

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

[genBlastA](#)

RRID:SCR_020951

Type: Tool

Proper Citation

genBlastA (RRID:SCR_020951)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2612959/>

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Description: Software tool to enable BLAST to identify homologous gene sequences. Graph based algorithm, which automatically filters High Scoring Pairs into well defined groups, each representing candidate gene in target genome. Used for identifying homologous sequences. Used for extracting relevant HSPs that represent candidate homologous genes from the entire HSP report.

Synonyms: GenBlastA

Resource Type: data processing software, software application, software resource

Defining Citation: [PMID:18838612](#)

Keywords: Identify homologous gene sequences, High Scoring Pairs filtering, target genome, candidate gene, homologous genes,

Funding: Michael Smith Foundation for Health Research ;
Natural Sciences and Engineering Research Council of Canada

Availability: Free, Available for download, Freely available

Resource Name: genBlastA

Resource ID: SCR_020951

Alternate URLs: <http://genome.sfu.ca/genblast/index.html>

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260905T133057+0000

Ratings and Alerts

No rating or validation information has been found for genBlastA.

No alerts have been found for genBlastA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Pfeifer M, et al. (2026) High-quality haplotype-resolved genome assembly and annotation of *Malus baccata* 'Jackii'. *Scientific data*, 13(1), 14.

Wang D, et al. (2026) Seroprevalence, isolation, comprehensive characterization, and pathogenicity of *Clostridium perfringens* strain from yak in Xizang, China. *Scientific reports*, 16(1).

Chen G, et al. (2026) Draft assemblies for 177 bird species enhance genus-level coverage. *GigaScience*, 15.

Lo BW, et al. (2026) Genomes of *Wiebesia* Fig Wasps Reveal the Adaptation and Codiversification in the Fig-Fig Wasp Mutualism. *Genome biology and evolution*, 18(4).

Chen Z, et al. (2026) Integrated Multi-Omics Analysis of a *Periplaneta americana* Symbiont *Streptomyces sampsonii* Strain WA1-19 Against *Candida albicans*. *Microbial biotechnology*, 19(4), e70333.

Henriquez T, et al. (2026) Establishment and application of a vesicle extraction method for clinical strains of *Pseudomonas aeruginosa*. *Microbiology spectrum*, 14(6), e0374625.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. *Journal of fungi (Basel, Switzerland)*, 11(3).

Hu Z, et al. (2025) Genomic epidemiology of antimicrobial resistance determinants in Chinese swine farm *Escherichia coli* isolates. *Frontiers in microbiology*, 16, 1575426.

Brejon Lamartinière E, et al. (2025) A haplotype-resolved chromosomal reference genome for the porcini mushroom *Boletus edulis*. *G3 (Bethesda, Md.)*, 15(6).

Li A, et al. (2025) Chromosomal-level genome assembly of an allotetraploid oyster. *Scientific data*, 12(1), 1492.

Liu Z, et al. (2025) C15-bacillomycin D produced by *Bacillus amyloliquefaciens* 4-9-2 suppress *Fusarium graminearum* infection and mycotoxin biosynthesis. *Frontiers in microbiology*, 16, 1599452.

Feng DD, et al. (2025) Chromosome-level genome assembly of a specialist walnut pest *Atrijuglans aristata*. *Scientific data*, 12(1), 434.

Qiu M, et al. (2025) Screening, Identification, and Whole-Genome Sequencing of Ferulic Acid Esterase-Producing Lactic Acid Bacteria from Sheep Rumen. *Microorganisms*, 13(6).

Yang J, et al. (2025) Genomic Analysis of *Penicillium griseofulvum* CF3 Reveals Potential for Plant Growth Promotion and Disease Resistance. *Journal of fungi (Basel, Switzerland)*, 11(2).

Huang D, et al. (2025) *Streptomyces huangiella* sp. nov., an endophytic actinomycete isolated from *Pheretima aspergillum*, a promising candidate for biological pathogen control. *Microbiology spectrum*, 13(10), e0071725.

Shi X, et al. (2024) A Genomic Sequence Resource of *Diaporthe mahothocarpus* GZU-Y2 Causing Leaf Spot Blight in *Camellia oleifera*. *Journal of fungi (Basel, Switzerland)*, 10(9).

Li A, et al. (2024) Chromosome-level genome assembly of the Suminoe oyster *Crassostrea ariakensis* in south China. *Scientific data*, 11(1), 1296.

Zhao S, et al. (2024) *Stenotrophomonas pavanii* MY01 induces phosphate precipitation of Cu(II) and Zn(II) by degrading glyphosate: performance, pathway and possible genes involved. *Frontiers in microbiology*, 15, 1479902.

Yu J, et al. (2024) Whole-Genome Sequencing of the Entomopathogenic Fungus *Fusarium solani* KMZW-1 and Its Efficacy Against *Bactrocera dorsalis*. *Current issues in molecular biology*, 46(10), 11593.

Wang Y, et al. (2023) Time-ordering japonica/geng genomes analysis indicates the importance of large structural variants in rice breeding. *Plant biotechnology journal*, 21(1), 202.