

Resource Summary Report

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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: data access protocol, service resource, production service resource, software resource, web service, 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: 20260801T190614+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 [RRID](#).

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

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.

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.

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.

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.

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.

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.

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.

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.

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

Gautam V, et al. (2025) Fungal-derived ZnO nanoparticles functionalized with riboflavin and UDP-GlcNAc exhibit potent nematocidal activity against *M. incognita*. *Scientific reports*, 15(1), 38427.