

Resource Summary Report

Generated by [RRID](#) on Aug 14, 2026

C-IMMSIM

RRID:SCR_018775

Type: Tool

Proper Citation

C-IMMSIM (RRID:SCR_018775)

Resource Information

URL: <http://150.146.2.1/C-IMMSIM/>

Proper Citation: C-IMMSIM (RRID:SCR_018775)

Description: Web prediction tool for molecular binding in simulation of immune system. Agent based simulator of immune response that represents pathogens, as well as lymphocytes receptors, by means of their amino acid sequences and makes use of bioinformatics methods for T and B cell epitope prediction. Calculates immune response to generic pathogenic secondary structure. Allows users to submit antigen protein sequence and specify schedule of its injection as well as host haplotype.

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

Defining Citation: [PMID:20419125](#)

Keywords: Molecular binding prediction, molecular binding simulation, immune system, pathogen, lymphocyte receptor, amino acid sequence, T cell epitope prediction, B cell epitope prediction, calculate immune response, generic pathogenic secondary structure, antigen protein sequence, host haplotype, immunogenic part, invading pathogen

Funding: European Community

Availability: Restricted

Resource Name: C-IMMSIM

Resource ID: SCR_018775

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260814T043008+0000

Ratings and Alerts

No rating or validation information has been found for C-IMMSIM.

No alerts have been found for C-IMMSIM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Cao H, et al. (2025) Development of a CTL Epitope-Based Vaccine Targeting Tumor Antigens in Esophageal Cancer: An Immunoinformatic Study. Iranian journal of biotechnology, 23(4), e4084.

Oluwagbemi OO, et al. (2022) Computational construction of a glycoprotein multi-epitope subunit vaccine candidate for old and new South-African SARS-CoV-2 virus strains. Informatics in medicine unlocked, 28, 100845.

Susithra Priyadarshni M, et al. (2022) In silico approach to design a multi-epitopic vaccine candidate targeting the non-mutational immunogenic regions in envelope protein and surface glycoprotein of SARS-CoV-2. Journal of biomolecular structure & dynamics, 40(23), 12948.

Das NC, et al. (2021) Therapeutic Efficacy of Anti-Bestrophin Antibodies against Experimental Filariasis: Immunological, Immune-Informatics and Immune Simulation Investigations. Antibodies (Basel, Switzerland), 10(2).

Mobini S, et al. (2020) Computational Design of a Novel VLP-Based Vaccine for Hepatitis B Virus. Frontiers in immunology, 11, 2074.