

Resource Summary Report

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JGI Genome Portal

RRID:SCR_002383

Type: Tool

Proper Citation

JGI Genome Portal (RRID:SCR_002383)

Resource Information

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

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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: data or information resource, department portal, organization portal, 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: 20260821T193641+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 869 mentions in open access literature.

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

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in Dictyostelium. Molecular biology of the cell, 36(8), ar98.

Zheng Z, et al. (2025) Atypical RXLR effectors are involved in Phytophthora cactorum pathogenesis. aBIOTECH, 6(1), 50.

Fierro Morales JC, et al. (2024) Reduced PaxillinB localization to cell-substrate adhesions promotes cell migration in Dictyostelium. bioRxiv : the preprint server for biology.

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).

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.

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

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.

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.

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.

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

Kumar M, et al. (2022) Corrigendum to "Cholesterol-Lowering Probiotics as Potential Biotherapeutics for Metabolic Diseases". *Journal of diabetes research*, 2022, 3952529.

Baloch AA, et al. (2022) Comparative genomics and evolutionary analysis of plant CNGCs. *Biology methods & protocols*, 7(1), bpac018.

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

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).