Resource Summary Report

Generated by <u>dkNET</u> on May 2, 2025

JGI Genome Portal

RRID:SCR_002383 Type: Tool

Proper Citation

JGI Genome Portal (RRID:SCR_002383)

Resource Information

URL: http://genome.jgi.doe.gov/

Proper Citation: JGI Genome Portal (RRID:SCR_002383)

Description: Portal providing access to all JGI genomic databases and analytical tools, sequencing projects and their status, search for and download assemblies and annotations of sequenced genomes, and interactively explore those genomes and compare them with other sequenced microbes, fungi, plants or metagenomes using specialized systems tailored to each particular class of organisms. The Department of Energy (DOE) Joint Genome Institute (JGI) is a national user facility with massive-scale DNA sequencing and analysis capabilities dedicated to advancing genomics for bioenergy and environmental applications. Beyond generating tens of trillions of DNA bases annually, the Institute develops and maintains data management systems and specialized analytical capabilities to manage and interpret complex genomic data sets, and to enable an expanding community of users around the world to analyze these data in different contexts over the web.

Synonyms: JGI Genome Portal, DOE Joint Genome Institute Genome Portal

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

Defining Citation: PMID:24225321, PMID:22110030

Keywords: gene, computation, genome, genomics, model organism, assembly, annotation, sequenced genome, metagenome, bio.tools

Funding: Department of Energy

Resource Name: JGI Genome Portal

Resource ID: SCR_002383

Alternate IDs: nif-0000-21230, SCR_004706, OMICS_01654, biotools:jgi_genome_portal, nlx_69965

Alternate URLs: http://genome.jgi-psf.org, https://bio.tools/jgi_genome_portal

Old URLs: http://genome.jgi-psf.org/

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250502T055324+0000

Ratings and Alerts

No rating or validation information has been found for JGI Genome Portal.

No alerts have been found for JGI Genome Portal.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 863 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Tamayo E, et al. (2024) Correlating sugar transporter expression and activities to identify transporters for an orphan sugar substrate. Applied microbiology and biotechnology, 108(1), 83.

Velle KB, et al. (2023) A conserved pressure-driven mechanism for regulating cytosolic osmolarity. Current biology : CB, 33(16), 3325.

Liu D, et al. (2023) The Weimberg pathway: an alternative for Myceliophthora thermophila to utilize D-xylose. Biotechnology for biofuels and bioproducts, 16(1), 13.

Ling ZL, et al. (2023) Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. Microbial genomics, 9(3).

Wang D, et al. (2023) Hypothetical Protein VDAG_07742 Is Required for Verticillium dahliae Pathogenicity in Potato. International journal of molecular sciences, 24(4).

Zhong J, et al. (2023) Metagenomic next-generation sequencing for rapid detection of pulmonary infection in patients with acquired immunodeficiency syndrome. Annals of clinical microbiology and antimicrobials, 22(1), 57.

Li?yt? J, et al. (2022) Distribution and regulatory roles of oxidized 5-methylcytosines in DNA and RNA of the basidiomycete fungi Laccaria bicolor and Coprinopsis cinerea. Open biology, 12(3), 210302.

Walker PL, et al. (2022) A Ubiquitously Conserved Cyanobacterial Protein Phosphatase Essential for High Light Tolerance in a Fast-Growing Cyanobacterium. Microbiology spectrum, 10(4), e0100822.

Salazar OR, et al. (2022) The coral Acropora loripes genome reveals an alternative pathway for cysteine biosynthesis in animals. Science advances, 8(38), eabq0304.

Vicedomini R, et al. (2022) Multiple Profile Models Extract Features from Protein Sequence Data and Resolve Functional Diversity of Very Different Protein Families. Molecular biology and evolution, 39(4).

Podowski JC, et al. (2022) Genome Streamlining, Proteorhodopsin, and Organic Nitrogen Metabolism in Freshwater Nitrifiers. mBio, 13(3), e0237921.

Stéger A, et al. (2022) The evolution of plant proton pump regulation via the R domain may have facilitated plant terrestrialization. Communications biology, 5(1), 1312.

Sharaf A, et al. (2022) Phylogenetic profiling resolves early emergence of PRC2 and illuminates its functional core. Life science alliance, 5(7).

Wang L, et al. (2022) A histone H3K9 methyltransferase Dim5 mediates repression of sorbicillinoid biosynthesis in Trichoderma reesei. Microbial biotechnology, 15(10), 2533.

Fernandes C, et al. (2021) Pyomelanin Synthesis in Alternaria alternata Inhibits DHN-Melanin Synthesis and Decreases Cell Wall Chitin Content and Thickness. Frontiers in microbiology, 12, 691433.

Martin K, et al. (2021) The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature communications, 12(1), 5483.

Kosina SM, et al. (2021) Biofilm Interaction Mapping and Analysis (BIMA) of Interspecific Interactions in Pseudomonas Co-culture Biofilms. Frontiers in microbiology, 12, 757856.

Nie Y, et al. (2021) The Gene Rearrangement, Loss, Transfer, and Deep Intronic Variation in Mitochondrial Genomes of Conidiobolus. Frontiers in microbiology, 12, 765733.

Amira MB, et al. (2021) Fungal X-Intrinsic Protein Aquaporin from Trichoderma atroviride: Structural and Functional Considerations. Biomolecules, 11(2).

Chen Y, et al. (2021) Multivariate linear mixed model enhanced the power of identifying genome-wide association to poplar tree heights in a randomized complete block design. G3

(Bethesda, Md.), 11(2).