

Resource Summary Report

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AlgPred

RRID:SCR_018780

Type: Tool

Proper Citation

AlgPred (RRID:SCR_018780)

Resource Information

URL: <http://crdd.osdd.net/raghava/algpred/>

Proper Citation: AlgPred (RRID:SCR_018780)

Description: Web tool for prediction of allergens based on similarity of known epitope with any region of protein. Used for prediction of allergenic proteins and mapping of IgE epitopes.

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

Defining Citation: [PMID:16844994](#)

Keywords: Allergen prediction, allergenic protein, allergenic protein prediction, IgE epitopes mapping, epitope, protein region, prediction, bio.tools

Funding: Council of Scientific and Industrial Research

Availability: Free, Freely available

Resource Name: AlgPred

Resource ID: SCR_018780

Alternate IDs: biotools:algpred

Alternate URLs: <https://webs.iitd.edu.in/raghava/algpred/submission.html>,
<https://bio.tools/algpred>

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260903T235531+0000

Ratings and Alerts

No rating or validation information has been found for AlgPred.

No alerts have been found for AlgPred.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 94 mentions in open access literature.

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

Valotto RS, et al. (2026) Consensus-based computational mapping of NS1 antigenic determinants in dengue and Zika viruses to improve diagnostic specificity. BMC infectious diseases, 26(1), 380.

Mahdeen AA, et al. (2026) A novel mRNA-based multiepitope vaccine candidate against Cryptosporidium hominis and Cryptosporidium parvum employing reverse-vaccinology and immunoinformatics approaches. PloS one, 21(2), e0343643.

Ali A, et al. (2026) TZ1391: a computationally designed circular mRNA multi-epitope vaccine candidate against Mycobacterium tuberculosis via TLR3 immunomodulation. BMC immunology, 27(1).

Sripath K, et al. (2026) Proteome-Based Antigen Screening and Multi-Epitope Design Against Cutibacterium acnes: An In Silico Study. Biology, 15(12).

Doostmohammadi A, et al. (2026) Phylogeny-guided multi-epitope vaccine design targeting conserved and divergent regions of Brucella OMP2, OMP25, and OMP31: an immunoinformatics study. BMC immunology, 27(1).

Bigdeli Z, et al. (2026) An In Silico Omics Investigation of the Lactobacillus Genus Complex for Allergenicity Mitigation. Immunity, inflammation and disease, 14(2), e70365.

Runtunuwu SVBE, et al. (2026) Immunoinformatics-driven multi-epitope vaccine design targeting PSMA, STEAP1, and B7H3 for prostate cancer. Frontiers in medicine, 13, 1716345.

Ashayeripanah M, et al. (2026) Screening and in silico evaluation of candidate late-stage antigens for incorporation into multi-stage and post-exposure vaccines against tuberculosis. NPJ vaccines, 11(1).

Luo JR, et al. (2025) Design of a multi-Epitope mRNA vaccine against Brucella type IV secretion system using reverse vaccinology and immunogenicity approaches. Scientific reports, 15(1), 30698.

Souod N, et al. (2025) In silico design and evaluation of a multiepitope vaccine against Bordetella pertussis: structural, immunological, and biological properties. Genomics &

informatics, 23(1), 16.

Masum MHU, et al. (2025) Revolutionizing Chikungunya Vaccines: mRNA Breakthroughs With Molecular and Immune Simulations. *Bioinformatics and biology insights*, 19, 11779322251324859.

Kashiri L, et al. (2025) In silico multi-epitope-based vaccine design for *Mycobacterium avium* complex species. *Frontiers in immunology*, 16, 1589083.

Beig M, et al. (2025) Development of a multi-epitope vaccine against *Acinetobacter baumannii*: A comprehensive approach to combating antimicrobial resistance. *PloS one*, 20(3), e0319191.

Patil SM, et al. (2025) Protocol for isolation, fractionation, and system biology-based profiling of gastrointestinal digested dairy colostrum and milk proteome. *STAR protocols*, 6(1), 103657.

Ashayeripanah M, et al. (2025) Enhanced immunogenicity in mouse by recombinant BCG prime and protein boost based on latency antigen Rv1733c and/or reactivation antigen RpfE. *BMC infectious diseases*, 25(1), 1338.

J Saadh M, et al. (2025) Designing of multi-epitope vaccine against Varicella zoster virus (VZV) using immunoinformatics and structural analysis: In silico study. *BioImpacts : BI*, 15, 30994.

Khazaei S, et al. (2025) Designing and Evaluation of a Plasmid Encoding Immunogenic Epitopes From *Echinococcus granulosus* Eg95-1-6, P29, and GST Against Hydatid Cyst in BALB/c Mice. *Journal of parasitology research*, 2025, 1655679.

Khazani Asforooshani M, et al. (2025) Exploiting subtractive genomics to identify novel drug targets and new immunogenic candidates against *Bordetella pertussis*: an in silico study. *Frontiers in bioinformatics*, 5, 1570054.

Fatahi G, et al. (2025) Designing of an efficient DC-inducing multi-epitope vaccine against Epstein Barr virus targeting the GP350 using immunoinformatics and molecular dynamic simulation. *Biochemistry and biophysics reports*, 42, 101966.

Moosavi-Kohnehsari RS, et al. (2025) A new vaccination approach for Salmonellosis employing a multi-epitope vaccine based on live microbial cell factory from *Lactococcus lactis*. *Poultry science*, 104(2), 104789.