

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

AllerHunter: Cross-reactive Allergen Prediction Home

RRID:SCR_002950

Type: Tool

Proper Citation

AllerHunter: Cross-reactive Allergen Prediction Home (RRID:SCR_002950)

Resource Information

URL: <http://tiger.dbs.nus.edu.sg/AllerHunter>

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Description: A cross-reactive allergen prediction program built on a combination of Support Vector Machine (SVM) and pairwise sequence similarity. Cross-reactivity is based on similarity of proteins to allergens. However, not all proteins with similar sequence or structure to known allergens are cross-reactive allergens. AllerHunter aims to predict allergens and non-allergens with high sensitivity and specificity, without compromising efficiency at classification of proteins with similar sequence to known allergens. There are distinct differences between prediction of allergenicity and cross-reactivity of allergens. Allergenicity is the immunogenic potential of an allergen to induce IgE antibody production, whereas cross-reactivity is the potential of a substance to bind to IgE previously induced by a known allergen. It is difficult to predict allergenicity because causes of immunogenicity of allergens are still not completely clear. However it is possible to predict cross-reactivity since it implies similarity in IgE binding sites. Please provide protein sequence in fasta format.

Abbreviations: AllerHunter

Synonyms: AllerHunter: Cross-reactive Allergen Prediction Program

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:19516900](#)

Keywords: fasta, allergen, prediction program, support vector machine

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: AllerHunter: Cross-reactive Allergen Prediction Home

Resource ID: SCR_002950

Alternate IDs: nif-0000-30082

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260905T133119+0000

Ratings and Alerts

No rating or validation information has been found for AllerHunter: Cross-reactive Allergen Prediction Home.

No alerts have been found for AllerHunter: Cross-reactive Allergen Prediction Home.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Canales BI, et al. (2026) map3k1 is required for spatial restriction of progenitor differentiation in planarians. eLife, 14.

Laganaro M, et al. (2025) Enhancing allergenicity risk assessment for novel foods in the EU: insights from the updated EFSA guidance - requirements, knowledge gaps and research needs. Frontiers in toxicology, 7, 1701391.

Kuri PR, et al. (2023) Current Update on Rotavirus in-Silico Multiepitope Vaccine Design. ACS omega, 8(1), 190.

Lata KS, et al. (2018) Exploring Leptospiral proteomes to identify potential candidates for vaccine design against Leptospirosis using an immunoinformatics approach. Scientific reports, 8(1), 6935.

Dash R, et al. (2017) In silico-based vaccine design against Ebola virus glycoprotein. Advances and applications in bioinformatics and chemistry : AABC, 10, 11.

Adhikari UK, et al. (2017) Overlapping CD8+ and CD4+ T-cell epitopes identification for the progression of epitope-based peptide vaccine from nucleocapsid and glycoprotein of emerging Rift Valley fever virus using immunoinformatics approach. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 56, 75.

Oany AR, et al. (2017) Vaccinomics Approach for Designing Potential Peptide Vaccine by Targeting Shigella spp. Serine Protease Autotransporter Subfamily Protein SigA. Journal of immunology research, 2017, 6412353.

Chen J, et al. (2016) dRHP-PseRA: detecting remote homology proteins using profile-based pseudo protein sequence and rank aggregation. Scientific reports, 6, 32333.

Shi J, et al. (2015) Epitope-Based Vaccine Target Screening against Highly Pathogenic MERS-CoV: An In Silico Approach Applied to Emerging Infectious Diseases. PloS one, 10(12), e0144475.

Oany AR, et al. (2015) Highly conserved regions in Ebola virus RNA dependent RNA polymerase may be act as a universal novel peptide vaccine target: a computational approach. In silico pharmacology, 3(1), 7.

Ng XY, et al. (2015) Prediction of antimicrobial peptides based on sequence alignment and support vector machine-pairwise algorithm utilizing LZ-complexity. BioMed research international, 2015, 212715.

Dimitrov I, et al. (2013) AllerTOP--a server for in silico prediction of allergens. BMC bioinformatics, 14 Suppl 6(Suppl 6), S4.