

Resource Summary Report

Generated by [dkNET](#) on Aug 27, 2026

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/>

Proper Citation: DTU Center for Biological Sequence Analysis (RRID:SCR_003590)

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, data access protocol, production service resource, service resource, software resource, web service

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 ;
Danish Research Councils ;
Danish Center for Scientific Computing ;
Villum Kann Rasmussen Foundation ;
Novo Nordisk Foundation ;
European Union ;

NIH

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>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260821T193713+0000

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 1475 mentions in open access literature.

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

Feng CH, et al. (2026) Genome-Wide Characterization and Expression Profiling of the CCR Gene Family Associated with Stem Strength in Upland Cotton (*Gossypium hirsutum* L.). *Life* (Basel, Switzerland), 16(5).

Meng F, et al. (2026) Structural, Evolutionary, and Regulatory Divergence of FAH12 from FAD2 Reveals Recurrent Independent Neofunctionalization Underlying Ricinoleic Acid Biosynthesis in *Ricinus communis*. *Plants* (Basel, Switzerland), 15(10).

Noskova Y, et al. (2026) Characterization of an Atypical GH19 Family Chitinase from *Vibrio jasicida* KMM 6832. *Microorganisms*, 14(2).

Mu Y, et al. (2026) Pathogen identification and analysis of broiler bronchial obstruction syndrome using high-throughput sequencing technology. *Poultry science*, 105(8), 107032.

Marks J, et al. (2026) Early occurrence of caffeoylshikimic acid esterase (CSE) activity in the hornwort *Anthoceros agrestis*. *Planta*, 263(2), 49.

Wen S, et al. (2026) Identification of Genes Associated with the Pan-Vibrios Resistance (PVR) Trait of Pacific White Shrimp (*Litopenaeus vannamei*) Using a Genome-Wide Association Study. *Biology*, 15(3).

Yang H, et al. (2025) Global analysis of transcription factors using both the reference genome and the multi-transcriptome of *Akebia trifoliata* reveals a sophisticated functional strategy. *Frontiers in plant science*, 16, 1529326.

Zhang K, et al. (2025) Whole Exome Sequencing Identifies Novel Splicing Variants in the PTPRQ Gene and Their Mechanisms in Autosomal Recessive Non-Syndromic Hearing Loss. *Journal of otology*, 20(3), 204.

Li S, et al. (2025) Genome-wide analysis of TMEM38 family revealed functional roles of TMEM38B in fat deposition and its miRNA-mediated regulation in chicken. *Poultry science*, 104(11), 105694.

Falkenstein K, et al. (2025) A Novel Missense Variant in Ultrarare SLC35A1-CDG Alters Cellular Glycosylation, Lipid, and Energy Metabolism Without Affecting CDG Serum Markers. *Human mutation*, 2025, 6290620.

Wang Y, et al. (2025) Study on the High-Efficiency Expression of Horseradish Peroxidase in *Pichia pastoris*. *Molecules (Basel, Switzerland)*, 30(22).

Zhang S, et al. (2025) Robust BICP0-gB indirect ELISA for the accurate diagnosis of bovine alphaherpesvirus 1 infections. *Veterinary and animal science*, 30, 100507.

Pietrow RE, et al. (2025) Wb5, a novel biomarker for monitoring efficacy and success of mass drug administration programs for *Wuchereria bancrofti* elimination. *PLoS neglected tropical diseases*, 19(5), e0013146.

Ezediuno LO, et al. (2025) Developing cancer vaccine with carcinoembryonic antigen and IGF-1R as immunostimulants using immunoinformatics approach. *Korean journal of clinical oncology*, 21(1), 20.

Timothy FM, et al. (2025) Comparative Characterization of *Plasmodium falciparum* Small Heat Shock Proteins and Their Inhibition by Quercetin (3,3',4',5,7-Pentahydroxyflavone). *The protein journal*, 44(5), 580.

Wen Q, et al. (2025) Molecular epidemiological characterization of human bocavirus (HBoV) in acute respiratory infection (ARI) patients in Yucheng, China. *Frontiers in public health*, 13, 1548907.

Najafian J, et al. (2025) Designing a vaccine candidate against egg drop syndrome virus: an in silico approach. *Veterinary research forum : an international quarterly journal*, 16(11), 655.

George S, et al. (2025) Evolutionary dynamics and molecular epidemiology of H1N1 pandemic 2009 influenza A viruses across swine farms in Denmark. *Virus evolution*, 11(1), veaf014.

Youmans L, et al. (2025) Focal Adhesion Kinase Variants May Contribute to Risk of Human Myelomeningocele. *medRxiv : the preprint server for health sciences*.

Acciarri G, et al. (2025) Dissecting the contribution of Kup and KimA to *Enterococcus faecalis* potassium homeostasis. *Scientific reports*, 15(1), 27027.