

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

Defining Citation: [PMID:20934990](#)

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

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

Availability: Free, Freely available

Resource Name: ANTIGENpro

Resource ID: SCR_018779

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260821T194151+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 343 mentions in open access literature.

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

Siddiquee NH, et al. (2026) Design of a global population-covering multi-epitope mRNA vaccine against Lassa virus using immunoinformatics. *Scientific reports*, 16(1).

Abebe MA, et al. (2026) In silico Design and Analysis of Engineered Proteins Containing Multi-Epitope and Immunodominant Domains Derived From *Rickettsia prowazekii* Antigens. *Bioinformatics and biology insights*, 20, 11779322261461934.

Akter S, et al. (2026) Immunoinformatics approach to engineer a multi-epitope vaccine against SdrG in skin commensal *Staphylococcus epidermidis*. *PloS one*, 21(3), e0327534.

Seifi N, et al. (2026) Design and in silico evaluation of an mRNA vaccine against HTLV-1 using AI-driven reverse vaccinology approaches. *PloS one*, 21(5), e0340201.

Li S, et al. (2026) In silico design of the multi-epitope vaccine for lung adenocarcinoma based on hub gene-derived neoantigens. *BMC cancer*, 26(1).

Dinata R, et al. (2026) Honey Bee AMPs as a Novel Carrier Protein for the Development of a Subunit Vaccine: An Immunoinformatic Approach. *Current issues in molecular biology*, 48(1).

Batool N, et al. (2026) In Silico Design and Subsequent Expression of Human Papillomavirus-16 and -18 L1 Vaccine Antigens in Broccoli. *Vaccines*, 14(3).

Ahmad S, et al. (2026) Multi-epitope vaccine design against Monkeypox virus: An immunoinformatics approach. *PloS one*, 21(2), e0342087.

Gollapalli P, et al. (2026) Designing and immuno-informatics evaluation of a multi-epitope vaccine targeting lipoprotein A-4'-phosphatase (LpxF) for *Helicobacter pylori* infection control. *Frontiers in bioinformatics*, 6, 1779654.

Khadka S, et al. (2026) In silico design of a multiepitope vaccine against antibiotic drug-resistant *Acinetobacter baumannii*. *Scientific reports*, 16(1).

Rivera MV, et al. (2026) Expression, Solubilization, and Refolding Recovery of a Novel I???Asparaginase-Arginase 1 Chimera from *E. coli* Inclusion Bodies. *ACS omega*, 11(10), 16333.

Zheng J, et al. (2026) Construction of the Multi-Epitope HFMD Vaccine Based on an Attenuated CVB3 Vector and Evaluation of Immunological Responses in Mice. *Vaccines*,

14(4).

Ali A, et al. (2026) TZ1391: a computationally designed circular mRNA multi-epitope vaccine candidate against *Mycobacterium tuberculosis* via TLR3 immunomodulation. *BMC immunology*, 27(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.

Dowran R, et al. (2026) Designing a Vaccine for the Monkeypox Virus Using Immunoinformatics and Structural Tools. *Advanced biomedical research*, 15, 5.

Liu J, et al. (2026) The hydatid cyst fluid protein EgAgB8/1 demonstrates potent immunogenicity by eliciting robust humoral and cellular immune responses in mice. *PLoS neglected tropical diseases*, 20(5), e0014260.

Asadi M, et al. (2026) Design and evaluation of a novel fusion antigen for diagnosing human strongyloidiasis: An immunoinformatics approach. *PloS one*, 21(6), e0351189.

Stong Tangan YA, et al. (2026) In-silico design of a multi-epitope vaccine candidate against *Strongyloides stercoralis*. *BMC infectious diseases*, 26(1).

Farhani I, et al. (2026) Design and immunogenicity of a recombinant *Saccharomyces boulardii* secreting the P2-VP8 subunit rotavirus vaccine. *Scientific reports*, 16(1), 6932.

Rezaei R, et al. (2026) Immunoinformatics-driven design of a conserved RNA-dependent RNA polymerase-based multi-epitope vaccine against avian infectious bronchitis virus. *Veterinary world*, 19(1), 448.