Resource Summary Report

Generated by dkNET on May 18, 2025

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, analysis service resource, web service, software 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

Funding:

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

Record Last Update: 20250517T060129+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 112 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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.

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, amnestic 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.

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.

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

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.

Torungkitmangmi N, et al. (2024) Molecular and biochemical characterizations of a Fasciola gigantica retinoid X receptor-? isoform A (FgRXR?-A). Scientific reports, 14(1), 12347.

Khan J, et al. (2024) Designing multi-epitope vaccines against Echinococcus granulosus: an in-silico study using immuno-informatics. BMC molecular and cell biology, 25(1), 29.

Bui BN, et al. (2024) Enrichment of cell cycle pathways in progesterone-treated endometrial organoids of infertile women compared to fertile women. Journal of assisted reproduction and genetics, 41(9), 2405.

Chen Y, et al. (2024) Epitope screening and self-assembled nanovaccine molecule design of PDCoV-S protein based on immunoinformatics. Frontiers in microbiology, 15, 1402963.

Lin Y, et al. (2024) A programmable, open-source robot that scratches cultured tissues to investigate cell migration, healing, and tissue sculpting. Cell reports methods, 4(12), 100915.

Bui BN, et al. (2024) The endometrial transcriptome of infertile women with and without implantation failure. Acta obstetricia et gynecologica Scandinavica, 103(7), 1348.

Chao P, et al. (2024) Proteomics-based vaccine targets annotation and design of multi-epitope vaccine against antibiotic-resistant Streptococcus gallolyticus. Scientific reports, 14(1), 4836.

Kaur B, et al. (2024) An Immunoinformatic-Based In Silico Identification on the Creation of a Multiepitope-Based Vaccination Against the Nipah Virus. BioMed research international, 2024, 4066641.

Moin AT, et al. (2023) A computational approach to design a polyvalent vaccine against human respiratory syncytial virus. Scientific reports, 13(1), 9702.

Jiang Y, et al. (2023) Explainable Deep Hypergraph Learning Modeling the Peptide Secondary Structure Prediction. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 10(11), e2206151.

Prakash S, et al. (2023) Cross-Protection Induced by Highly Conserved Human B, CD4+, and CD8+ T Cell Epitopes-Based Coronavirus Vaccine Against Severe Infection, Disease, and Death Caused by Multiple SARS-CoV-2 Variants of Concern. bioRxiv : the preprint server for biology.

Genth J, et al. (2023) Identification of proteoforms of short open reading frame-encoded peptides in Blautia producta under different cultivation conditions. Microbiology spectrum, 11(6), e0252823.