

Resource Summary Report

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ABACAS

RRID:SCR_015852

Type: Tool

Proper Citation

ABACAS (RRID:SCR_015852)

Resource Information

URL: <http://abacas.sourceforge.net>

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Description: Software that contiguates (align, order, orientate), visualizes and designs primers to close gaps on shotgun assembled contigs based on a reference sequence. ABACAS finds alignment positions and identifies syntenies of assembled contigs against the reference, then generates a pseudomolecule taking overlapping contigs and gaps into account.

Abbreviations: ABACAS

Synonyms: ABACAS: Algorithm Based Automatic Contiguation of Assembled Sequences, Algorithm Based Automatic Contiguation of Assembled Sequences (ABACAS), Algorithm Based Automatic Contiguation of Assembled Sequences

Resource Type: software resource, software application

Keywords: contiguation, primer, shotgun assembled contig, reference sequence, assembled sequence

Funding: European Union LSHP-LT-2004-503578;
Wellcome Trust Sanger Institute

Availability: Free, Available for download

Resource Name: ABACAS

Resource ID: SCR_015852

Alternate IDs: OMICS_06933

Alternate URLs: <https://sourceforge.net/projects/abacas/files/>,
<https://sources.debian.org/src/abacas/>

License: GNU General Public License 2.0

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T191058+0000

Ratings and Alerts

No rating or validation information has been found for ABACAS.

No alerts have been found for ABACAS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 174 mentions in open access literature.

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

Safari M, et al. (2026) Comprehensive genomic analysis of a novel *Bacillus cereus* decomposing toluene potentially applicable in bioremediation. *Microbiology spectrum*, 14(1), e0289224.

Alam M, et al. (2025) A novel virulent core genome multilocus sequence type CT 11424 of *Listeria monocytogenes* isolate causing stillbirth in Bangladesh. *BMC microbiology*, 25(1), 61.

Cheng HR, et al. (2025) Genomic analysis of the *Streptococcus pneumoniae* in Taiwan: a nationwide study from 2006 to 2022. *Microbial genomics*, 11(9).

White RT, et al. (2024) Genomic epidemiology reveals geographical clustering of multidrug-resistant *Escherichia coli* ST131 associated with bacteraemia in Wales. *Nature communications*, 15(1), 1371.

Aguirre-Sánchez JR, et al. (2024) Genomic insights of *S. aureus* associated with bovine mastitis in a high livestock activity region of Mexico. *Journal of veterinary science*, 25(4), e42.

Belman S, et al. (2024) Geographical migration and fitness dynamics of *Streptococcus pneumoniae*. *Nature*, 631(8020), 386.

Cheng HR, et al. (2024) Estimating geographical spread of *Streptococcus pneumoniae* within Israel using genomic data. *Microbial genomics*, 10(6).

Miari VF, et al. (2024) Carriage and antimicrobial susceptibility of commensal *Neisseria* species from the human oropharynx. *Scientific reports*, 14(1), 25017.

Belman S, et al. (2024) Estimating between-country migration in pneumococcal populations. *G3 (Bethesda, Md.)*, 14(6).

Monzón S, et al. (2024) Monkeypox virus genomic accordion strategies. *Nature communications*, 15(1), 3059.

Briercheck EL, et al. (2024) Geographic EBV variants confound disease-specific variant interpretation and predict variable immune therapy responses. *Blood advances*, 8(14), 3731.

Bourdin T, et al. (2023) High-Throughput Short Sequence Typing Schemes for *Pseudomonas aeruginosa* and *Stenotrophomonas maltophilia* Pure Culture and Environmental DNA. *Microorganisms*, 12(1).

Baral B, et al. (2023) Co-factor independent oxidases *ncnN* and *actVA-3* are involved in the dimerization of benzoisochromanquinone antibiotics in naphthocyclinone and actinorhodin biosynthesis. *FEMS microbiology letters*, 370.

Bah SY, et al. (2023) Genomic Characterization of Skin and Soft Tissue *Streptococcus pyogenes* Isolates from a Low-Income and a High-Income Setting. *mSphere*, 8(1), e0046922.

Chung The H, et al. (2023) Multidrug resistance plasmids underlie clonal expansions and international spread of *Salmonella enterica* serotype 1,4,[5],12:i:- ST34 in Southeast Asia. *Communications biology*, 6(1), 1007.

Vieira AA, et al. (2023) Pipeline validation for the identification of antimicrobial-resistant genes in carbapenem-resistant *Klebsiella pneumoniae*. *Scientific reports*, 13(1), 15189.

Willard KA, et al. (2023) Viral and host factors drive a type 1 Epstein-Barr virus spontaneous lytic phenotype. *mBio*, 14(6), e0220423.

Wu D, et al. (2023) Achieving health-oriented air pollution control requires integrating unequal toxicities of industrial particles. *Nature communications*, 14(1), 6491.

Nguyen TT, et al. (2023) Whole-Genome Analysis of Antimicrobial-Resistant *Salmonella enterica* Isolated from Duck Carcasses in Hanoi, Vietnam. *Current issues in molecular biology*, 45(3), 2213.

Thurlow CM, et al. (2022) Selective Whole-Genome Amplification as a Tool to Enrich Specimens with Low *Treponema pallidum* Genomic DNA Copies for Whole-Genome Sequencing. *mSphere*, 7(3), e0000922.