Resource Summary Report

Generated by NIF on May 20, 2025

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, software resource, data access protocol, service resource

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

Funding:

Availability: Free, Freely available

Resource Name: Random DNA Sequence Generator

Resource ID: SCR_018768

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250519T204043+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 16 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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.

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).

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.