

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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>

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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, data access protocol, production service resource, service resource, software resource, web service

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: 20260905T132837+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 316 mentions in open access literature.

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

Pajand O, et al. (2026) Computational design of a novel multi-epitope vaccine candidate against group A rotavirus. *Virology journal*, 23(1).

Shuvo MN, et al. (2026) Computational and immunoinformatics approaches for designing phytocompound-based drugs and a multi-epitope vaccine targeting FemA, a cell wall protein of *Staphylococcus aureus*. *PloS one*, 21(4), e0346271.

Núñez-Muñoz LA, et al. (2026) Recombinant Production and Immunological Evaluation of Tobamovirus fructirugosum (ToBRFV) Capsid and Movement Proteins. *Molecular biotechnology*, 68(7), 3206.

Kousar S, et al. (2026) Immunoinformatic-based design of a multi-epitope subunit vaccine against *Ruminococcus torques* using subtractive proteomics and molecular dynamics simulations. *Scientific reports*, 16(1).

Nandish V, et al. (2026) Comparative pangenomics of *Pasteurella multocida* uncovers adhesins specific to capsular serogroup B strains associated with bovine host tropism. *BMC microbiology*, 26(1).

Doostmohammadi A, et al. (2026) Phylogeny-guided multi-epitope vaccine design targeting conserved and divergent regions of *Brucella* OMP2, OMP25, and OMP31: an immunoinformatics study. *BMC immunology*, 27(1).

Chundru D, et al. (2026) In silico design of a multiepitope subunit vaccine targeting *Salmonella enterica* serovar *Infantis*: an immunoinformatics and reverse vaccinology approach. *Frontiers in immunology*, 17, 1717278.

Ahad A, et al. (2026) Ethylene signaling and metabolite reprogramming in salt tolerance of *Triticum aestivum*. *Scientific reports*, 16(1).

Rafi MO, et al. (2026) Predicting the Impact of Deleterious Single-Nucleotide Polymorphisms in the p47ING1a Isoform of Human ING1 Gene. *Genetics research*, 2026(1), e2859448.

Ali A, et al. (2026) TZ1391: a computationally designed circular mRNA multi-epitope vaccine candidate against *Mycobacterium tuberculosis* via TLR3 immunomodulation. *BMC*

immunology, 27(1).

Chatterjee D, et al. (2026) From computational screening to in vitro validation: exploring antimicrobial peptides against *Pseudomonas aeruginosa*. *Frontiers in microbiology*, 17, 1796090.

Stong Tangan YA, et al. (2026) In-silico design of a multi-epitope vaccine candidate against *Strongyloides stercoralis*. *BMC infectious diseases*, 26(1).

Naveed M, et al. (2026) Computational design of a multiepitope vaccine targeting VP1 and VP2 capsid proteins of simian virus 40 (SV40) for enhanced immune activation. *Open medicine (Warsaw, Poland)*, 21(1), 20251284.

Naveed M, et al. (2026) Immunoinformatics-based design and evaluation of a multi-epitope vaccine against *Vibrio fluvialis*. *Scientific reports*, 16(1), 4100.

Youssef DG, et al. (2026) Computational characterization of GRP78 binding sites on mitochondrial GPX4: implications for targeting ferroptosis in triple-negative breast cancer. *Scientific reports*, 16(1), 1330.

Zhu F, et al. (2026) Computational Validation of Multi-Epitope mRNA Vaccine Targeting *Streptococcus anginosus* Surface Protein (TMPC) as an Effective Alternative Treatment to Reduce Gastric Cancer. *MicrobiologyOpen*, 15(1), e70230.

Afshan G, et al. (2026) A mutation-aware proteomics approach for designing a multi-epitope vaccine against multidrug-resistant *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. *Microbiology spectrum*, 14(4), e0309525.

Saber MA, et al. (2026) Pan-genome and reverse vaccinology for a multi-epitope vaccine against circulating post-2022 Monkeypox virus strains. *PloS one*, 21(6), e0351881.

Yuan L, et al. (2026) Clinical Serum-Anchored Computational Design Pipeline for a Broad-Spectrum Influenza Multi-Epitope mRNA Vaccine. *Biology*, 15(4).

Zheng N, et al. (2026) In silico design of a novel multi-epitope mRNA vaccine candidate for BtHKU5-CoV-2 using immunoinformatics. *PLoS neglected tropical diseases*, 20(4), e0013517.