Resource Summary Report

Generated by <u>RRID</u> on Apr 28, 2025

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, web service, software resource, data access protocol

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.iiitd.edu.in/raghava/algpred/submission.html, https://bio.tools/algpred

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250428T054143+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 52 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>RRID</u>.

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.

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.

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.

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.

Hakimian M, et al. (2024) A novel chimeric vaccine containing multiple epitopes for simulating robust immune activation against Klebsiella pneumoniae. BMC immunology, 25(1), 27.

Shi J, et al. (2024) In silico designed novel multi-epitope mRNA vaccines against Brucella by targeting extracellular protein BtuB and LptD. Scientific reports, 14(1), 7278.

Albutti A, et al. (2024) An Integrated Approach to Develop a Potent Vaccine Candidate Construct Against Prostate Cancer by Utilizing Machine Learning and Bioinformatics. Cancer reports (Hoboken, N.J.), 7(12), e70079.

Momajadi L, et al. (2024) Designing a multi-epitope influenza vaccine: an immunoinformatics

approach. Scientific reports, 14(1), 25382.

Sánchez-Arroyo A, et al. (2024) Aspergillus niger Ochratoxinase Is a Highly Specific, Metal-Dependent Amidohydrolase Suitable for OTA Biodetoxification in Food and Feed. Journal of agricultural and food chemistry, 72(33), 18658.

Hussain M, et al. (2024) Computational modeling of cyclotides as antimicrobial agents against Neisseria gonorrhoeae PorB porin protein: integration of docking, immune, and molecular dynamics simulations. Frontiers in chemistry, 12, 1493165.

Liang S, et al. (2024) Combined Immunoinformatics to Design and Evaluate a Multi-Epitope Vaccine Candidate against Streptococcus suis Infection. Vaccines, 12(2).

Ramalingam PS, et al. (2024) Design and development of dual targeting CAR protein for the development of CAR T-cell therapy against KRAS mutated pancreatic ductal adenocarcinoma using computational approaches. Discover oncology, 15(1), 592.

Pillay K, et al. (2024) In silico design of Mycobacterium tuberculosis multi-epitope adhesin protein vaccines. Heliyon, 10(18), e37536.

Mahdeen AA, et al. (2024) Designing novel multiepitope mRNA vaccine targeting Hendra virus (HeV): An integrative approach utilizing immunoinformatics, reverse vaccinology, and molecular dynamics simulation. PloS one, 19(10), e0312239.

Ashoori N, et al. (2024) In silico vaccine design: Targeting highly epitopic regions of Clostridium perfringens type D epsilon toxin and Clostridium novyi type B alpha toxin for optimal immunogenicity. Computational and structural biotechnology journal, 25, 153.

Moin AT, et al. (2023) A computational approach to design a polyvalent vaccine against human respiratory syncytial virus. Scientific reports, 13(1), 9702.

Wróblewska B, et al. (2023) Immunoreactive proteins of Capsicum-based spices as a threat to human health: mass spectrometry analysis and in silico mapping. Scientific reports, 13(1), 17723.

Prakash S, et al. (2023) Cross-Protection Induced by Highly Conserved Human B, CD4+, and CD8+ T Cell Epitopes-Based Coronavirus Vaccine Against Severe Infection, Disease, and Death Caused by Multiple SARS-CoV-2 Variants of Concern. bioRxiv : the preprint server for biology.

Fereshteh S, et al. (2023) Defeating a superbug: A breakthrough in vaccine design against multidrug-resistant Pseudomonas aeruginosa using reverse vaccinology. PloS one, 18(8), e0289609.