

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

SCRATCH

RRID:SCR_014291

Type: Tool

Proper Citation

SCRATCH (RRID:SCR_014291)

Resource Information

URL: <http://scratch.proteomics.ics.uci.edu/index.html>

Proper Citation: SCRATCH (RRID:SCR_014291)

Description: Web protein structure and structural feature prediction server. Software suite includes predictors for secondary structure, relative solvent accessibility, disordered regions, domains, disulfide bridges, single mutation stability, residue contacts versus average, individual residue contacts and tertiary structure. User provides amino acid sequence and selects desired predictions, then submits to the server.

Synonyms: Scratch Protein Predictor

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

Defining Citation: [PMID:15980571](#)

Keywords: Protein predictor, secondary structure, relative solvent accessibility, disordered regions, domains, disulfide bridges, single mutation stability, residue contacts versus average, individual residue contacts, tertiary structure prediction, bio.tools

Availability: Free, Freely available

Resource Name: SCRATCH

Resource ID: SCR_014291

Alternate IDs: biotools:scratch

Alternate URLs: <https://bio.tools/scratch>

Old URLs: <http://www.igb.uci.edu/servers/psss.html>

Record Creation Time: 20220129T080319+0000

Ratings and Alerts

No rating or validation information has been found for SCRATCH.

No alerts have been found for SCRATCH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 141 mentions in open access literature.

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

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.

Feng J, et al. (2026) A temperate phage encoding a catalytically active endolysin: characterization of phage P7869 and its Lys7869 against Pseudomonas aeruginosa. BMC microbiology, 26(1).

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

Fowles DJ, et al. (2025) Physics-Based Solubility Prediction for Organic Molecules. Chemical reviews, 125(15), 7057.

Luo JR, et al. (2025) Design of a multi-Epitope mRNA vaccine against Brucella type IV secretion system using reverse vaccinology and immunogenicity approaches. Scientific reports, 15(1), 30698.

Bukhari K, et al. (2025) Multi-epitope vaccine design against human metapneumovirus via reverse vaccinology and molecular modelling. Scientific reports, 15(1), 45014.

Parvin R, et al. (2025) Designing of a multiepitope-based vaccine against echinococcosis utilizing the potent Ag5 antigen: Immunoinformatics and simulation approaches. PloS one, 20(2), e0310510.

Ullah S, et al. (2025) In Silico Designed Multi-Epitope Vaccine Based on the Conserved Fragments in Viral Proteins for Broad-Spectrum Protection Against Porcine Reproductive and Respiratory Syndrome Virus. Veterinary sciences, 12(6).

Kashiri L, et al. (2025) In silico multi-epitope-based vaccine design for Mycobacterium avium complex species. Frontiers in immunology, 16, 1589083.

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.

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.

Vural O, et al. (2025) Machine learning approaches for predicting protein-ligand binding sites from sequence data. *Frontiers in bioinformatics*, 5, 1520382.

Christensen MO, et al. (2025) Prevalence of Asthma and Asthma Severity Among Patients with Moderate-Severe Atopic Dermatitis Treated with Advanced Systemics. *Acta dermato-venereologica*, 105, adv43415.

Li S, et al. (2025) Immunoinformatics method to design universal multi-epitope nanoparticle vaccine for TGEV S protein. *Scientific reports*, 15(1), 10931.

Salehinejad H, et al. (2025) Machine learning models predicting inpatient falls. *Scientific reports*, 15(1), 45248.

Karakavuk T, et al. (2025) Recombinant ROP6 protein expressed in *Saccharomyces cerevisiae* INVSc1 cells induced strong immune response and provided significant protection against toxoplasmosis. *Scientific reports*, 15(1), 32979.

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.

Khanam A, et al. (2024) An immunoinformatics approach for a potential NY-ESO-1 and WT1 based multi-epitope vaccine designing against triple-negative breast cancer. *Heliyon*, 10(17), e36935.

Echevarria-Cooper SL, et al. (2024) Evaluation of the NIH Toolbox Odor Identification Test across normal cognition, amnesic mild cognitive impairment, and dementia due to Alzheimer's disease. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 20(1), 288.