

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: service resource, software resource, data access protocol, 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: 20260729T044449+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 68 mentions in open access literature.

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

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

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.

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.

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.

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

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.

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.

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.

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.

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.

Siddiki AZ, et al. (2025) Development of a multi-epitope chimeric vaccine in silico against *Babesia bovis*, *Theileria annulata*, and *Anaplasma marginale* using computational biology tools and reverse vaccinology approach. *PloS one*, 20(1), e0312262.

Naz H, et al. (2025) Utilizing the subtractive proteomics approach to design ensemble vaccine against *Candida lusitanae* for immune response stimulation; a bioinformatics study. *PloS one*, 20(2), e0316264.

Rahman MM, et al. (2025) Designing of an mRNA vaccine against high-risk human papillomavirus targeting the E6 and E7 oncoproteins exploiting immunoinformatics and dynamic simulation. *PloS one*, 20(1), e0313559.

Yu L, et al. (2025) Multimodal deep learning for allergenic proteins prediction. *BMC biology*, 23(1), 232.

Moradkasani S, et al. (2025) Development of a multi-epitope vaccine from outer membrane proteins and identification of novel drug targets against *Francisella tularensis*: an In Silico approach. *Frontiers in immunology*, 16, 1479862.

Karakavuk T, et al. (2025) Recombinant ROP6 protein expressed in *Saccharomyces cerevisiae* INVSc1 cells induced strong immune response and provided significant protection against toxoplasmosis. *Scientific reports*, 15(1), 32979.

Ranjan M, et al. (2024) Predictions of Immunodominant Epitope Peptides From the AsaA Type VI Secretion System in *Acinetobacter baumannii*: A Computational Approach. *Cureus*, 16(5), e59618.

Trabelsi K, et al. (2024) A novel approach to designing viral precision vaccines applied to SARS-CoV-2. *Frontiers in cellular and infection microbiology*, 14, 1346349.

Perez-Soria MME, et al. (2024) Immunization of cattle with a *Rhipicephalus microplus* chitinase peptide containing predicted B-cell epitopes reduces tick biological fitness. *Parasitology*, 151(9), 1053.