Resource Summary Report

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EBI Genomes

RRID:SCR_002426
Type: Tool

Proper Citation

EBI Genomes (RRID:SCR_002426)

Resource Information

URL: http://www.ebi.ac.uk/genomes

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Description: The EBI genomes pages give access to a large number of complete genomes including bacteria, archaea, viruses, phages, plasmids, viroids and eukaryotes. Methods using whole genome shotgun data are used to gain a large amount of genome coverage for an organism. WGS data for a growing number of organisms are being submitted to DDBJ/EMBL/GenBank. Genome entries have been listed in their appropriate category which may be browsed using the website navigation tool bar on the left. While organelles are all listed in a separate category, any from Eukaryota with chromosome entries are also listed in the Eukaryota page. Within each page, entries are grouped and sorted at the species level with links to the taxonomy page for that species separating each group. Within each species, entries whose source organism has been categorized further are grouped and numbered accordingly. Links are made to: * taxonomy * complete EMBL flatfile * CON files * lists of CON segments * Project * Proteomes pages * FASTA file of Proteins * list of Proteins

Synonyms: Genomes Pages - At the EBI, ENA Genomes Server

Resource Type: data or information resource, data set

Keywords: eukaryote genome, gene, gene browser, genome, archaea genome, bacteria genome, phage genome, plasmid genome, viroid genome, viruse genome, sequence, protein, nucleotide, complete genome, gold standard

Funding:

Resource Name: EBI Genomes

Resource ID: SCR_002426

Alternate IDs: nif-0000-02778

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250429T054733+0000

Ratings and Alerts

No rating or validation information has been found for EBI Genomes.

No alerts have been found for EBI Genomes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Hajj M, et al. (2021) Phylogenetic Diversity of Lhr Proteins and Biochemical Activities of the Thermococcales aLhr2 DNA/RNA Helicase. Biomolecules, 11(7).

Maibach V, et al. (2019) Reduced bonobo MHC class I diversity predicts a reduced viral peptide binding ability compared to chimpanzees. BMC evolutionary biology, 19(1), 14.

Bahari MNA, et al. (2018) Transciptome profiling at early infection of Elaeis guineensis by Ganoderma boninense provides novel insights on fungal transition from biotrophic to necrotrophic phase. BMC plant biology, 18(1), 377.

Ugarte A, et al. (2018) A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. Microbiome, 6(1), 149.

Quentin Y, et al. (2018) Single-strand DNA processing: phylogenomics and sequence diversity of a superfamily of potential prokaryotic HuH endonucleases. BMC genomics, 19(1), 475.

Sharma AK, et al. (2017) A novel approach for the prediction of species-specific biotransformation of xenobiotic/drug molecules by the human gut microbiota. Scientific reports, 7(1), 9751.

Scholz HC, et al. (2016) The Change of a Medically Important Genus: Worldwide

Occurrence of Genetically Diverse Novel Brucella Species in Exotic Frogs. PloS one, 11(12), e0168872.

Rihtman B, et al. (2016) Assessing Illumina technology for the high-throughput sequencing of bacteriophage genomes. PeerJ, 4, e2055.

Goldberg T, et al. (2016) Computational prediction shines light on type III secretion origins. Scientific reports, 6, 34516.

Perez Sepulveda B, et al. (2016) Marine phage genomics: the tip of the iceberg. FEMS microbiology letters, 363(15).

Pastrello C, et al. (2014) Integration, visualization and analysis of human interactome. Biochemical and biophysical research communications, 445(4), 757.

Vo NS, et al. (2014) RandAL: a randomized approach to aligning DNA sequences to reference genomes. BMC genomics, 15 Suppl 5(Suppl 5), S2.

Goldberg T, et al. (2014) LocTree3 prediction of localization. Nucleic acids research, 42(Web Server issue), W350.

Phung DK, et al. (2013) Archaeal ?-CASP ribonucleases of the aCPSF1 family are orthologs of the eukaryal CPSF-73 factor. Nucleic acids research, 41(2), 1091.

Burge SW, et al. (2013) Rfam 11.0: 10 years of RNA families. Nucleic acids research, 41(Database issue), D226.

Schüller A, et al. (2012) Computer-based annotation of putative AraC/XylS-family transcription factors of known structure but unknown function. Journal of biomedicine & biotechnology, 2012, 103132.

Accetto T, et al. (2011) Inability of Prevotella bryantii to form a functional Shine-Dalgarno interaction reflects unique evolution of ribosome binding sites in Bacteroidetes. PloS one, 6(8), e22914.

Cochrane G, et al. (2009) Petabyte-scale innovations at the European Nucleotide Archive. Nucleic acids research, 37(Database issue), D19.

Cochrane G, et al. (2008) Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. Nucleic acids research, 36(Database issue), D5.

Kulikova T, et al. (2007) EMBL Nucleotide Sequence Database in 2006. Nucleic acids research, 35(Database issue), D16.