

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 application, software resource

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: 20260829T183121+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 178 mentions in open access literature.

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

Pantoja L, et al. (2026) Genomic Analysis of Gut Bacteria in Tecia Solanivora: Insights into Host Functions and Their Potential in Biocontrol. Current microbiology, 83(8).

Saleh KJ, et al. (2026) One Health genomic surveillance identified high-risk carbapenem-resistant ST821 clones of Acinetobacter baumannii in Nigerian clinical and community settings. Microbial genomics, 12(6).

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

Cañas-Duarte SJ, et al. (2026) An integrative multi-omics approach points to membrane composition as a key factor in E. coli persistence. PloS one, 21(6), e0351161.

Koroleva A, et al. (2026) Metabolic engineering of doxorubicin biosynthesis through P450-redox partner optimization and structural analysis of DoxA. Nature communications, 17(1).

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

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.

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.

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

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.

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).

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

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

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.

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

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.

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.