Resource Summary Report

Generated by T1D on Jul 29, 2026

3DRefine

RRID:SCR_021883
Type: Tool

Proper Citation

3DRefine (RRID:SCR_021883)

Resource Information

URL: http://sysbio.rnet.missouri.edu/3Drefine/

Proper Citation: 3DRefine (RRID:SCR_021883)

Description: Interactive web server for efficient protein structure refinement with capability to perform web based statistical and visual analysis.

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

Defining Citation: DOI:10.1093/nar/gkw336

Keywords: efficient protein structure refinement, statistical and visual analysis

Funding: NIGMS R01 GM093123

Availability: Free, Freely available

Resource Name: 3DRefine

Resource ID: SCR_021883

Record Creation Time: 20220421T050137+0000

Record Last Update: 20260729T044535+0000

Ratings and Alerts

No rating or validation information has been found for 3DRefine.

No alerts have been found for 3DRefine.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ma S, et al. (2025) Development of a novel multi-epitope subunit mRNA vaccine candidate to combat Acinetobacter baumannii. Scientific reports, 15(1), 1410.

Zhu F, et al. (2025) Designing a multi-epitope vaccine against Pseudomonas aeruginosa via integrating reverse vaccinology with immunoinformatics approaches. Scientific reports, 15(1), 10425.

Tombari W, et al. (2025) A novel mRNA-based multi-epitope vaccine for rabies virus computationally designed via reverse vaccinology and immunoinformatics. Scientific reports, 15(1), 30355.

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against Brucella melitensis in mice. Scientific reports, 15(1), 27210.

Gül A, et al. (2024) Immunogenicity and protection efficacy of a COVID-19 DNA vaccine encoding spike protein with D614G mutation and optimization of large-scale DNA vaccine production. Scientific reports, 14(1), 13865.

Ma S, et al. (2023) Development of a novel multi-epitope mRNA vaccine candidate to combat HMPV virus. Human vaccines & immunotherapeutics, 19(3), 2293300.

Baig DI, et al. (2023) Genome-wide identification and comparative in-silico characterization of ?-galactosidase (GH-35) in ascomycetes and its role in germ tube development of Aspergillus fumigatus via RNA-seq analysis. PloS one, 18(6), e0286428.

Usman M, et al. (2023) Vaccinomics Approach for Multi-Epitope Vaccine Design against Group A Rotavirus Using VP4 and VP7 Proteins. Vaccines, 11(4).

Mashhadi Abolghasem Shirazi M, et al. (2023) Alum and a TLR7 agonist combined with built-in TLR4 and 5 agonists synergistically enhance immune responses against HPV RG1 epitope. Scientific reports, 13(1), 16801.

Wang C, et al. (2022) Abnormal global alternative RNA splicing in COVID-19 patients. PLoS genetics, 18(4), e1010137.

Antonelli ACB, et al. (2022) In silico construction of a multiepitope Zika virus vaccine using immunoinformatics tools. Scientific reports, 12(1), 53.

Mahmoudvand S, et al. (2022) Design of a multi-epitope-based vaccine consisted of immunodominant epitopes of structural proteins of SARS-CoV-2 using immunoinformatics approach. Biotechnology and applied biochemistry.

Shamkh IM, et al. (2022) Nontoxic and Naturally Occurring Active Compounds as Potential Inhibitors of Biological Targets in Liriomyza trifolii. International journal of molecular sciences, 23(21).

Adebayo JO, et al. (2022) Iloneoside, an antimalarial pregnane glycoside isolated from Gongronema latifolium leaf, potentiates the activity of chloroquine against multidrug resistant Plasmodium falciparum. Molecular and biochemical parasitology, 249, 111474.

Yadav ML, et al. (2021) Implication of rare genetic variants of NODAL and ACVR1B in congenital heart disease patients from Indian population. Experimental cell research, 409(1), 112869.

Jabarzadeh S, et al. (2021) In Silico Design of a New Multi-Epitope Peptide-Based Vaccine Candidate Against Q Fever. Molecular biology, 55(6), 950.

Chen Q, et al. (2021) Broaden the sugar donor selectivity of blackberry glycosyltransferase UGT78H2 through residual substitutions. International journal of biological macromolecules, 166, 277.

Abdollahi S, et al. (2021) Physicochemical and structural characterization, epitope mapping and vaccine potential investigation of a new protein containing Tetratrico Peptide Repeats of Acinetobacter baumannii: An in-silico and in-vivo approach. Molecular immunology, 140, 22.

Rolando Alberto RF, et al. (2020) In silico and in vivo studies of gp120-HIV-derived peptides in complex with G4-PAMAM dendrimers. RSC advances, 10(35), 20414.

de Albuquerque PPLF, et al. (2020) Structural insights into NS5B protein of novel equine hepaciviruses and pegiviruses complexed with polymerase inhibitors. Virus research, 278, 197867.