## **Resource Summary Report**

Generated by NIF on May 5, 2025

# **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:** analysis service resource, production service resource, software resource, web service, data access protocol, 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.

Availability: Free, Freely available

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**: 20250505T054629+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 206 mentions in open access literature.

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

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.

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.

Bhat RAH, et al. (2024) Antibacterial activity of a short de novo designed peptide against fish bacterial pathogens. Amino acids, 56(1), 28.

Morgan RN, et al. (2024) Multi-epitope peptide vaccines targeting dengue virus serotype 2 created via immunoinformatic analysis. Scientific reports, 14(1), 17645.

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

Pumchan A, et al. (2024) Computational design of novel chimeric multiepitope vaccine against bacterial and viral disease in tilapia (Oreochromis sp.). Scientific reports, 14(1), 14048.

Karimipour-Saryazdi A, et al. (2024) In Silico Analysis of the ROP29 Protein as a Vaccine Candidate Against Toxoplasma gondii. Journal of parasitology research, 2024, 1918202.

Mubarak AS, et al. (2024) Enhancing tuberculosis vaccine development: a deconvolution neural network approach for multi-epitope prediction. Scientific reports, 14(1), 10375.

Nguyen TL, et al. (2024) Immunoinformatics and computational approaches driven designing a novel vaccine candidate against Powassan virus. Scientific reports, 14(1), 5999.

Ehsasatvatan M, et al. (2024) Designing and immunomolecular analysis of a new broadspectrum multiepitope vaccine against divergent human papillomavirus types. PloS one, 19(12), e0311351.

Amjad H, et al. (2024) Comprehensive bioinformatics-based annotation and functional characterization of bovine chymosin protein revealed novel biological insights. Food chemistry. Molecular sciences, 8, 100191.

David H, et al. (2024) Mitigating candidiasis with acarbose by targeting Candida albicans ?-glucosidase: in-silico, in-vitro and transcriptomic approaches. Scientific reports, 14(1), 11890.

Zhu L, et al. (2024) Design and evaluation of a multi-epitope DNA vaccine against HPV16. Human vaccines & immunotherapeutics, 20(1), 2352908.

Ghaffar SA, et al. (2024) Designing of a multi-epitopes based vaccine against Haemophilius parainfluenzae and its validation through integrated computational approaches. Frontiers in immunology, 15, 1380732.

Barazesh M, et al. (2024) Bioinformatics analysis to design a multi-epitope mRNA vaccine against S. agalactiae exploiting pathogenic proteins. Scientific reports, 14(1), 28294.

Bappy MNI, et al. (2024) Screening of Novel Drug Targets and Drug Design for Bordetella pertussis: A Subtractive Proteomics Approach. Current research in microbial sciences, 7, 100291.

Hashempour A, et al. (2024) Design of multivalent-epitope vaccine models directed toward the world's population against HIV-Gag polyprotein: Reverse vaccinology and immunoinformatics. PloS one, 19(9), e0306559.

Nebangwa DN, et al. (2024) Predictive immunoinformatics reveal promising safety and antionchocerciasis protective immune response profiles to vaccine candidates (Ov-RAL-2 and Ov-103) in anticipation of phase I clinical trials. PloS one, 19(10), e0312315.

Y?lmaz Çolak Ç, et al. (2024) In silico analysis of virulence factors of Streptococcus uberis for a chimeric vaccine design. In silico pharmacology, 12(1), 7.

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multiepitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. Scientific reports, 14(1), 10297.