Resource Summary Report

Generated by NIF on May 20, 2025

ANTIGENpro

RRID:SCR_018779
Type: Tool

Proper Citation

ANTIGENpro (RRID:SCR_018779)

Resource Information

URL: http://scratch.proteomics.ics.uci.edu/

Proper Citation: ANTIGENpro (RRID:SCR_018779)

Description: Web tool as sequence-based, alignment-free and pathogen-independent predictor of protein antigenicity.Predicts likelihood that protein is protective antigen. Integrated in SCRATCH suite of predictors.

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

Defining Citation: PMID:20934990

Keywords: Protein antigenicity, sequence based predictior, alignment free predictor, pathogen independent predictor, protein antigenicity predictor, SCRATCH suite, predictor

Funding: NLM LM 07443;
NSF EIA 0321390;
NSF 0513376;
Microsoft Faculty Research Award

Availability: Free, Freely available

Resource Name: ANTIGENpro

Resource ID: SCR_018779

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250519T204043+0000

Ratings and Alerts

No rating or validation information has been found for ANTIGENpro.

No alerts have been found for ANTIGENpro.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 208 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhou X, et al. (2025) Transethnic analysis identifies SORL1 variants and haplotypes protective against Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14214.

Zubair S, et al. (2025) Computational design of multi-epitope vaccine against Hepatitis C Virus infection using immunoinformatics techniques. PloS one, 20(1), e0317520.

Aganja RP, et al. (2025) Expression and delivery of HA1-M2e antigen using an innovative attenuated Salmonella-mediated delivery system confers promising protection against H9N2 avian influenza challenge. Poultry science, 104(1), 104602.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Nahian M, et al. (2025) Development of a broad-spectrum epitope-based vaccine against Streptococcus pneumoniae. PloS one, 20(1), e0317216.

Mall R, et al. (2025) Benchmarking protein language models for protein crystallization. Scientific reports, 15(1), 2381.

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.

Alshiekheid MA, et al. (2024) Bioinformatics and immunoinformatics assisted multiepitope vaccine construct against Burkholderia anthina. Saudi pharmaceutical journal : SPJ : the official publication of the Saudi Pharmaceutical Society, 32(1), 101917.

Khichi S, et al. (2024) A Multi-epitope Subunit Vaccine Identification and Development Against Scrub Typhus (Orientia tsutsugamushi) Using Immunoinformatics Approaches. Cureus, 16(5), e61009.

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.

Liu D, et al. (2024) Epitope screening and vaccine molecule design of PRRSV GP3 and GP5 protein based on immunoinformatics. Journal of cellular and molecular medicine, 28(3), e18103.

Omer I, et al. (2024) Design of an epitope-based peptide vaccine against Cryptococcus neoformans. FEBS open bio, 14(9), 1471.

Yun JS, et al. (2024) In silico analysis for the development of multi-epitope vaccines against Mycobacterium tuberculosis. Frontiers in immunology, 15, 1474346.

Shetty S, et al. (2024) Immunoinformatics design of a multi-epitope vaccine for Chlamydia trachomatis major outer membrane proteins. Scientific reports, 14(1), 29919.

Pang F, et al. (2024) Designing a multi-epitope subunit vaccine against Orf virus using molecular docking and molecular dynamics. Virulence, 15(1), 2398171.

Nafian F, et al. (2024) In Silico Design of a Trans-Amplifying RNA-Based Vaccine against SARS-CoV-2 Structural Proteins. Advances in virology, 2024, 3418062.

Zhuang L, et al. (2024) Leveraging computer-aided design and artificial intelligence to develop a next-generation multi-epitope tuberculosis vaccine candidate. Infectious medicine, 3(4), 100148.

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multi-epitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. Scientific reports, 14(1), 10297.

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.

Li M, et al. (2024) Designing a conjugate vaccine targeting Klebsiella pneumoniae ST258 and ST11. Heliyon, 10(5), e27417.