

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/>

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

Defining Citation: [PMID:22649060](#)

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

Funding: Ministry of Land ;
Transport and Maritime Affairs of Korea ;
National Research Foundation 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: 20260919T195353+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 231 mentions in open access literature.

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

Wonkam A, et al. (2026) Exome sequencing identifies known and candidate genes in hearing impairment in Cameroon. Communications medicine, 6(1).

Kolla HB, et al. (2026) Unleashing the immune arsenal: development of broad spectrum multiepitope bluetongue vaccine targeting conserved T cell epitopes of structural proteins. BMC genomics, 27(1).

Elrashedy A, et al. (2026) Immunoinformatics-based design of artificial chimeric proteins as universal vaccine candidates against foot-and-mouth disease virus serotypes A, O, and SAT2. Scientific reports, 16(1).

Garay E, et al. (2026) A High-Coverage Epitope-Based Vaccine Design for EIAV Envelope Polyprotein Using an Immunoinformatic Approach. Veterinary sciences, 13(3).

Khan N, et al. (2026) Comparative evolutionary and structural bioinformatic analysis of the human N-Acetyltransferase-2 (NAT2) gene with different mammalian and avian taxa. BMC genomics, 27(1), 143.

Zubair A, et al. (2026) Integrative immunogenomic strategy for designing a multi-epitope vaccine against Zika and Dengue viruses. Scientific reports, 16(1).

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).

Gollapalli P, et al. (2026) Designing and immuno-informatics evaluation of a multi-epitope vaccine targeting lipoprotein A-4'-phosphatase (LpxF) for Helicobacter pylori infection control. Frontiers in bioinformatics, 6, 1779654.

Tao X, et al. (2026) Preparation of a multiepitope vaccine candidate for camel bocavirus and evaluation of its immunogenicity in a mouse model. Frontiers in immunology, 17, 1786028.

Nieto-Giraldo DF, et al. (2026) Analysis of the Effect of the Magnetic Field on Water Flux Through TIP3;1 Aquaporins Using Molecular Dynamics in GROMACS. *The Journal of membrane biology*, 259(1), 7.

Ulloa-Aguilar JM, et al. (2026) Human respiratory syncytial virus regulates the expression of interferon-stimulated genes through modulation of fibrillarin. *Frontiers in cellular and infection microbiology*, 16, 1706028.

Li T, et al. (2026) Unraveling the potential carcinogenic risk of bisphenols: a comprehensive network analysis and computational toxicology insights. *Human genomics*, 20(1).

Jung E, et al. (2026) Ebastine targets HER2/HER3 signaling and cancer stem cell traits to overcome trastuzumab resistance in HER2???positive breast cancer. *International journal of molecular medicine*, 57(4).

Dabiri M, et al. (2026) Computational optimization of DEK1 calpain domain solubility through integrated structural modelling and data-driven targeted mutagenesis. *Scientific reports*, 16(1).

Rezaei R, et al. (2026) Immunoinformatics-driven design of a conserved RNA-dependent RNA polymerase-based multi-epitope vaccine against avian infectious bronchitis virus. *Veterinary world*, 19(1), 448.

Vo TTB, et al. (2026) Mild to Virulent: Coat Protein Mutations Restore Mosaic Symptom Induction in a Korean PepMV Isolate. *Viruses*, 18(2).

Workneh YA, et al. (2026) In silico design of novel recombinant antigens containing immunologically relevant regions of wild-type and escape mutant variants of HBsAg. *PloS one*, 21(3), e0344362.

Fuad M, et al. (2026) A comprehensive in silico investigation into the deleterious nonsynonymous single nucleotide polymorphisms of the human transcription factor EB (TFEB) gene and their predicted association with cancer. *Journal, genetic engineering & biotechnology*, 24(2), 100686.

Puagsopa J, et al. (2025) Development of a Broad-Spectrum Pan-Mpox Vaccine via Immunoinformatic Approaches. *International journal of molecular sciences*, 26(15).

Tusar MTT, et al. (2025) Designing a Multi-Epitope Vaccine Against HPV 16, 18, 33, and 45 Targeting L1 and E7 Proteins: An Immunoinformatics Approach for Cervical Cancer Prevention and Therapy. *Bioinformatics and biology insights*, 19, 11779322251391076.