Resource Summary Report

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DTU Center for Biological Sequence Analysis

RRID:SCR_003590
Type: Tool

Proper Citation

DTU Center for Biological Sequence Analysis (RRID:SCR_003590)

Resource Information

URL: https://services.healthtech.dtu.dk/

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Description: Center for Biological Sequence Analysis of the Technical University of Denmark conducts basic research in the field of bioinformatics and systems biology and directs its research primarily towards topics related to the elucidation of the functional aspects of complex biological mechanisms. A large number of computational methods have been produced, which are offered to others via WWW servers. Several data sets are also available. The center also has experimental efforts in gene expression analysis using DNA chips and data generation in relation to the physical and structural properties of DNA. The on-line prediction services at CBS are available as interactive input forms. Most of the servers are also available as stand-alone software packages with the same functionality. In addition, for some servers, programmatic access is provided in the form of SOAP-based Web Services. The center also educates engineering students in biotechnology and systems biology and offers a wide range of courses in bioinformatics, systems biology, human health, microbiology and nutrigenomics.

Abbreviations: CBS, DTU CBS

Resource Type: analysis service resource, web service, production service resource, data access protocol, software resource, service resource

Keywords: nucleotide, sequence, amino acid, dna, microarray, molecule, immunology, protein function, protein structure, protein, post-translational, whole genome, sequence analysis

Funding: Danish National Research Foundation ;
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Resource Name: DTU Center for Biological Sequence Analysis

Resource ID: SCR_003590

Alternate IDs: nlx_12329

Old URLs: http://www.cbs.dtu.dk/index.shtml

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Ratings and Alerts

No rating or validation information has been found for DTU Center for Biological Sequence Analysis.

No alerts have been found for DTU Center for Biological Sequence Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1413 mentions in open access literature.

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

Chakrabarti S, et al. (2020) Phosphorylation of unique C-terminal sites of the mu-opioid receptor variants 1B2 and 1C1 influences their Gs association following chronic morphine. Journal of neurochemistry, 152(4), 449.

Hou H, et al. (2018) Overexpression of a SBP-Box Gene (VpSBP16) from Chinese Wild Vitis Species in Arabidopsis Improves Salinity and Drought Stress Tolerance. International journal of molecular sciences, 19(4).

Whiten SR, et al. (2018) Characterization of the adult Aedes aegypti early midgut peritrophic matrix proteome using LC-MS. PloS one, 13(3), e0194734.

Nevoa JC, et al. (2018) An insight into the salivary gland and fat body transcriptome of

Panstrongylus lignarius (Hemiptera: Heteroptera), the main vector of Chagas disease in Peru. PLoS neglected tropical diseases, 12(2), e0006243.

Salas-Perez RA, et al. (2018) RNA-Seq transcriptome analysis of Amaranthus palmeri with differential tolerance to glufosinate herbicide. PloS one, 13(4), e0195488.

Kim P, et al. (2018) Glycosylation of Hemagglutinin and Neuraminidase of Influenza A Virus as Signature for Ecological Spillover and Adaptation among Influenza Reservoirs. Viruses, 10(4).

Allan ER, et al. (2017) Schistosome infectivity in the snail, Biomphalaria glabrata, is partially dependent on the expression of Grctm6, a Guadeloupe Resistance Complex protein. PLoS neglected tropical diseases, 11(2), e0005362.

Schmöckel SM, et al. (2017) Identification of Putative Transmembrane Proteins Involved in Salinity Tolerance in Chenopodium quinoa by Integrating Physiological Data, RNAseq, and SNP Analyses. Frontiers in plant science, 8, 1023.

Nasher F, et al. (2017) Streptococcus pneumoniae Proteins AmiA, AliA, and AliB Bind Peptides Found in Ribosomal Proteins of Other Bacterial Species. Frontiers in microbiology, 8, 2688.

Moreno LF, et al. (2017) Phylogenomic analyses reveal the diversity of laccase-coding genes in Fonsecaea genomes. PloS one, 12(2), e0171291.

Machado H, et al. (2017) FurIOS: A Web-Based Tool for Identification of Vibrionaceae Species Using the fur Gene. Frontiers in microbiology, 8, 414.

Marshall CW, et al. (2017) Metabolic Reconstruction and Modeling Microbial Electrosynthesis. Scientific reports, 7(1), 8391.

Hou H, et al. (2017) The SBP-Box Gene VpSBP11 from Chinese Wild Vitis Is Involved in Floral Transition and Affects Leaf Development. International journal of molecular sciences, 18(7).

Tischer S, et al. (2016) Discovery of immunodominant T-cell epitopes reveals penton protein as a second immunodominant target in human adenovirus infection. Journal of translational medicine, 14(1), 286.

Jimenez-Lopez JC, et al. (2016) Identification and Assessment of the Potential Allergenicity of 7S Vicilins in Olive (Olea europaea L.) Seeds. BioMed research international, 2016, 4946872.

Saldaña-Ahuactzi Z, et al. (2016) Effects of lng Mutations on LngA Expression, Processing, and CS21 Assembly in Enterotoxigenic Escherichia coli E9034A. Frontiers in microbiology, 7, 1201.

Li FC, et al. (2016) Molecular characterization of the Haemonchus contortus phosphoinositide-dependent protein kinase-1 gene (Hc-pdk-1). Parasites & vectors, 9, 65.

Ariani P, et al. (2016) Genome-wide characterisation and expression profile of the grapevine ATL ubiquitin ligase family reveal biotic and abiotic stress-responsive and development-related members. Scientific reports, 6, 38260.

Kamprom W, et al. (2016) Endothelial Progenitor Cell Migration-Enhancing Factors in the Secretome of Placental-Derived Mesenchymal Stem Cells. Stem cells international, 2016, 2514326.

Shen HQ, et al. (2015) Isolation and phylogenetic analysis of hemagglutinin gene of H9N2 influenza viruses from chickens in South China from 2012 to 2013. Journal of veterinary science, 16(3), 317.