

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 2026

GalaxyRefine

RRID:SCR_018531

Type: Tool

Proper Citation

GalaxyRefine (RRID:SCR_018531)

Resource Information

URL: <http://galaxy.seoklab.org/cgi-bin/submit.cgi?type=REFINE>

Proper Citation: GalaxyRefine (RRID:SCR_018531)

Description: Web server for protein structure prediction, refinement, and related methods. First rebuilds side chains and performs side-chain repacking and subsequent overall structure relaxation by molecular dynamics simulation.

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

Defining Citation: [PMID:23737448](#)

Keywords: Protein structure prediction, protein, structure prediction, protein structure, molecular dynamics simulation, bio.tools

Funding: National Research Foundation of Korea ;
Seoul National University.

Resource Name: GalaxyRefine

Resource ID: SCR_018531

Alternate IDs: biotools:galaxyrefine

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

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260806T054702+0000

Ratings and Alerts

No rating or validation information has been found for GalaxyRefine.

No alerts have been found for GalaxyRefine.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 248 mentions in open access literature.

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

Kumar A, et al. (2025) Protocol for designing a peptide-based multi-epitope vaccine targeting monkeypox using reverse vaccine technology. STAR protocols, 6(1), 103671.

Zhou P, et al. (2025) In silico design and in vitro validation of a multi-epitope peptide vaccine targeting triple-negative breast cancer. Frontiers in oncology, 15, 1611991.

Shehri ZSA, et al. (2025) Immuno-informatics analyses of important esophageal cancer associated viruses for multi-epitope vaccine design. Frontiers in immunology, 16, 1587224.

Jiang J, et al. (2025) A comprehensive strategy for the development of a multi-epitope vaccine targeting Treponema pallidum, utilizing heat shock proteins, encompassing the entire process from vaccine design to in vitro evaluation of immunogenicity. Frontiers in microbiology, 16, 1551437.

Molari WS, et al. (2025) Amblyostatin-1, the first salivary cystatin with host immunomodulatory and anti-inflammatory properties from the Neotropical tick Amblyomma sculptum, vector of Brazilian spotted fever. Frontiers in immunology, 16, 1585703.

Pineda-Suazo D, et al. (2025) Insights into Octopus maya cathepsins from metatranscriptome and genome: structure evolutionary relationships and functional role prediction in digestive processes. Biology open, 14(4).

Fatahi G, et al. (2025) Designing of an efficient DC-inducing multi-epitope vaccine against Epstein Barr virus targeting the GP350 using immunoinformatics and molecular dynamic simulation. Biochemistry and biophysics reports, 42, 101966.

Motamedi H, et al. (2025) Immunoinformatic evaluation for the development of a potent multi-epitope vaccine against bacterial vaginosis caused by Gardnerella vaginalis. PloS one, 20(2), e0316699.

Hossain S, et al. (2025) In silico evaluation of missense SNPs in cancer-associated Cystatin A protein and their potential to disrupt Cathepsin B interaction. Heliyon, 11(3), e42478.

Gupta S, et al. (2025) Screening of Oncogenic Proteins and Development of a Multiepitope Peptide Vaccine Targeting AKT1 and PARP1 for Breast Cancer by Integrating Reverse Vaccinology and Immune-Informatics Approaches. *Asian Pacific journal of cancer prevention : APJCP*, 26(1), 327.

Tepjanta P, et al. (2025) In vitro and in silico analyses of amino acid substitution effects at the conserved N-linked glycosylation site in hepatitis B virus surface protein on antigenicity, immunogenicity, HBV replication and secretion. *PloS one*, 20(1), e0316328.

Chick JA, et al. (2025) Computational design, expression, and characterization of a *Plasmodium falciparum* multi-epitope, multi-stage vaccine candidate (PfCTMAG). *Heliyon*, 11(2), e42014.

Sadeh S, et al. (2025) Designing influenza virus-derived cell-penetrating peptides for antigen delivery: Integrating uptake efficiency, safety, and receptor targeting. *PloS one*, 20(12), e0338028.

Siddiki AZ, et al. (2025) Development of a multi-epitope chimeric vaccine in silico against *Babesia bovis*, *Theileria annulata*, and *Anaplasma marginale* using computational biology tools and reverse vaccinology approach. *PloS one*, 20(1), e0312262.

Zhong R, et al. (2025) Identification of new HLA-A*0201-restricted cytotoxic T lymphocyte epitopes from LDHC in lung adenocarcinoma. *Frontiers in immunology*, 16, 1564731.

Manna T, et al. (2025) Investigations on genomic, topological and structural properties of diguanylate cyclases involved in *Vibrio cholerae* biofilm signalling using in silico techniques: Promising drug targets in combating cholera. *Current research in structural biology*, 9, 100166.

Ramalingam PS, et al. (2025) Unveiling reverse vaccinology and immunoinformatics toward Saint Louis encephalitis virus: a ray of hope for vaccine development. *Frontiers in immunology*, 16, 1576557.

Zubair A, et al. (2025) Targeting HIV-1 conserved regions: An immunoinformatic pathway to vaccine innovation for the Asia. *PloS one*, 20(3), e0317382.

Chowdhury ZJ, et al. (2025) Deciphering the potential of plant metabolites as insecticides against melon fly (*Zeugodacus cucurbitae*): Exposing control alternatives to assure food security. *Heliyon*, 11(2), e42034.

Arriagada V, et al. (2025) In Silico Design and Characterization of a Multiepitope Vaccine Candidate Against *Brucella canis* Using a Reverse Vaccinology Approach. *Journal of immunology research*, 2025, 6348238.