

Resource Summary Report

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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/>

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

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: 20260821T193651+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 480 mentions in open access literature.

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

Dos Santos MJM, et al. (2026) In Silico Analysis and Expression Profiling of Adhesin-Like Flocculins in *Trichosporon asahii*. *Mycopathologia*, 191(1), 28.

Ma Y, et al. (2026) Checkpoint blockade-related CNS adverse events are characterized by neurotoxic T helper cells with sustained neuroantigen reactivity. *Cell reports. Medicine*, 7(4), 102700.

Fu Y, et al. (2026) Disruption of yellow-e3 impairs both adult molting and cuticular melanization in the honeybee (*Apis mellifera*). *Frontiers in zoology*, 23(1).

Zhang YK, et al. (2026) miR-let-7 Targeting ZcCTL-S1 to Regulate Reproductive Development in *Zeugodacus cucurbitae*. *Insects*, 17(3).

Shuvo MN, et al. (2026) Computational and immunoinformatics approaches for designing phytocompound-based drugs and a multi-epitope vaccine targeting FemA, a cell wall protein of *Staphylococcus aureus*. *PloS one*, 21(4), e0346271.

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).

Tusar MTT, et al. (2025) Designing a Multi-Epitope Vaccine Against HPV 16, 18, 33, and 45 Targeting L1 and E7 Proteins: An Immunoinformatics Approach for Cervical Cancer Prevention and Therapy. *Bioinformatics and biology insights*, 19, 11779322251391076.

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.

Xu JT, et al. (2025) FoCup, a secreted protein, is essential for virulence of *Fusarium oxysporum* f. sp. *cucumerinum* on cucumber. *Frontiers in microbiology*, 16, 1728884.

Li P, et al. (2025) A novel exo-lytic and disaccharide-yielding glycosaminoglycan lyase from a marine-derived polysaccharide-degrading actinobacterium *Microbacterium* sp. strain WS15. *Frontiers in microbiology*, 16, 1680841.

Zeng L, et al. (2024) Alginate-Degrading Modes, Oligosaccharide-Yielding Properties, and Potential Applications of a Novel Bacterial Multifunctional Enzyme, Aly16-1. *Microorganisms*, 12(11).

Niu Y, et al. (2024) scTRIM44 Positively Regulated Siniperca Chuatsi Rhabdovirus Through RIG-I- and MDA5-Mediated Interferon Signaling. *Viruses*, 16(12).

Folgueira C, et al. (2024) Remodeling p38 signaling in muscle controls locomotor activity via IL-15. *Science advances*, 10(33), eadn5993.

Mugunthan SP, et al. (2024) Systems approach to design multi-epitopic peptide vaccine candidate against fowl adenovirus structural proteins for *Gallus gallus domesticus*. *Frontiers in cellular and infection microbiology*, 14, 1351303.

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

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.

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.

Moens C, et al. (2024) Genomic comparison between *Mycobacterium bovis* and *Mycobacterium microti* and in silico analysis of peptide-based biomarkers for serodiagnosis. *Frontiers in veterinary science*, 11, 1446930.

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.