

Resource Summary Report

Generated by [dkNET](#) on Sep 22, 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: data access protocol, software resource, web service

Defining Citation: [DOI:10.1093/nar/gkw336](https://doi.org/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: 20260919T195459+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

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Mehdi AMK, et al. (2026) Bioinformatics-Driven Design of Fusion Recombinant Protein (EgFABP1-EgTeg) for Enhanced Immunodiagnosis of Hydatid Cysts. *Immunity, inflammation and disease*, 14(5), e70401.

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.

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.

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.

Shojaeian A, et al. (2025) Design of a multi-epitope vaccine candidate against *Helicobacter pylori* in gastric cancer: an immunoinformatic approach. *GMS hygiene and infection control*, 20, Doc27.

Krishna SV, et al. (2024) Promising antiviral inhibitors against lumpy skin disease: A vetinformatics approach. *Open veterinary journal*, 14(11), 2806.

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.

Claudia B, et al. (2024) A multi-epitope self-amplifying mRNA SARS-CoV-2 vaccine design using a reverse vaccinology approach. *Research in pharmaceutical sciences*, 19(5), 520.

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

Leal CS, et al. (2023) In Silico Physicochemical Characterization of Fusion Proteins from Emerging Amazonian Arboviruses. *Life (Basel, Switzerland)*, 13(8).

Sharifi F, et al. (2023) Bioinformatics evaluation of anticancer properties of GP63 protein-derived peptides on MMP2 protein of melanoma cancer. *Journal of pathology informatics*, 14, 100190.

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.

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

Ghandadi M, et al. (2022) An Immunoinformatic Strategy to Develop New *Mycobacterium tuberculosis* Multi-epitope Vaccine. *International journal of peptide research and therapeutics*, 28(3), 99.

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

Kochanowski M, et al. (2022) Proteomic Profiling and In Silico Characterization of the Secretome of *Anisakis simplex* Sensu Stricto L3 Larvae. *Pathogens (Basel, Switzerland)*, 11(2).

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

Williams ME, et al. (2022) Molecular Modeling of Subtype-Specific Tat Protein Signatures to Predict Tat-TAR Interactions That May Be Involved in HIV-Associated Neurocognitive Disorders. *Frontiers in microbiology*, 13, 866611.