Resource Summary Report

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Toolbox at the European Bioinformatics Institute

RRID:SCR_002872
Type: Tool

Proper Citation

Toolbox at the European Bioinformatics Institute (RRID:SCR_002872)

Resource Information

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

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Description: The European Bioinformatics Institute (EBI) toolbox area provides a comprehensive range of tools for the field of bioinformatics. These are subdivided into categories in the left menu for convenience. EBI has developed a large number of very useful bioinformatics tools. A few examples include: - Similarity & Homology - the BLAST or FASTA programs can be used to look for sequence similarity and infer homology. - Protein Functional Analysis - InterProScan can be used to search for motifs in your protein sequence. - Proteomic Services NEW - UniProt DAS server allows researchers to show their research results in the context of UniProtKB/Swiss-Prot annotation. - Sequence Analysis - ClustalW2 a sequence alignment tool. - Structural Analysis - MSDfold can be used to query your protein structure and compare it to those in the Protein Data Bank (PDB). - Web Services - provide programmatic access to the various databases and retrieval/analysis services EBI provides. - Tools Miscellaneous - Expression Profiler a set of tools for clustering, analysis and visualization of gene expression and other genomic data. Sponsors: This resource is sponsored by EBI.

Synonyms: EBI Bioinformatics Tools

Resource Type: software toolkit, software resource

Keywords: expression, functional, gene, bioinformatics, database, genomic, homology, protein, proteomic, sequence, structural, toolbox

Funding:

Resource Name: Toolbox at the European Bioinformatics Institute

Resource ID: SCR_002872

Alternate IDs: nif-0000-25553

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250503T055539+0000

Ratings and Alerts

No rating or validation information has been found for Toolbox at the European Bioinformatics Institute.

No alerts have been found for Toolbox at the European Bioinformatics Institute.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 85 mentions in open access literature.

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

Mandal S, et al. (2024) Fluoride and gallein regulate polyphosphate accumulation in dental caries-associated Lacticaseibacillus. Microbiology (Reading, England), 170(11).

Du J, et al. (2021) Phylogenetic Analysis of the Dengue Virus Strains Causing the 2019 Dengue Fever Outbreak in Hainan, China. Virologica Sinica, 36(4), 636.

Yousefipour F, et al. (2021) Identification of two novel homozygous nonsense mutations in TRAPPC9 in two unrelated consanguineous families with intellectual Disability from Iran. Molecular genetics & genomic medicine, 9(12), e1610.

Wang G, et al. (2021) Identification and genome analysis of a novel picornavirus from captive belugas (Delphinapterus leucas) in China. Scientific reports, 11(1), 21018.

Wu Z, et al. (2021) Decoding the RNA viromes in rodent lungs provides new insight into the origin and evolutionary patterns of rodent-borne pathogens in Mainland Southeast Asia. Microbiome, 9(1), 18.

Vetrici MA, et al. (2021) Douglas-fir LEAFY COTYLEDON1 (PmLEC1) is an active transcription factor during zygotic and somatic embryogenesis. Plant direct, 5(7), e00333.

Kong F, et al. (2021) Arabidopsis Toxicos en Levadura 12 (ATL12): A Gene Involved in Chitin-Induced, Hormone-Related and NADPH Oxidase-Mediated Defense Responses. Journal of fungi (Basel, Switzerland), 7(10).

Sun X, et al. (2021) Identification and Characterization of the Seed Storage Proteins and Related Genes of Cannabis sativa L. Frontiers in nutrition, 8, 678421.

Pourrezaei S, et al. (2021) Molecular epidemiology and phylogenetic analysis of human T-lymphotropic virus type 1 in the tax gene and it association with adult t-cell leukemia/lymphoma disorders. Iranian journal of microbiology, 13(4), 509.

Tian Y, et al. (2021) Cloning and expression analysis of GATA1 gene in Carassius auratus red var. BMC genomic data, 22(1), 12.

Chansaenroj J, et al. (2020) High prevalence of DS-1-like rotavirus infection in Thai adults between 2016 and 2019. PloS one, 15(6), e0235280.

Du J, et al. (2019) Identification of a Novel Ichthyic Parvovirus in Marine Species in Hainan Island, China. Frontiers in microbiology, 10, 2815.

Hirano Y, et al. (2019) Structural basis of phosphatidylcholine recognition by the C2-domain of cytosolic phospholipase A2?. eLife, 8.

Bale NJ, et al. (2019) Fatty Acid and Hopanoid Adaption to Cold in the Methanotroph Methylovulum psychrotolerans. Frontiers in microbiology, 10, 589.

Wu Z, et al. (2018) Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome, 6(1), 178.

Wu Z, et al. (2018) Discovery of Diverse Rodent and Bat Pestiviruses With Distinct Genomic and Phylogenetic Characteristics in Several Chinese Provinces. Frontiers in microbiology, 9, 2562.

Avwioroko OJ, et al. (2018) Isolation, identification and in silico analysis of alpha-amylase gene of Aspergillus niger strain CSA35 obtained from cassava undergoing spoilage. Biochemistry and biophysics reports, 14, 35.

Wang YF, et al. (2018) Glycan-binding preferences and genetic evolution of human seasonal influenza A(H3N2) viruses during 1999-2007 in Taiwan. PloS one, 13(5), e0196727.

Alousi S, et al. (2018) Genomic Characterization of MDR Escherichia coli Harboring blaOXA-48 on the IncL/M-type Plasmid Isolated from Blood Stream Infection. BioMed research international, 2018, 3036143.

Yu W, et al. (2018) Functional analysis of eliciting plant response protein Epl1-Tas from Trichoderma asperellum ACCC30536. Scientific reports, 8(1), 7974.