

Resource Summary Report

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DNABASER

RRID:SCR_009138

Type: Tool

Proper Citation

DNABASER (RRID:SCR_009138)

Resource Information

URL: <http://gaow.github.io/genetic-analysis-software/d-1.html#dnabaser>

Proper Citation: DNABASER (RRID:SCR_009138)

Description: Software tool for manual and automatic DNA sequence assembly, DNA sequence analysis, automatic sample processing, contig editing, metadata integration, file format conversion and mutation detection. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: DNABASER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DNABASER

Resource ID: SCR_009138

Alternate IDs: nlx_154256

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260801T191044+0000

Ratings and Alerts

No rating or validation information has been found for DNABASER.

No alerts have been found for DNABASER.

Data and Source Information

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Wangui J, et al. (2025) Molecular Analysis of Human Respiratory Syncytial Virus Group B Strains Isolated in Kenya Before and During the Emergence of Pandemic Influenza A/H1N1. *Influenza and other respiratory viruses*, 19(2), e70082.

Mutungi PM, et al. (2024) Fungal endophytes from saline-adapted shrubs induce salinity stress tolerance in tomato seedlings. *FEMS microbes*, 5, xtae012.

Bel Hadj Ali I, et al. (2024) Recombinase-based amplification coupled with lateral flow chromatography for the specific and sensitive detection and identification of *Leishmania major* in cutaneous leishmaniasis patients. *Frontiers in microbiology*, 15, 1514684.

Cambronero-Heinrichs JC, et al. (2023) *Erwiniaceae* bacteria play defensive and nutritional roles in two widespread ambrosia beetles. *FEMS microbiology ecology*, 99(12).

Lan Y, et al. (2023) Luobuma Leaf Spot Disease Caused by *Alternaria tenuissima* in China. *Journal of fungi (Basel, Switzerland)*, 9(11).

Miltiadous A, et al. (2022) A de novo SFMBT1 pathogenic variant identified in a boy with Poland syndrome. *Cold Spring Harbor molecular case studies*, 8(3).

Sproles AE, et al. (2022) Improved high-throughput screening technique to rapidly isolate *Chlamydomonas* transformants expressing recombinant proteins. *Applied microbiology and biotechnology*, 106(4), 1677.

Youseif SH, et al. (2022) A new source of bacterial myrosinase isolated from endophytic *Bacillus* sp. NGB-B10, and its relevance in biological control activity. *World journal of microbiology & biotechnology*, 38(11), 215.

Bel Hadj Ali I, et al. (2021) Dipeptidyl peptidase III as a DNA marker to investigate epidemiology and taxonomy of Old World *Leishmania* species. *PLoS neglected tropical diseases*, 15(7), e0009530.

Samarasinghe H, et al. (2021) Global patterns in culturable soil yeast diversity. *iScience*, 24(10), 103098.

Hoyos J, et al. (2021) Host selection pattern and flavivirus screening of mosquitoes in a disturbed Colombian rainforest. *Scientific reports*, 11(1), 18656.

Cortázar-Chinarro M, et al. (2020) Antimicrobial peptide and sequence variation along a latitudinal gradient in two anurans. *BMC genetics*, 21(1), 38.

Gemilyan M, et al. (2019) Prevalence of *Helicobacter pylori* infection and antibiotic resistance profile in Armenia. *Gut pathogens*, 11, 28.

Strandwitz P, et al. (2019) GABA-modulating bacteria of the human gut microbiota. *Nature microbiology*, 4(3), 396.

Sarkar A, et al. (2019) Genotypes of glycoprotein B gene among the Indian symptomatic neonates with congenital CMV infection. *BMC pediatrics*, 19(1), 291.

Al-Wahaibi ASM, et al. (2019) Secretion of DNases by Marine Bacteria: A Culture Based and Bioinformatics Approach. *Frontiers in microbiology*, 10, 969.

El Karkouri K, et al. (2019) Rapid MALDI-TOF MS identification of commercial truffles. *Scientific reports*, 9(1), 17686.

Mayerhofer J, et al. (2019) A species-specific multiplexed PCR amplicon assay for distinguishing between *Metarhizium anisopliae*, *M. brunneum*, *M. pingshaense* and *M. robertsii*. *Journal of invertebrate pathology*, 161, 23.

Leite J, et al. (2018) Genomic identification and characterization of the elite strains *Bradyrhizobium yuanmingense* BR 3267 and *Bradyrhizobium pachyrhizi* BR 3262 recommended for cowpea inoculation in Brazil. *Brazilian journal of microbiology* : [publication of the Brazilian Society for Microbiology], 49(4), 703.

Cortázar-Chinarro M, et al. (2017) Drift, selection, or migration? Processes affecting genetic differentiation and variation along a latitudinal gradient in an amphibian. *BMC evolutionary biology*, 17(1), 189.