

Resource Summary Report

Generated by T1D on Jul 31, 2026

GalaxyWEB

RRID:SCR_018558

Type: Tool

Proper Citation

GalaxyWEB (RRID:SCR_018558)

Resource Information

URL: <http://galaxy.seoklab.org/>

Proper Citation: GalaxyWEB (RRID:SCR_018558)

Description: Web server for protein structure prediction and refinement. Used to predict protein structure from sequence by template based modeling. Used for refinement after providing starting model structure and locations of loops or termini to be refined.

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

Defining Citation: [PMID:22649060](https://pubmed.ncbi.nlm.nih.gov/22649060/)

Keywords: Protein structure prediction, protein structure refinement, protein sequence, template based modeling, model structure, loop location, bio.tools

Funding: National Research Foundation of Korea ;
Ministry of Land ;
Transport and Maritime Affairs of Korea ;
Seoul National University

Availability: Free, Freely available

Resource Name: GalaxyWEB

Resource ID: SCR_018558

Alternate IDs: biotools:galaxyweb

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

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260731T043032+0000

Ratings and Alerts

No rating or validation information has been found for GalaxyWEB.

No alerts have been found for GalaxyWEB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 157 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Sheikhi A, et al. (2025) Novel sACE2-Anti-CD16VHH Fusion Protein Surreptitiously Inhibits SARS-CoV-2 Variant Spike Proteins and Macrophage Cytokines, and Activates Natural Killer Cell Cytotoxicity. *Vaccines*, 13(2).

Masum MHU, et al. (2025) Revolutionizing Chikungunya Vaccines: mRNA Breakthroughs With Molecular and Immune Simulations. *Bioinformatics and biology insights*, 19, 11779322251324859.

Khan S, et al. (2025) Immunoinformatics-based strategies for developing DNA and mRNA vaccines against monkeypox virus (MPXV). *Virology journal*, 22(1), 377.

Aali F, et al. (2025) Bioinformatics analysis of innovative multi-epitope vaccine utilizing MAGE-A, MAM-A, and Gal-3 for breast cancer management. *Scientific reports*, 15(1), 19774.

Yalcouyé A, et al. (2025) Whole-exome sequencing reveals known and candidate genes for hearing impairment in Mali. *HGG advances*, 6(1), 100391.

Mosalanejad Z, et al. (2025) Designing an optimized theta-defensin peptide for HIV therapy using in-silico approaches. *Journal of integrative bioinformatics*, 22(1).

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.

Ranjbar KJ, et al. (2025) Bioinformatics analysis of the in silico engineered protein vaccine with and without Escherichia coli heat labile enterotoxin adjuvant on the model of Klebsiella pneumoniae. *Scientific reports*, 15(1), 7321.

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.

Tan X, et al. (2025) Development of ZHPV16E7- granzyme B immunoaffitoxin: dual mechanisms targeting hpv16-positive cervical cancer through epithelial-mesenchymal

transition inhibition and cell death. *Frontiers in immunology*, 16, 1616715.

Yarmohammadi H, et al. (2025) Development of a novel bivalent vaccine candidate against hepatitis A virus and rotavirus using reverse vaccinology and immunoinformatics. *Journal of virus eradication*, 11(1), 100578.

Zubair S, et al. (2025) Computational design of multi-epitope vaccine against Hepatitis C Virus infection using immunoinformatics techniques. *PloS one*, 20(1), e0317520.

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

Nirob MNH, et al. (2025) A multi-epitope vaccine targeting a key virulence factor ClfA: An In-silico approach to combat *Staphylococcus aureus* infections. *PloS one*, 20(10), e0334885.

Liang S, et al. (2025) The ABC type fucose operon regulated by XtrSs through CcpA contributes to *Streptococcus suis* survival in macrophages. *Virulence*, 16(1), 2553790.

Heidarinia H, et al. (2025) Design a multi-epitope vaccine candidate against *Acinetobacter baumannii* using advanced computational methods. *AMB Express*, 15(1), 103.

Adelusi TI, et al. (2025) Designing of an innovative conserved multiepitope subunit vaccine targeting SARS-CoV-2 glycoprotein and nucleoprotein through immunoinformatic. *Scientific reports*, 15(1), 2563.

Tariq TB, et al. (2025) Molecular modelling and gene expression analysis to probe the GT-? trihelix transcription factors in *Solanum tuberosum* under drought stress. *Scientific reports*, 15(1), 12471.

Gharazi H, et al. (2025) Brucellosis novel multi-epitope vaccine design based on in silico analysis focusing on *Brucella abortus*. *BMC immunology*, 26(1), 46.

Adeleke MA, et al. (2025) Computational Development of Transmission-Blocking Vaccine Candidates Based on Fused Antigens of Pre- and Post-fertilization Gametocytes Against *Plasmodium falciparum*. *Bioinformatics and biology insights*, 19, 11779322241306215.