

Resource Summary Report

Generated by ASWG on Aug 3, 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: web service, software resource, production service resource, data access protocol, service resource, analysis 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 ;
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: 20260803T040344+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 1434 mentions in open access literature.

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

Almujri SS, et al. (2025) MetE: a promising protective antigen for tuberculosis vaccine development. *Frontiers in immunology*, 16, 1593263.

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*.

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.

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.

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.

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.

Wang N, et al. (2025) Structural Homology Fails to Predict Secretion Efficiency in Pichia pastoris: Divergent Responses of Architecturally Similar scFvs to Multi-Parametric Genetic Engineering. International journal of molecular sciences, 26(10).

Laheurte C, et al. (2025) UCPVax, a CD4 helper peptide vaccine, induces polyfunctional Th1 cells, antibody response, and epitope spreading to improve antitumor immunity. Cell reports. Medicine, 6(7), 102196.

Liu J, et al. (2025) Protective Efficacy of an mRNA Vaccine Against HP-PRRSV Challenge in Piglets. Microorganisms, 13(6).

Ozubek S, et al. (2025) Molecular characterization and recombinant expression of Babesia ovis SBP4 protein as a potential serodiagnostic antigen. Scientific reports, 15(1), 45001.

Zhao Z, et al. (2025) Computational design and evaluation of multiepitope vaccines against herpes simplex virus type 1. Frontiers in immunology, 16, 1581571.

Persello A, et al. (2025) A Mg-Chelatase Subunit I Missense Mutant in Barley Exhibits a Cold-Sensitive Phenotype Under Field Conditions. Physiologia plantarum, 177(4), e70434.

Colombini M, et al. (2025) Phenotypic dichotomy in Crotalus durissus ruruima venom and potential consequences for clinical management of snakebite envenomations. PLoS neglected tropical diseases, 19(8), e0013296.

Szathmari B, et al. (2025) Orthrus: a Pumilio-family gene involved in fruiting body and dark stipe development in Coprinopsis cinerea. Frontiers in fungal biology, 6, 1633301.

Park K, et al. (2025) Discovery and genomic characterization of Ulleung virus harbored by Crocidura utsuryoensis on Ulleung Island in Republic of Korea. Scientific reports, 15(1), 21748.

Lou H, et al. (2025) Regulation and functional analysis of BvMBF1c in response to Cercospora leaf spot (CLS) stresses in sugar beet (Beta vulgaris L.). BMC plant biology, 25(1), 1574.