

Resource Summary Report

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CAP3 Sequence Assembly Program

RRID:SCR_007250

Type: Tool

Proper Citation

CAP3 Sequence Assembly Program (RRID:SCR_007250)

Resource Information

URL: <http://pbil.univ-lyon1.fr/cap3.php>

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Description: This form allows you to assemble a set of contiguous sequences (contigs) with the CAP3 program. The CAP3 program has a capability to clip 5' and 3' low-quality regions of reads. It uses base quality values in computation of overlaps between reads, construction of multiple sequence alignments of reads, and generation of consensus sequences. The program also uses forward-reverse constraints to correct assembly errors and link contigs. Results of CAP3 on four BAC data sets are presented. The performance of CAP3 was compared with that of PHRAP on a number of BAC data sets. PHRAP often produces longer contigs than CAP3 whereas CAP3 often produces fewer errors in consensus sequences than PHRAP. It is easier to construct scaffolds with CAP3 than with PHRAP on low-pass data with forward-reverse constraints. Sponsors: This project was supported by NIH Grant R01HG01502-02 from NHGRI. Keywords: CAP3, Program, Form, Computation, DNA, Dataset, Database, Program,, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: CAP3

Resource Type: data or information resource, topical portal, portal

Keywords: FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CAP3 Sequence Assembly Program

Resource ID: SCR_007250

Alternate IDs: nif-0000-30233

Record Creation Time: 20220129T080240+0000

Ratings and Alerts

No rating or validation information has been found for CAP3 Sequence Assembly Program.

No alerts have been found for CAP3 Sequence Assembly Program.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 781 mentions in open access literature.

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

Yeager R, et al. (2025) Wild yeast isolation by middle-school students reveals features of populations residing on North American oaks. *G3* (Bethesda, Md.), 15(1).

Arick li MA, et al. (2025) Assessment of the genetic diversity of Atlantic bottlenose dolphin (*Tursiops truncatus*) strandings in the Mississippi Sound (USA). *PloS one*, 20(6), e0314249.

Maneeprasert P, et al. (2025) Molecular Characterization of CnHd3a and Spatial Expression of Its Alternative Splicing Forms Associated with Flowering Transition and Flower Development in Coconut Palm (*Cocos nucifera* L.). *Genes*, 16(6).

Samarelli R, et al. (2025) Treatment of avian malaria in captive African penguins (*Spheniscus demersus*) by the combination of atovaquone and proguanil hydrochloride. *International journal of veterinary science and medicine*, 13(1), 1.

Kaboré DPA, et al. (2025) A metagenomics survey of viral diversity in mosquito vectors allows the first detection of Sindbis virus in Burkina Faso. *PloS one*, 20(6), e0323767.

Lanclos VC, et al. (2025) New isolates refine the ecophysiology of the *Roseobacter* CHAB-I-5 lineage. *ISME communications*, 5(1), ycaf068.

Shen L, et al. (2025) Identification and bioinformatics analysis of cilia-associated gene families in *Euplotes amieti* (Ciliophora, Hypotrichia). *Frontiers in microbiology*, 16, 1486189.

Williams J, et al. (2025) Harmonization and integration of data from prospective cohort studies across the Region of the Americas. *Revista panamericana de salud publica = Pan American journal of public health*, 49, e54.

Ishihara S, et al. (2025) Endogenous retrovirus loci and induced changes in gene expression in Japanese indigenous chickens. *Scientific reports*, 15(1), 12290.

Kaufmann H, et al. (2025) Genomic Repertoire of Twenty-Two Novel Vibrionaceae Species Isolated from Marine Sediments. *Microbial ecology*, 88(1), 36.

Frese AN, et al. (2024) Quantitative proteome dynamics across embryogenesis in a model chordate. *iScience*, 27(4), 109355.

Andradi-Brown C, et al. (2024) A novel computational pipeline for var gene expression augments the discovery of changes in the *Plasmodium falciparum* transcriptome during transition from in vivo to short-term in vitro culture. *eLife*, 12.

Manzulli V, et al. (2024) *Psychrobacter raelei* sp. nov., isolated from a dog with peritonitis. *International journal of systematic and evolutionary microbiology*, 74(4).

Yeager R, et al. (2024) Wild yeast isolation by middle school students reveals features of North American oak populations of *Saccharomyces cerevisiae* and *Kluyveromyces lactis*. *bioRxiv* : the preprint server for biology.

Matias BF, et al. (2024) Molecular Detection by Rolling Circle Amplification Combined with Deep Sequencing of Mixed Infection by Bovine Papillomaviruses 2 and 4 in Carcinoma In Situ of the Bovine Esophageal Mucosa. *Viruses*, 16(10).

Vasileiadis A, et al. (2024) A Novel Dhillonvirus Phage against *Escherichia coli* Bearing a Unique Gene of Intergeneric Origin. *Current issues in molecular biology*, 46(9), 9312.

Lauber C, et al. (2024) Deep mining of the Sequence Read Archive reveals major genetic innovations in coronaviruses and other nidoviruses of aquatic vertebrates. *PLoS pathogens*, 20(4), e1012163.

Ho WK, et al. (2024) A genomic toolkit for winged bean *Psophocarpus tetragonolobus*. *Nature communications*, 15(1), 1901.

Guimarães LC, et al. (2024) Methicillin-resistant *Staphylococcus aureus* and coagulase-negative *Staphylococcus* produce antimicrobial substances against members of the skin microbiota in children with atopic dermatitis. *FEMS microbiology ecology*, 100(6).

Manigat FO, et al. (2024) pUdOs: Concise Plasmids for Bacterial and Mammalian Cells. *ACS synthetic biology*, 13(2), 485.