Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2025

genBlastA

RRID:SCR_020951
Type: Tool

Proper Citation

genBlastA (RRID:SCR_020951)

Resource Information

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

Proper Citation: genBlastA (RRID:SCR_020951)

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 resource, software application

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: 20250426T060751+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 23 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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.

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.

Jia J, et al. (2022) Multi-omics perspective on studying reproductive biology in Daphnia

sinensis. Genomics, 114(2), 110309.

Wu C, et al. (2022) Genomic features of the polyphagous cotton leafworm Spodoptera littoralis. BMC genomics, 23(1), 353.

Jiang F, et al. (2022) Chromosome-level genome assembly of Bactrocera dorsalis reveals its adaptation and invasion mechanisms. Communications biology, 5(1), 25.

Zheng J, et al. (2022) Molecular mechanisms underlying hematophagia revealed by comparative analyses of leech genomes. GigaScience, 12.

Yang Y, et al. (2022) Chromosome-level genome assembly of the shuttles hoppfish, Periophthalmus modestus. GigaScience, 11(1).

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.

He J, et al. (2022) A chromosome-level genome assembly of Artocarpus nanchuanensis (Moraceae), an extremely endangered fruit tree. GigaScience, 11.

He X, et al. (2022) The whole-genome assembly of an endangered Salicaceae species: Chosenia arbutifolia (Pall.) A. Skv. GigaScience, 11.

Wang Y, et al. (2021) A draft genome, resequencing, and metabolomes reveal the genetic background and molecular basis of the nutritional and medicinal properties of loquat (Eriobotrya japonica (Thunb.) Lindl). Horticulture research, 8(1), 231.

Zhao T, et al. (2021) A chromosome-level reference genome of the hazelnut, Corylus heterophylla Fisch. GigaScience, 10(4).

Li XJ, et al. (2021) The De Novo Genome Sequencing of Silver Pheasant (Lophura nycthemera). Genome biology and evolution, 13(12).

Yin D, et al. (2020) Comparison of Arachis monticola with Diploid and Cultivated Tetraploid Genomes Reveals Asymmetric Subgenome Evolution and Improvement of Peanut. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 7(4), 1901672.

Yi XG, et al. (2020) The genome of Chinese flowering cherry (Cerasus serrulata) provides new insights into Cerasus species. Horticulture research, 7, 165.