research*, 53(1).

Nesta A, et al. (2025) Alternative splicing of transposable elements in human breast cancer. *Mobile DNA*, 16(1), 6.