Resource Summary Report

Generated by NIF on May 19, 2025

GenomeCompiler

RRID:SCR_013988
Type: Tool

Proper Citation

GenomeCompiler (RRID:SCR_013988)

Resource Information

URL: http://www.genomecompiler.com

Proper Citation: GenomeCompiler (RRID:SCR_013988)

Description: A software platform which enables users to conduct genetic engineering with genomic manipulation tools (provided in the platform). Genome Compiler includes multiple DNA synthesis providers, lab facility services, and advanced bioinformatics tools and genetic repositories. Data can be imported from VectorNTI, SnapGene, ApE, Clone Manager, and others. The Gibson Assembly and Restriction Ligation methods are supported by Genome Compiler.

Resource Type: software application, data visualization software, data processing software, data management software, software resource, collaboration tool

Keywords: software application, genetic engineering, genomic maniplation, tool, data visualization, data management, collaboration, platform

Funding:

Availability: Free, Available to the research community

Resource Name: GenomeCompiler

Resource ID: SCR_013988

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250517T060122+0000

Ratings and Alerts

No rating or validation information has been found for GenomeCompiler.

No alerts have been found for GenomeCompiler.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Abou-Shaara HF, et al. (2021) Exploring the non-coding regions in the mtDNA of some honey bee species and subspecies. Saudi journal of biological sciences, 28(1), 204.

McLean T, et al. (2020) Inactivated tetanus as an immunological smokescreen: A major step towards harnessing tetanus-based therapeutics. Molecular immunology, 127, 164.

Razmara E, et al. (2020) Whole-exome sequencing identified a novel variant in an Iranian patient affected by pycnodysostosis. Molecular genetics & genomic medicine, 8(3), e1118.

Ramesh T, et al. (2019) Gold-Hybridized Zinc Oxide Nanorods as Real-Time Low-Cost NanoBiosensors for Detection of virulent DNA signature of HPV-16 in Cervical Carcinoma. Scientific reports, 9(1), 17039.

Bruzzese DJ, et al. (2019) Phylogeny, host use, and diversification in the moth family Momphidae (Lepidoptera: Gelechioidea). PloS one, 14(6), e0207833.

Razmara E, et al. (2018) Whole-exome sequencing identifies R1279X of MYH6 gene to be associated with congenital heart disease. BMC cardiovascular disorders, 18(1), 137.

Wang WB, et al. (2018) Identification of a novel mutation of the NTRK1 gene in patients with congenital insensitivity to pain with anhidrosis (CIPA). Gene, 679, 253.

Guo CJ, et al. (2017) Discovery of Reactive Microbiota-Derived Metabolites that Inhibit Host Proteases. Cell, 168(3), 517.

Carbonell P, et al. (2016) Bioinformatics for the synthetic biology of natural products: integrating across the Design-Build-Test cycle. Natural product reports, 33(8), 925.

Kahl LJ, et al. (2013) A survey of enabling technologies in synthetic biology. Journal of biological engineering, 7(1), 13.