

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

AllerTop

RRID:SCR_018496

Type: Tool

Proper Citation

AllerTop (RRID:SCR_018496)

Resource Information

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

Proper Citation: AllerTop (RRID:SCR_018496)

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: production service resource, web service, data access protocol, software resource, service resource, 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: 20260815T182552+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 352 mentions in open access literature.

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

Ali S, et al. (2026) Immunoinformatics-guided design of a universal chimeric multi-epitope subunit vaccine against Marburg virus disease and Ravn virus co-infection. Scientific reports, 16(1), 6984.

Pajand O, et al. (2026) Computational design of a novel multi-epitope vaccine candidate against group A rotavirus. Virology journal, 23(1).

Emadi SH, et al. (2026) Design and computational evaluation of a prophylactic and therapeutic multi-epitope vaccine candidate against cervical cancer. Virology journal, 23(1), 45.

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.

Ishwar D, et al. (2026) In silico design of a multi-epitope vaccine targeting DENV-1 and DENV-3. Scientific reports, 16(1), 5308.

Ali SR, et al. (2026) In Silico Approach for Fluorene Biodegradation, and the Impacts of Derivatives on the Environment and Health. Journal of xenobiotics, 16(2).

Cai T, et al. (2026) Identification and Characterization of Novel Umami and Umami-Enhancing Peptides from Soy Sauce Using an In Silico Approach and Electronic Tongue. Foods (Basel, Switzerland), 15(4).

Aljumaa MA, et al. (2026) Integrative Spatial Transcriptomics and Immunoinformatics for Prognostic Multi-Epitope Vaccine Construct Prediction Against Synovial Sarcoma. Pharmaceuticals (Basel, Switzerland), 19(2).

He S, et al. (2026) Integrative bioinformatics approach to the mRNA vaccine development for the human papillomavirus using the capsid protein. Biology direct, 21(1).

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.

Aljumaa MA, et al. (2026) Genome-Guided Discovery of Vaccine Targets for a Multi-Epitope Construct Against Multidrug-Resistant Enterobacter cloacae. MicrobiologyOpen, 15(3), e70350.

Zepeda-Cervantes J, et al. (2026) Identification of Conserved B and T Cell Epitopes in Glycoprotein S of Mexican Porcine Epidemic Diarrhea Virus (PEDV) Strains via Immunoinformatics Analysis, Molecular Docking, and Immunofluorescence. Viruses,

18(4).

Naveed M, et al. (2026) Designing a multi-epitope vaccine against yellow fever virus using immunoinformatics approaches. *Open medicine (Warsaw, Poland)*, 21(1), 20261453.

Nguyen TL, et al. (2026) Identification and evaluation of tumor pyroptosis-associated antigens for design a vaccine candidate against lung cancer. *Scientific reports*, 16(1).

Naveed M, et al. (2026) Computational design of a multiepitope vaccine targeting VP1 and VP2 capsid proteins of simian virus 40 (SV40) for enhanced immune activation. *Open medicine (Warsaw, Poland)*, 21(1), 20251284.

Naveed M, et al. (2026) Immunoinformatics-based design and evaluation of a multi-epitope vaccine against *Vibrio fluvialis*. *Scientific reports*, 16(1), 4100.

Nava-Cuamatzi V, et al. (2026) In Silico Design and Evaluation of TcGAPDH as a Vaccine Against Chagas Disease: A Reverse Vaccinology Approach. *Acta parasitologica*, 71(1), 40.

Zhu F, et al. (2026) Computational Validation of Multi-Epitope mRNA Vaccine Targeting *Streptococcus anginosus* Surface Protein (TMPC) as an Effective Alternative Treatment to Reduce Gastric Cancer. *MicrobiologyOpen*, 15(1), e70230.

Karaca Ocak ??, et al. (2026) Computational screening of AI-derived cyclotides as putative VEGFR2 binders for wound-site angiogenesis. *Scientific reports*, 16(1).

Kousar S, et al. (2026) Immunoinformatic-based design of a multi-epitope subunit vaccine against *Ruminococcus torques* using subtractive proteomics and molecular dynamics simulations. *Scientific reports*, 16(1).