

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

CBS Prediction Servers

RRID:SCR_002874

Type: Tool

Proper Citation

CBS Prediction Servers (RRID:SCR_002874)

Resource Information

URL: <http://www.cbs.dtu.dk/services/>

Proper Citation: CBS Prediction Servers (RRID:SCR_002874)

Description: A portal to the on-line prediction services at Center for Biological Sequence Analysis. All of the servers are available as interactive input forms, and most of the servers are also available as stand-alone software packages with the same functionality. Ready-to-ship packages exist for the most common UNIX platforms. In addition, for some servers, programmatic access is provided in the form of SOAP-based Web Services.

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

Keywords: nucleotide sequence, amino acid sequence, prediction service, web service, biological sequence analysis, data analysis service, stand alone software

Funding: Center for Biological Sequence Analysis

Availability: Free, Freely available

Resource Name: CBS Prediction Servers

Resource ID: SCR_002874

Alternate IDs: nif-0000-25555

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260731T042637+0000

Ratings and Alerts

No rating or validation information has been found for CBS Prediction Servers.

No alerts have been found for CBS Prediction Servers.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 456 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ren J, et al. (2025) Control of Rhizobia Endosymbiosis by Coupling ER Expansion with Enhanced UPR. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(15), e2414519.

Shao D, et al. (2025) The Functional Identification of the CYP2E1 Gene in the Kidney of *Lepus yarkandensis*. *International journal of molecular sciences*, 26(2).

Razzak A, et al. (2025) Development of a multi-epitope vaccine against *Helicobacter pylori* using a novel saRNA technology through an immunoinformatics approach. *Scientific reports*, 15(1), 33753.

Adedeji EO, et al. (2024) Combination of computational techniques and RNAi reveal targets in *Anopheles gambiae* for malaria vector control. *PloS one*, 19(7), e0305207.

Aarthy M, et al. (2024) Identification and prioritisation of potential vaccine candidates using subtractive proteomics and designing of a multi-epitope vaccine against *Wuchereria bancrofti*. *Scientific reports*, 14(1), 1970.

Meraj S, et al. (2024) A novel prolixicin identified in common bed bugs with activity against both bacteria and parasites. *Scientific reports*, 14(1), 13818.

Yu JB, et al. (2024) Death-Associated Protein-1 Plays a Role in the Reproductive Development of *Nilaparvata lugens* and the Transovarial Transmission of Its Yeast-Like Symbiont. *Insects*, 15(6).

Barazesh M, et al. (2024) Bioinformatics analysis to design a multi-epitope mRNA vaccine against *S. agalactiae* exploiting pathogenic proteins. *Scientific reports*, 14(1), 28294.

Li W, et al. (2024) A plant cell death-inducing protein from litchi interacts with *Peronophythora litchii* pectate lyase and enhances plant resistance. *Nature communications*, 15(1), 22.

Long S, et al. (2023) A New Gene SCY3 Homologous to Scygonadin Showing Antibacterial Activity and a Potential Role in the Sperm Acrosome Reaction of *Scylla paramamosain*. *International journal of molecular sciences*, 24(6).

Mohammadi Y, et al. (2023) In silico design and evaluation of a novel mRNA vaccine against BK virus: a reverse vaccinology approach. *Immunologic research*, 71(3), 422.

Huang L, et al. (2023) A brown fat-enriched adipokine, ASRA, is a leptin receptor antagonist that stimulates appetite. *bioRxiv : the preprint server for biology*.

Rezvannejad E, et al. (2023) Identification genetic variations in some heat shock protein genes of Tali goat breed and study their structural and functional effects on relevant proteins. *Veterinary medicine and science*, 9(5), 2247.

Sun X, et al. (2023) Genome characteristics of atypical porcine pestivirus from abortion cases in Shandong Province, China. *Virology journal*, 20(1), 282.

Moens C, et al. (2023) Identification of New *Mycobacterium bovis* antigens and development of a multiplexed serological bead-immunoassay for the diagnosis of bovine tuberculosis in cattle. *PloS one*, 18(10), e0292590.

Yao G, et al. (2023) Identification, characterization and expression analysis of rLcn13, an epididymal lipocalin in rats. *Acta biochimica et biophysica Sinica*, 55(2), 314.

Moeini S, et al. (2023) Phylogenetic analysis and docking study of neuraminidase gene of influenza A/H1N1 viruses circulating in Iran from 2010 to 2019. *Virus research*, 334, 199182.

Khan AT, et al. (2022) A computational and bioinformatic analysis of ACE2: an elucidation of its dual role in COVID-19 pathology and finding its associated partners as potential therapeutic targets. *Journal of biomolecular structure & dynamics*, 40(4), 1813.

Huang T, et al. (2022) Expression of GALNT8 and O-glycosylation of BMP receptor 1A suppress breast cancer cell proliferation by upregulating ER α levels. *Biochimica et biophysica acta. General subjects*, 1866(1), 130046.

Nawade B, et al. (2022) Longer Duration of Active Oil Biosynthesis during Seed Development Is Crucial for High Oil Yield-Lessons from Genome-Wide In Silico Mining and RNA-Seq Validation in Sesame. *Plants (Basel, Switzerland)*, 11(21).