

Resource Summary Report

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DOE Joint Genome Institute

RRID:SCR_003045

Type: Tool

Proper Citation

DOE Joint Genome Institute (RRID:SCR_003045)

Resource Information

URL: <http://www.jgi.doe.gov/>

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Description: Institute to advance genomics in support of the DOE missions related to clean energy generation and environmental characterization and cleanup. Supported by the DOE Office of Science, the DOE JGI unites the expertise at Lawrence Berkeley National Laboratory, Lawrence Livermore National Laboratory, and the HudsonAlpha Institute for Biotechnology. The facility provides integrated high-throughput sequencing and computational analysis that enable systems-based scientific approaches to these challenges.

Abbreviations: DOE JGI, JGI,

Synonyms: DOE Joint Genome Institute - Enabling Advances in Bioenergy & Environmental Research, Department of Energy Joint Genome Institute, Joint Genome Institute

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

Keywords: genomics, sequencing, computational analysis, clean energy, environment, biotechnology, nucleotide sequence, protein, genome, bacteria, microorganism, fungal colony, fungal community, dna, phenotype, molecular biology, life science, genomics, genetics, nature, nurture, ecology, bioenergetics, high-throughput sequencing

Funding: DOE

Availability: Free, Freely available

Resource Name: DOE Joint Genome Institute

Resource ID: SCR_003045

Alternate IDs: nif-0000-30425

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260821T042611+0000

Ratings and Alerts

No rating or validation information has been found for DOE Joint Genome Institute.

No alerts have been found for DOE Joint Genome Institute.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 701 mentions in open access literature.

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

Merk LN, et al. (2025) Presence of group II introns in phage genomes. Nucleic acids research, 53(15).

Guo Y, et al. (2025) Identification of a Biosynthetic Gene Cluster for the Production of the Blue-Green Pigment Xylindein by the Fungus Chlorociboria aeruginascens. Journal of natural products, 88(2), 233.

??mon J, et al. (2025) A non-canonical fungal peroxisome PTS-1 signal, SYM, and its evolutionary aspects. Scientific reports, 15(1), 28088.

LaPorte MF, et al. (2025) AlgaeOrtho, a bioinformatics tool for processing ortholog inference results in algae. Frontiers in microbiology, 16, 1541898.

Reyes C, et al. (2025) Siderophores and secondary metabolites produced by Ganoderma adspersum. Microbiology (Reading, England), 171(11).

Merk LN, et al. (2025) Prevalence of Group II Introns in Phage Genomes. bioRxiv : the preprint server for biology.

Piot A, et al. (2025) Exon disruptive variants in Populus trichocarpa associated with wood properties exhibit distinct gene expression patterns. The plant genome, 18(1), e20541.

Jonca J, et al. (2024) Comprehensive phenomic and genomic studies of the species, Pectobacterium cacticida and proposal for reclassification as Alcorniella cacticida comb. nov. Frontiers in plant science, 15, 1323790.

Cong Z, et al. (2024) Genome Mining of Fungal Unique Trichodiene Synthase-like Sesquiterpene Synthases. Journal of fungi (Basel, Switzerland), 10(5).

Peck LD, et al. (2024) Horizontal transfers between fungal *Fusarium* species contributed to successive outbreaks of coffee wilt disease. *PLoS biology*, 22(12), e3002480.

Sheng H, et al. (2024) A conserved oomycete effector RxLR23 triggers plant defense responses by targeting ERD15La to release NbNAC68. *Nature communications*, 15(1), 6336.

Wang Y, et al. (2024) MASH-Ocean 1.0: Interactive platform for investigating microbial diversity, function, and biogeography with marine metagenomic data. *iMeta*, 3(3), e201.

Wang Z, et al. (2024) A novel and ubiquitous miRNA-involved regulatory module ensures precise phosphorylation of RNA polymerase II and proper transcription. *PLoS pathogens*, 20(4), e1012138.

Zhang X, et al. (2024) Genomic Localization Bias of Secondary Metabolite Gene Clusters and Association with Histone Modifications in *Aspergillus*. *Genome biology and evolution*, 16(11).

Flipphi M, et al. (2024) An ascomycete H4 variant with an unknown function. *Royal Society open science*, 11(2), 231705.

Borowska-Beszta M, et al. (2024) Comparative genomics, pangenomics, and phenomic studies of *Pectobacterium betavascularum* strains isolated from sugar beet, potato, sunflower, and artichoke: insights into pathogenicity, virulence determinants, and adaptation to the host plant. *Frontiers in plant science*, 15, 1352318.

Qiu C, et al. (2024) Positive selection and functional diversification of transcription factor Cmr1 homologs in *Alternaria*. *Applied microbiology and biotechnology*, 108(1), 133.

Reyes-Umana V, et al. (2023) Integration of molecular and computational approaches paints a holistic portrait of obscure metabolisms. *mBio*, 14(6), e0043123.

Lo YC, et al. (2023) Domestication in dry-cured meat *Penicillium* fungi: Convergent specific phenotypes and horizontal gene transfers without strong genetic subdivision. *Evolutionary applications*, 16(9), 1637.

Flipphi M, et al. (2023) Mutations in the Second Alternative Oxidase Gene: A New Approach to Group *Aspergillus niger* Strains. *Journal of fungi (Basel, Switzerland)*, 9(5).