

Resource Summary Report

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SAFA Footprinting Software

RRID:SCR_002707

Type: Tool

Proper Citation

SAFA Footprinting Software (RRID:SCR_002707)

Resource Information

URL: <https://simtk.org/home/safa>

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Description: A software package that analyzes the structural details of RNA molecules through rapid quantification of a footprinting gel. By automating many of the steps involved in gel analysis, approximately one entire gel with thousands of bands can be quantified in less than 10 minutes using SAFA. In general, all the automated features have a manual override, such that even difficult or exceptional gels can be analyzed with the package.

Abbreviations: SAFA

Synonyms: Semi-Automated Footprinting Analysis Software

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

Defining Citation: [PMID:15701734](#), [PMID:18772866](#)

Keywords: footprint, gel, data analysis, software, RNA, RNA folding, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SAFA Footprinting Software

Resource ID: SCR_002707

Alternate IDs: nif-0000-23336, biotools:safa

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

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260728T043133+0000

Ratings and Alerts

No rating or validation information has been found for SAFA Footprinting Software.

No alerts have been found for SAFA Footprinting Software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Wierzbaj AJ, et al. (2025) Unveiling the promise of peptide nucleic acids as functional linkers for an RNA imaging platform. RSC chemical biology, 6(2), 249.

Siwik SH, et al. (2025) Structural basis for ring-opening fluorescence by the RhoBAST RNA aptamer. Nucleic acids research, 53(12).

Perez-Lombardini F, et al. (2021) Assessing Sustainability in Cattle Silvopastoral Systems in the Mexican Tropics Using the SAFA Framework. Animals : an open access journal from MDPI, 11(1).

Stewart H, et al. (2016) Identification of novel RNA secondary structures within the hepatitis C virus genome reveals a cooperative involvement in genome packaging. Scientific reports, 6, 22952.

Ge P, et al. (2015) Computational analysis of RNA structures with chemical probing data. Methods (San Diego, Calif.), 79-80, 60.

Ranpura H, et al. (2014) Finding and characterizing the complexes of drug like molecules with quadruplex DNA: combined use of an enhanced hydroxyl radical cleavage protocol and NMR. PloS one, 9(4), e96218.

Gilmour DS, et al. (2009) Detecting transcriptionally engaged RNA polymerase in eukaryotic cells with permanganate genomic footprinting. Methods (San Diego, Calif.), 48(4), 368.

Wang JX, et al. (2008) Riboswitches that sense S-adenosylhomocysteine and activate genes involved in coenzyme recycling. Molecular cell, 29(6), 691.