Resource Summary Report

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NCBI Genome

RRID:SCR_002474
Type: Tool

Proper Citation

NCBI Genome (RRID:SCR_002474)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/genome

Proper Citation: NCBI Genome (RRID:SCR_002474)

Description: Database that organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations in six major organism groups: Archaea, Bacteria, Eukaryotes, Viruses, Viroids, and Plasmids. Genomes of over 1,200 organisms can be found in this database, representing both completely sequenced organisms and those for which sequencing is in progress. Users can browse by organism, and view genome maps and protein clusters. Links to other prokaryotic and archaeal genome projects, as well as BLAST tools and access to the rest of the NCBI online resources are available.

Abbreviations: Genome

Synonyms: Entrez Genomes, Entrez Genome, NCBI, Genome, Genome Database, Genome: Information by genome sequence

Resource Type: data or information resource, storage service resource, database, service resource, data repository

Keywords: chromosome, organelle, plasmid, viroid, virus, genome, sequence, map, assembly, annotation, gene mapping, dna, blast, protein cluster, gold standard

Funding:

Availability: Free, Freely avaialble

Resource Name: NCBI Genome

Resource ID: SCR_002474

Alternate IDs: nif-0000-02802

Alternate URLs: http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Genome

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250425T055256+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Genome.

No alerts have been found for NCBI Genome.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 523 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Gong X, et al. (2025) Chromosome-level genome assembly of Iodes seguinii and its metabonomic implications for rheumatoid arthritis treatment. The plant genome, 18(1), e20534.

Megrian D, et al. (2025) Evolutionary plasticity and functional repurposing of the essential metabolic enzyme MoeA. Communications biology, 8(1), 49.

Futas J, et al. (2024) Comparative genomics of the Natural Killer Complex in carnivores. Frontiers in immunology, 15, 1459122.

Lan Z, et al. (2024) Whole-genome resequencing and transcriptional profiling association analysis revealed the intraspecies difference response to oligosaccharides utilization in Bifidobacterium animalis subsp. lactis. Frontiers in microbiology, 15, 1375384.

Li XT, et al. (2024) Acidithiobacillus acidisediminis sp. nov., an acidophilic sulphur-oxidizing chemolithotroph isolated from acid mine drainage sediment. International journal of systematic and evolutionary microbiology, 74(5).

Huang YH, et al. (2024) PhyloAln: A Convenient Reference-Based Tool to Align Sequences and High-Throughput Reads for Phylogeny and Evolution in the Omic Era. Molecular biology

and evolution, 41(7).

Wang Y, et al. (2024) Identifying potential anthocyanin biosynthesis regulator in Chinese cherry by comprehensive genome-wide characterization of the R2R3-MYB transcription factor gene family. BMC genomics, 25(1), 784.

Zamba-Campero M, et al. (2024) Broadly conserved FlgV controls flagellar assembly and Borrelia burgdorferi dissemination in mice. bioRxiv : the preprint server for biology.

Abdullah S, et al. (2024) Dissemination of clinical Escherichia coli harboring the mcr-1 gene in Pakistan. Frontiers in microbiology, 15, 1502528.

Shekhar MS, et al. (2024) Genome assembly, Full-length transcriptome, and isoform diversity of Red Snapper, Lutjanus argentimaculatus. Scientific data, 11(1), 796.

Sipiczki M, et al. (2024) Reversible stochastic epigenetic like silencing of the production of pulcherriminic acid in the antimicrobial antagonist Metschnikowia Pulcherrima. Scientific reports, 14(1), 29677.

Das S, et al. (2024) Phylogenomics of Psammodynastes and Buhoma (Elapoidea: Serpentes), with the description of a new Asian snake family. Scientific reports, 14(1), 9489.

Du Z, et al. (2024) The Genome Architecture of the Copepod Eurytemora carolleeae - the Highly Invasive Atlantic Clade of the Eurytemoraaffinis Species Complex. Genomics, proteomics & bioinformatics, 22(5).

Helal P, et al. (2024) Changes in the Firmicutes to Bacteriodetes ratio in the gut microbiome in individuals with anorexia nervosa following inpatient treatment: A systematic review and a case series. Brain and behavior, 14(9), e70014.

Qi Z, et al. (2024) Adaptive advantages of restorative RNA editing in fungi for resolving survival-reproduction trade-offs. Science advances, 10(1), eadk6130.

Rachid Zaim S, et al. (2024) MOCHA's advanced statistical modeling of scATAC-seq data enables functional genomic inference in large human cohorts. Nature communications, 15(1), 6828.

Chen P, et al. (2024) Comparative genomic analyses of Cutibacterium granulosum provide insights into genomic diversity. Frontiers in microbiology, 15, 1343227.

André A, et al. (2024) Genomics unveils country-to-country transmission between animal hospitals of a multidrug-resistant and sequence type 2 Acinetobacter baumannii clone. Microbial genomics, 10(10).

Salehi-Najafabadi A, et al. (2024) Insights into additional lactone-based signaling circuits in Streptomyces: existence of acyl-homoserine lactones and LuxI/LuxR homologs in six Streptomyces species. Frontiers in microbiology, 15, 1342637.

Wu H, et al. (2024) A drug-free cardiovascular stent functionalized with tailored collagen supports in-situ healing of vascular tissues. Nature communications, 15(1), 735.