

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Random DNA Sequence Generator

RRID:SCR_018768

Type: Tool

Proper Citation

Random DNA Sequence Generator (RRID:SCR_018768)

Resource Information

URL: <http://faculty.ucr.edu/~mmaduro/random.htm>

Proper Citation: Random DNA Sequence Generator (RRID:SCR_018768)

Description: Web application to generate random DNA sequences.

Resource Type: data access protocol, service resource, software resource, web service

Keywords: Random DNA, random DNA sequence, generate random DNA, sequence, generation

Availability: Free, Freely available

Resource Name: Random DNA Sequence Generator

Resource ID: SCR_018768

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260903T235517+0000

Ratings and Alerts

No rating or validation information has been found for Random DNA Sequence Generator.

No alerts have been found for Random DNA Sequence Generator.

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 [kravitz2](#) .

Clarke JE, et al. (2026) A platform for CRISPRi-seq in *Streptomyces albidoflavus*. *mBio*, 17(2), e0306525.

Wei L, et al. (2026) The landscape and regulatory potential of eccDNAs in mammalian preimplantation embryos. *Nature communications*, 17(1).

Wu N, et al. (2025) Extrachromosomal circular DNA expressing miRNA promotes ovarian cancer progression. *Clinical and translational medicine*, 15(9), e70445.

Ruehmkorff C, et al. (2025) In vivo pathway optimization in yeast via loxpsym-mediated shuffling of upstream activating sequences. *Nucleic acids research*, 53(17).

Cheng Z, et al. (2025) Comprehensive landscape and oncogenic role of extrachromosomal circular DNA in malignant biliary strictures. *Cell & bioscience*, 15(1), 16.

Shand EL, et al. (2024) Live-cell analysis of IMPDH protein levels during yeast colony growth provides insights into the regulation of GTP synthesis. *mBio*, 15(8), e0102124.

Kobo A, et al. (2024) Nonspecific N-terminal tetrapeptide insertions disrupt the translation arrest induced by ribosome-arresting peptide sequences. *The Journal of biological chemistry*, 300(6), 107360.

Lin Z, et al. (2024) Integrating Circle-Seq with transcriptomics reveals genome-wide characterization of extrachromosomal circular DNA for dilated cardiomyopathy. *Biology direct*, 19(1), 125.

Sharon JA, et al. (2023) Trumpet is an operating system for simple and robust cell-free biocomputing. *Nature communications*, 14(1), 2257.

Short AE, et al. (2023) Next generation synthetic memory via intercepting recombinase function. *Nature communications*, 14(1), 5255.

Jiang X, et al. (2023) Genome-wide characterization of extrachromosomal circular DNA in gastric cancer and its potential role in carcinogenesis and cancer progression. *Cellular and molecular life sciences : CMLS*, 80(7), 191.

Tomanek I, et al. (2022) Adaptation dynamics between copy-number and point mutations. *eLife*, 11.

Lambert M, et al. (2021) A New Specific and Sensitive RT-qPCR Method Based on Splinted 5' Ligation for the Quantitative Detection of RNA Species Shorter than microRNAs. *Non-coding RNA*, 7(3).

Hong SR, et al. (2021) Bisulfite-Converted DNA Quantity Evaluation: A Multiplex Quantitative Real-Time PCR System for Evaluation of Bisulfite Conversion. *Frontiers in genetics*, 12, 618955.

Wang Y, et al. (2021) eccDNAs are apoptotic products with high innate immunostimulatory activity. *Nature*, 599(7884), 308.

Lin Z, et al. (2021) Formation of artificial chromosomes in *Caenorhabditis elegans* and analyses of their segregation in mitosis, DNA sequence composition and holocentromere organization. *Nucleic acids research*, 49(16), 9174.

Jang WS, et al. (2020) Development of a multiplex isothermal amplification molecular diagnosis method for on-site diagnosis of influenza. *PloS one*, 15(9), e0238615.

Barra GB, et al. (2020) Analytical Sensitivity and Specificity of Two RT-qPCR Protocols for SARS-CoV-2 Detection Performed in an Automated Workflow. *Genes*, 11(10).

Schreiner S, et al. (2020) Design and application of circular RNAs with protein-sponge function. *Nucleic acids research*, 48(21), 12326.

Simko EAJ, et al. (2020) G-quadruplexes offer a conserved structural motif for NONO recruitment to NEAT1 architectural lncRNA. *Nucleic acids research*, 48(13), 7421.