

Resource Summary Report

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AllerTop

RRID:SCR_018496

Type: Tool

Proper Citation

AllerTop (RRID:SCR_018496)

Resource Information

URL: <https://www.ddg-pharmfac.net/AllerTOP/>

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Description: Web server for in silico prediction of allergens. Alignment free server for in silico prediction of allergens based on main physicochemical properties of proteins. Used to predict the route of allergen exposure: food, inhalant or toxin.

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

Defining Citation: [PMID:23735058](#)

Keywords: Allergen, allergen prediction, physicochemical protein property, protein, protein property, allergen exposure

Funding: National Research Fund of the Ministry of Education and Science ; Bulgaria

Resource Name: AllerTop

Resource ID: SCR_018496

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260801T042816+0000

Ratings and Alerts

No rating or validation information has been found for AllerTop.

No alerts have been found for AllerTop.

Data and Source Information

Usage and Citation Metrics

We found 225 mentions in open access literature.

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

Pasha AVK, et al. (2026) Immunoinformatics-Based Multi-Epitope Vaccine Targeting Helicobacter Pylori. Cancer reports (Hoboken, N.J.), 9(1), e70441.

Khan A, et al. (2026) HMPV-TherResDB: Comprehensive human metapneumovirus (HMPV) database for sequence-structure annotations, vaccine resources, and therapeutics research. Virus research, 363, 199665.

Fadahunsi AI, et al. (2025) Immunoinformatics-Aided Design of a Multiepitope Vaccine Against Eimeria Tenella-Associated Chicken Coccidiosis. Bioinformatics and biology insights, 19, 11779322251348307.

Kumar A, et al. (2025) Protocol for designing a peptide-based multi-epitope vaccine targeting monkeypox using reverse vaccine technology. STAR protocols, 6(1), 103671.

Ranjbar KJ, et al. (2025) Bioinformatics analysis of the in silico engineered protein vaccine with and without Escherichia coli heat labile enterotoxin adjuvant on the model of Klebsiella pneumoniae. Scientific reports, 15(1), 7321.

Zhu F, et al. (2025) Designing a multi-epitope vaccine against Pseudomonas aeruginosa via integrating reverse vaccinology with immunoinformatics approaches. Scientific reports, 15(1), 10425.

Naveed M, et al. (2025) Development of a novel multiepitope vaccine against Menangle virus (MenV) using in-silico approaches by targeting its transmembrane proteins. Scientific reports, 15(1), 13715.

Zhou P, et al. (2025) In silico design and in vitro validation of a multi-epitope peptide vaccine targeting triple-negative breast cancer. Frontiers in oncology, 15, 1611991.

Zaman N, et al. (2025) Molecular insights into pangenome localization and constructs design for Hemophilus influenza vaccine. Scientific reports, 15(1), 22316.

Hosseini SA, et al. (2025) Discovery of novel vaccine candidates based on the immunogenic epitopes derived from Toxoplasma membrane proteins. Clinical and experimental vaccine research, 14(1), 86.

Mashrur MN, et al. (2025) In silico design of novel multi-epitope peptide vaccine against Neospora caninum induced cattle abortion targeting extracellular GRA2 and Nc-p43 protein. Scientific reports, 15(1), 42169.

Mishra SK, et al. (2025) A Mutation-Based Reverse Vaccinology Approach Considering Variability in Epitopes to Combat Multi-Strains: A Study Using Glycoprotein of LASV. Journal of cellular and molecular medicine, 29(20), e70907.

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.

Parvin R, et al. (2025) Designing of a multiepitope-based vaccine against echinococcosis utilizing the potent Ag5 antigen: Immunoinformatics and simulation approaches. *PloS one*, 20(2), e0310510.

Chick JA, et al. (2025) Computational design, expression, and characterization of a *Plasmodium falciparum* multi-epitope, multi-stage vaccine candidate (PfCTMAG). *Heliyon*, 11(2), e42014.

Adeleke MA, et al. (2025) Computational Development of Transmission-Blocking Vaccine Candidates Based on Fused Antigens of Pre- and Post-fertilization Gametocytes Against *Plasmodium falciparum*. *Bioinformatics and biology insights*, 19, 11779322241306215.

da Silva MK, et al. (2025) Immunoinformatic profiling of parvovirus B19 VP1/VP2 epitopes: relevance to surgical transfusion safety. *International journal of surgery (London, England)*, 111(9), 6030.

Almofti YA, et al. (2025) Exploring varicella zoster virus proteome for construction and validation of a multi-epitope based subunit vaccine using multifaceted immunoinformatics approaches. *PloS one*, 20(6), e0324453.

Sadeghi SA, et al. (2025) Immunoinformatics study of CD40 ligand-targeting vaccine constructs: a novel immunotherapeutic approach. *Osong public health and research perspectives*, 16(4), 311.

Barreto AS, et al. (2025) Design and development of highly conserved, HLA-promiscuous T cell multiepitope vaccines against human visceral leishmaniasis. *Frontiers in immunology*, 16, 1540537.