

Resource Summary Report

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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, service resource, data access protocol, software resource

Defining Citation: [PMID:20934990](#)

Keywords: Protein antigenicity, sequence based predictor, 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: 20260728T043554+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 247 mentions in open access literature.

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

Mahafujul Alam SS, et al. (2025) Immunoinformatics based designing of a multi-epitope cancer vaccine targeting programmed cell death ligand??1. Scientific reports, 15(1), 12420.

Aali F, et al. (2025) Bioinformatics analysis of innovative multi-epitope vaccine utilizing MAGE-A, MAM-A, and Gal-3 for breast cancer management. Scientific reports, 15(1), 19774.

Masum MHU, et al. (2025) Revolutionizing Chikungunya Vaccines: mRNA Breakthroughs With Molecular and Immune Simulations. Bioinformatics and biology insights, 19, 11779322251324859.

Souod N, et al. (2025) In silico design and evaluation of a multiepitope vaccine against Bordetella pertussis: structural, immunological, and biological properties. Genomics & informatics, 23(1), 16.

Aram C, et al. (2025) Development of a candidate mRNA vaccine based on Multi-Peptide targeting VP4 of rotavirus A: an immunoinformatics and molecular dynamics approach. Scientific reports, 15(1), 22610.

Li C, et al. (2025) Design of a multi-epitope recombinant BCG vaccine targeting Brucella OMP31, LptE and VirB2 in immunoinformatics approaches. PloS one, 20(11), e0334843.

Naderian R, et al. (2025) Rational design of multi-epitope vaccine for Chandipura virus using an immunoinformatics approach. PloS one, 20(10), e0335147.

Nahian M, et al. (2025) Immunoinformatic strategy for developing multi-epitope subunit vaccine against Helicobacter pylori. PloS one, 20(2), e0318750.

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

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.

Arriagada V, et al. (2025) In Silico Design and Characterization of a Multiepitope Vaccine Candidate Against Brucella canis Using a Reverse Vaccinology Approach. Journal of immunology research, 2025, 6348238.

Chansap S, et al. (2025) Development of multi-epitope Cathepsin L driven short peptide vaccine against *Fasciola gigantica*. *Frontiers in veterinary science*, 12, 1547937.

Suneesh NS, et al. (2025) Reverse vaccinology-based design of multivalent multiepitope mRNA vaccines targeting key viral proteins of Herpes Simplex Virus type-2. *Frontiers in immunology*, 16, 1586271.

Heidarinia H, et al. (2025) Design a multi-epitope vaccine candidate against *Acinetobacter baumannii* using advanced computational methods. *AMB Express*, 15(1), 103.

Youssef EG, et al. (2025) In Silico Design of a Multiepitope Vaccine Against Intestinal Pathogenic *Escherichia coli* Based on the 2011 German O104:H4 Outbreak Strain Using Reverse Vaccinology and an Immunoinformatic Approach. *Diseases (Basel, Switzerland)*, 13(8).

Nirob MNH, et al. (2025) A multi-epitope vaccine targeting a key virulence factor ClfA: An In-silico approach to combat *Staphylococcus aureus* infections. *PloS one*, 20(10), e0334885.

Mashhadi Abolghasem Shirazi M, et al. (2025) Novel bioinformatics approaches to design epitope-based vaccine against HIV latency by inquiring CTL epitopes and built-in adjuvants. *Scientific reports*, 15(1), 32809.

Sahoo S, et al. (2025) An integrated structural and immunoinformatic approach to design a multi-epitope based vaccine against the foot-and-mouth disease virus. *Scientific reports*, 15(1), 35911.

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

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.