

Resource Summary Report

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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: data access protocol, service resource, analysis service resource, web service, software resource, production 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: 20250421T054246+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 127 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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

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.

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

Rahman MM, et al. (2025) Designing of an mRNA vaccine against high-risk human papillomavirus targeting the E6 and E7 oncoproteins exploiting immunoinformatics and dynamic simulation. PloS one, 20(1), e0313559.

Khanam A, et al. (2024) An immunoinformatics approach for a potential NY-ESO-1 and WT1 based multi-epitope vaccine designing against triple-negative breast cancer. Heliyon, 10(17), e36935.

Martínez-Valencia D, et al. (2024) The Entamoeba histolytica Vps26 (EhVps26) retromeric protein is involved in phagocytosis: Bioinformatic and experimental approaches. PloS one, 19(8), e0304842.

- Wen Z, et al. (2024) Exploring DIX-DIX Homo- and Hetero-Oligomers in Wnt Signaling with AlphaFold2. *Cells*, 13(19).
- Moin AT, et al. (2024) Computational design and evaluation of a polyvalent vaccine for viral nervous necrosis (VNN) in fish to combat Betanodavirus infection. *Scientific reports*, 14(1), 27020.
- Liu J, et al. (2024) A multi-epitope subunit vaccine providing broad cross-protection against diverse serotypes of *Streptococcus suis*. *NPJ vaccines*, 9(1), 216.
- Li M, et al. (2024) Designing a conjugate vaccine targeting *Klebsiella pneumoniae* ST258 and ST11. *Heliyon*, 10(5), e27417.
- Shi J, et al. (2024) In silico designed novel multi-epitope mRNA vaccines against *Brucella* by targeting extracellular protein BtuB and LptD. *Scientific reports*, 14(1), 7278.
- Sui B, et al. (2024) TRIM72 restricts lyssavirus infection by inducing K48-linked ubiquitination and proteasome degradation of the matrix protein. *PLoS pathogens*, 20(2), e1011718.
- Arshad SF, et al. (2024) Multi-epitopes vaccine design for surface glycoprotein against SARS-CoV-2 using immunoinformatic approach. *Heliyon*, 10(2), e24186.
- Nair G, et al. (2024) An intramolecular cross-talk in D29 mycobacteriophage endolysin governs the lytic cycle and phage-host population dynamics. *Science advances*, 10(6), eadh9812.
- 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.
- Elshafei SO, et al. (2024) Immunoinformatics, molecular docking and dynamics simulation approaches unveil a multi epitope-based potent peptide vaccine candidate against avian leukosis virus. *Scientific reports*, 14(1), 2870.
- Bamba S, et al. (2024) Case report: Novel variants cause developmental and epileptic encephalopathy in three unrelated families from Mali. *Frontiers in genetics*, 15, 1412442.
- Shabir A, et al. (2024) Exploring HMMR as a therapeutic frontier in breast cancer treatment, its interaction with various cell cycle genes, and targeting its overexpression through specific inhibitors. *Frontiers in pharmacology*, 15, 1361424.
- David H, et al. (2024) Mitigating candidiasis with acarbose by targeting *Candida albicans* α -glucosidase: in-silico, in-vitro and transcriptomic approaches. *Scientific reports*, 14(1), 11890.
- Zhu X, et al. (2024) Design of multi-epitope vaccine against porcine rotavirus using computational biology and molecular dynamics simulation approaches. *Virology journal*, 21(1), 160.