

# Resource Summary Report

Generated by [ASWG](#) on Aug 4, 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:** web service, data access protocol, service resource, software resource

**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:** 20260804T043705+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 19 mentions in open access literature.

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

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.

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).

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.

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.

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).

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.

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

Van Orden MJ, et al. (2020) CRISPR type II-A subgroups exhibit phylogenetically distinct mechanisms for prespacer insertion. *The Journal of biological chemistry*, 295(32), 10956.

Hagey DW, et al. (2016) Distinct transcription factor complexes act on a permissive chromatin landscape to establish regionalized gene expression in CNS stem cells. *Genome research*, 26(7), 908.