Resource Summary Report

Generated by dkNET on Apr 28, 2025

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: 20250428T053933+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 171 mentions in open access literature.

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

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).

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.

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.

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

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.

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.

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.

Samper-Cativiela C, et al. (2022) Genomic characterization of multidrug-resistant Salmonella serovar Kentucky ST198 isolated in poultry flocks in Spain (2011-2017). Microbial genomics, 8(3).

Gladstone RA, et al. (2022) International links between Streptococcus pneumoniae vaccine serotype 4 sequence type (ST) 801 in Northern European shipyard outbreaks of invasive pneumococcal disease. Vaccine, 40(7), 1054.

Le CT, et al. (2022) Comparative genomics of Nocardia seriolae reveals recent importation and subsequent widespread dissemination in mariculture farms in the South Central Coast region, Vietnam. Microbial genomics, 8(7).