Resource Summary Report

Generated by dkNET on May 19, 2025

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/

Proper Citation: DOE Joint Genome Institute (RRID:SCR_003045)

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: organization portal, data or information resource, 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

Resource Name: DOE Joint Genome Institute

Resource ID: SCR_003045

Alternate IDs: nif-0000-30425

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250517T055557+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 683 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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

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.

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.

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.

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).

Borowska-Beszta M, et al. (2024) Comparative genomics, pangenomics, and phenomic studies of Pectobacterium betavasculorum 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.

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).

Yu J, et al. (2023) Genomic Diversity and Phenotypic Variation in Fungal Decomposers Involved in Bioremediation of Persistent Organic Pollutants. Journal of fungi (Basel, Switzerland), 9(4).

Wang S, et al. (2023) Molecular and Functional Analyses of Characterized Sesquiterpene Synthases in Mushroom-Forming Fungi. Journal of fungi (Basel, Switzerland), 9(10).

Li L, et al. (2023) Globally distributed Myxococcota with photosynthesis gene clusters illuminate the origin and evolution of a potentially chimeric lifestyle. Nature communications, 14(1), 6450.

Mathieu Y, et al. (2023) Functional characterization of fungal lytic polysaccharide monooxygenases for cellulose surface oxidation. Biotechnology for biofuels and bioproducts, 16(1), 132.

Szebenyi C, et al. (2023) cotH Genes Are Necessary for Normal Spore Formation and Virulence in Mucor lusitanicus. mBio, 14(1), e0338622.

Flipphi M, et al. (2023) Generation, Transfer, and Loss of Alternative Oxidase Paralogues in the Aspergillaceae Family. Journal of fungi (Basel, Switzerland), 9(12).

Chen M, et al. (2022) Stable carbon isotope values of syndepositional carbonate spherules and micrite record spatial and temporal changes in photosynthesis intensity. Geobiology, 20(5), 667.

Chen G, et al. (2022) Genome?wide characterization of the G? subunit gene family in Rosaceae and expression analysis of PbrGPAs under heat stress. Gene, 810, 146056.

Liu Q, et al. (2022) Mating-Type Genes Play an Important Role in Fruiting Body Development in Morchella sextelata. Journal of fungi (Basel, Switzerland), 8(6).

Mosunova OV, et al. (2022) Evolution-Informed Discovery of the Naphthalenone Biosynthetic Pathway in Fungi. mBio, 13(3), e0022322.