

Resource Summary Report

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Dictyostelium discoideum genome database

RRID:SCR_008149

Type: Tool

Proper Citation

Dictyostelium discoideum genome database (RRID:SCR_008149)

Resource Information

URL: <http://dictybase.org>

Proper Citation: Dictyostelium discoideum genome database (RRID:SCR_008149)

Description: This website contains the genome sequence of Dictyostelium discoideum. The determination of the entire information content of the Dictyostelium genome will be of great value to those working with this organism directly, as well as to those who would like to determine the functions of homologous genes from other species. Dictyostelium discoideum, a soil-living amoeba, is an excellent organism for the study of the molecular mechanisms of cell motility, signal transduction, cell-type differentiation and developmental processes. Genes involved in any of these processes can be knocked-out rapidly by targeted homologous recombination. Since Dictyostelium is haploid, mutants are readily isolated and the REMI (restriction enzyme mediated integration) technique of insertional mutagenesis allows the facile cloning of disrupted genes. The Dictyostelium genome is being sequenced with the chromosomal shotgun methodology on a chromosome by chromosome basis. The six Dictyostelium chromosomes with sizes ranging from four to seven Mb are being separated by PFGE (Pulsed Field Gel Electrophoresis) by Edward Cox, Princeton University. Chromosomal libraries with insert sizes between 1 and 4 kb are being generated by the Sanger Centre using pUC18 as a vector. For shotgun sequencing both forward and reverse reads from each clone randomly selected from the chromosome-enriched libraries are being produced. The read pairs will represent a useful mapping resource to assess contig order. For every Mb of DNA an estimated number of 20,000 - 25,000 single shotgun reads will be necessary. The hereditary information is carried on 6 chromosomes with sizes ranging from 4 to 7 Mb resulting in a total of about 34 Mb of DNA, a multicopy 90 kb extrachromosomal element that harbours the rRNA genes, and the 55 kb mitochondrial genome. The estimated number of genes in the genome is 8,000 to 10,000 and many of the known genes show a high degree of sequence similarity to homologues in vertebrate species.

Abbreviations: Dictyostelium discoideum genome database

Resource Type: data or information resource, database

Keywords: element, gene, basic research knowledge base, cell, chromosomal, chromosome, cloning, developmental, dictyostelium, differentiation, discoideum, disrupted, genome, homologous, homologues, insertional, mechanism, methodology, mitochondrial, molecular, motility, mutagenesis, mutant, organism, pair, rrna, sequence, shotgun, signal, size, specie, technique, transduction, vertebrate

Funding: European Union ;
NIH ;
DFG

Resource Name: Dictyostelium discoideum genome database

Resource ID: SCR_008149

Alternate IDs: nif-0000-20974

Old URLs: <http://genome.imb-jena.de/dictyostelium/>

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260903T234937+0000

Ratings and Alerts

No rating or validation information has been found for Dictyostelium discoideum genome database.

No alerts have been found for Dictyostelium discoideum genome database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 183 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Allan CY, et al. (2024) Polycystin-2 Mediated Calcium Signalling in the Dictyostelium Model for Autosomal Dominant Polycystic Kidney Disease. Cells, 13(7).

Hüsler D, et al. (2023) The large GTPase Sey1/atlastin mediates lipid droplet- and FadL-dependent intracellular fatty acid metabolism of Legionella pneumophila. eLife, 12.

Vines JH, et al. (2023) A PI(3,5)P2 reporter reveals PIKfyve activity and dynamics on macropinosomes and phagosomes. The Journal of cell biology, 222(9).

Rijal R, et al. (2022) Dictyostelium discoideum cells retain nutrients when the cells are about to outgrow their food source. Journal of cell science, 135(18).

- Forbes G, et al. (2022) Interactome and evolutionary conservation of Dictyostelid small GTPases and their direct regulators. *Small GTPases*, 13(1), 239.
- Boland AW, et al. (2022) Oxygen-dependent regulation of E3(SCF)ubiquitin ligases and a Skp1-associated JmjD6 homolog in development of the social amoeba *Dictyostelium*. *The Journal of biological chemistry*, 298(9), 102305.
- Diesend J, et al. (2022) Fractional 2'-O-methylation in the ribosomal RNA of *Dictyostelium discoideum* supports ribosome heterogeneity in Amoebozoa. *Scientific reports*, 12(1), 1952.
- Itabangi H, et al. (2022) A bacterial endosymbiont of the fungus *Rhizopus microsporus* drives phagocyte evasion and opportunistic virulence. *Current biology : CB*, 32(5), 1115.
- Hiraoka H, et al. (2022) ATP levels influence cell movement during the mound phase in *Dictyostelium discoideum* as revealed by ATP visualization and simulation. *FEBS open bio*, 12(11), 2042.
- Martín-González J, et al. (2021) *Dictyostelium discoideum* as a non-mammalian biomedical model. *Microbial biotechnology*, 14(1), 111.
- Singh SP, et al. (2021) Extracellular Signalling Modulates Scar/WAVE Complex Activity through Abi Phosphorylation. *Cells*, 10(12).
- Biondo M, et al. (2021) The Dynamics of Aerotaxis in a Simple Eukaryotic Model. *Frontiers in cell and developmental biology*, 9, 720623.
- Pears CJ, et al. (2021) *Dictyostelium discoideum* as a Model to Assess Genome Stability Through DNA Repair. *Frontiers in cell and developmental biology*, 9, 752175.
- Heidorn-Czarna M, et al. (2021) Chronic Activation of AMPK Induces Mitochondrial Biogenesis through Differential Phosphorylation and Abundance of Mitochondrial Proteins in *Dictyostelium discoideum*. *International journal of molecular sciences*, 22(21).
- Fili? V, et al. (2021) Regulation of the Actin Cytoskeleton via Rho GTPase Signalling in *Dictyostelium* and Mammalian Cells: A Parallel Slalom. *Cells*, 10(7).
- Herman EK, et al. (2021) Genomics and transcriptomics yields a system-level view of the biology of the pathogen *Naegleria fowleri*. *BMC biology*, 19(1), 142.
- Riehl J, et al. (2021) Domain Organization of the UBX Domain Containing Protein 9 and Analysis of Its Interactions With the Homohexameric AAA + ATPase p97 (Valosin-Containing Protein). *Frontiers in cell and developmental biology*, 9, 748860.
- Kjellin J, et al. (2021) Abundantly expressed class of noncoding RNAs conserved through the multicellular evolution of dictyostelid social amoebas. *Genome research*, 31(3), 436.
- Huang LY, et al. (2021) Methylation-directed acetylation of histone H3 regulates developmental sensitivity to histone deacetylase inhibition. *Nucleic acids research*, 49(7), 3781.
- Arthur AL, et al. (2021) VASP-mediated actin dynamics activate and recruit a filopodia myosin. *eLife*, 10.