

Resource Summary Report

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Gentle

RRID:SCR_016127

Type: Tool

Proper Citation

Gentle (RRID:SCR_016127)

Resource Information

URL: <http://gentle.magnusmanske.de>

Proper Citation: Gentle (RRID:SCR_016127)

Description: Software for DNA and amino acid editing, database management, plasmid maps, It can also be used for restriction and ligation, alignments, sequencer data import, calculators, gel image display, PCR, and more.

Synonyms: GENTle

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

Keywords: editing, database, management, plasmid maps, restriction, ligation, alignments, sequence, data, import, calculator, gel, image, display, PCR, cloning, genetic

Funding: Free Software Foundation

Availability: Free, Available for download

Resource Name: Gentle

Resource ID: SCR_016127

Alternate IDs: OMICS_18307

Alternate URLs: <https://sources.debian.org/src/gentle/>

License: GNU General Public License, version 2

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260728T043511+0000

Ratings and Alerts

No rating or validation information has been found for Gentle.

No alerts have been found for Gentle.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Musah HS, et al. (2024) Antimicrobial resistance and molecular characteristics of *Neisseria gonorrhoea* isolates in Ghana. *Access microbiology*, 6(2).

de Carvalho JB, et al. (2019) miRNA Genetic Variants Alter Their Secondary Structure and Expression in Patients With RASopathies Syndromes. *Frontiers in genetics*, 10, 1144.

Havlicek J, et al. (2018) Rapid Microarray-Based Detection of Rifampin, Isoniazid, and Fluoroquinolone Resistance in *Mycobacterium tuberculosis* by Use of a Single Cartridge. *Journal of clinical microbiology*, 56(2).

Sao Emani C, et al. (2018) Generation and characterization of thiol-deficient *Mycobacterium tuberculosis* mutants. *Scientific data*, 5, 180184.

Havlicek J, et al. (2017) An application of competitive reporter monitored amplification (CMA) for rapid detection of single nucleotide polymorphisms (SNPs). *PloS one*, 12(8), e0183561.

Sirena D, et al. (2005) The nucleotide sequence and a first generation gene transfer vector of species B human adenovirus serotype 3. *Virology*, 343(2), 283.