

Resource Summary Report

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SCRATCH

RRID:SCR_014291

Type: Tool

Proper Citation

SCRATCH (RRID:SCR_014291)

Resource Information

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

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

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 136 mentions in open access literature.

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

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.

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.

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.

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).

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.

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

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.

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

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.

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.

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.

Simbulan AM, et al. (2024) Immunoinformatics-guided approach for designing a pan-proteome multi-epitope subunit vaccine against African swine fever virus. *Scientific reports*, 14(1), 1354.

Li S, et al. (2024) Epitopes screening and vaccine molecular design of PEDV S protein based on immunoinformatics. *Scientific reports*, 14(1), 19537.

Lin Y, et al. (2024) SCRATCH: A programmable, open-hardware, benchtop robot that automatically scratches cultured tissues to investigate cell migration, healing, and tissue sculpting. *bioRxiv : the preprint server for biology*.

Banico EC, et al. (2024) Advancing one health vaccination: In silico design and evaluation of a multi-epitope subunit vaccine against Nipah virus for cross-species immunization using immunoinformatics and molecular modeling. *PloS one*, 19(9), e0310703.