

# 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, 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 ;  
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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:** 20260905T132506+0000

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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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1475 mentions in open access literature.

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

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).

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

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

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.
- 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.
- 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.
- 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.
- Wang Y, et al. (2025) Study on the High-Efficiency Expression of Horseradish Peroxidase in *Pichia pastoris*. *Molecules (Basel, Switzerland)*, 30(22).
- 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.
- 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.
- 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.
- 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.
- 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.
- Almujri SS, et al. (2025) MetE: a promising protective antigen for tuberculosis vaccine development. *Frontiers in immunology*, 16, 1593263.
- 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.