

Resource Summary Report

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

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: 20260805T044441+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 32 mentions in open access literature.

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

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.

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.

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

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

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.

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

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.

- 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.
- 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.
- 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.
- Zhao H, et al. (2023) A high-quality chromosome-level wild rice genome of *Oryza coarctata*. *Scientific data*, 10(1), 701.
- Dai F, et al. (2023) Genomic Resequencing Unravels the Genetic Basis of Domestication, Expansion, and Trait Improvement in *Morus Atropurpurea*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 10(24), e2300039.
- Jia J, et al. (2022) Multi-omics perspective on studying reproductive biology in *Daphnia sinensis*. *Genomics*, 114(2), 110309.
- Zheng J, et al. (2022) Molecular mechanisms underlying hematophagia revealed by comparative analyses of leech genomes. *GigaScience*, 12.
- Jiang F, et al. (2022) Chromosome-level genome assembly of *Bactrocera dorsalis* reveals its adaptation and invasion mechanisms. *Communications biology*, 5(1), 25.
- Jiang D, et al. (2022) The gold-ringed octopus (*Amphioctopus fangsiao*) genome and cerebral single-nucleus transcriptomes provide insights into the evolution of karyotype and neural novelties. *BMC biology*, 20(1), 289.