

Resource Summary Report

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PROCHECK

RRID:SCR_019043

Type: Tool

Proper Citation

PROCHECK (RRID:SCR_019043)

Resource Information

URL: <https://www.ebi.ac.uk/thornton-srv/software/PROCHECK/>

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Description: Software tool to check stereochemical quality of protein structures. Its outputs comprise number of plots in PostScript format and comprehensive residue by residue listing. Includes PROCHECK-NMR for checking quality of structures solved by NMR.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [DOI:10.1107/S0021889892009944](https://doi.org/10.1107/S0021889892009944)

Keywords: Stereochemical quality, protein structure, plot, residue listing, protein, assessing protein quality,

Availability: Free, Available for download

Resource Name: PROCHECK

Resource ID: SCR_019043

License URLs: <https://www.ebi.ac.uk/thornton-srv/software/PROCHECK/confid.txt>

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260905T132845+0000

Ratings and Alerts

No rating or validation information has been found for PROCHECK.

No alerts have been found for PROCHECK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 122 mentions in open access literature.

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

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).

Attique L, et al. (2026) Multiepitope-Based Peptide Vaccine Against A35R Glycoprotein and E8L Membrane Protein of Monkeypox Virus Using an Immunoinformatics Approach. Biology, 15(7).

Hussain Z, et al. (2026) Phylogenetic Relationships and Structural Conservation of blaOXA-48-like Carbapenemase in Multispecies Clinical Strains from an Intensive Care Unit in Pakistan. International journal of molecular sciences, 27(12).

Wakid MH, et al. (2026) Kaempferol activity on Cryptosporidium parvum infection in an experimentally infected immunocompromised mouse model: In silico and in vivo investigations. Pharmaceutical biology, 64(1), 27.

Fathi S, et al. (2026) Systems Vaccinology-Integrated Proteomics to Develop a Novel Prophylactic and Therapeutic Vaccine Against Human Papillomavirus 16. Bioinformatics and biology insights, 20, 11779322261437247.

Rahaman HH, et al. (2026) In silico prediction, molecular docking and simulation of natural flavonoid apigenin and xanthoangelol E against human metapneumovirus. In silico pharmacology, 14(1), 40.

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.

Mallawarachchi S, et al. (2026) Evaluation of molecular interactions of vaping juice components with ACE2 receptor. Scientific reports, 16(1).

Ribeiro JA, et al. (2026) Molecular Characterization of Tomato Brown Rugose Fruit Virus in Portugal and Its Global Phylogenetic Context. Plants (Basel, Switzerland), 15(8).

Gómez-Escobedo R, et al. (2026) An In Silico and In Vitro Approach Identified Potential Trypanothione Synthetase Inhibitors with Trypanocidal Activity. Molecules (Basel, Switzerland), 31(7).

Aljumaa MA, et al. (2026) Integrative Spatial Transcriptomics and Immunoinformatics for Prognostic Multi-Epitope Vaccine Construct Prediction Against Synovial Sarcoma. Pharmaceuticals (Basel, Switzerland), 19(2).

Runtunuwu SVBE, et al. (2026) Immunoinformatics-driven multi-epitope vaccine design targeting PSMA, STEAP1, and B7H3 for prostate cancer. *Frontiers in medicine*, 13, 1716345.

Karkoutly O, et al. (2026) Computational Repurposing and Experimental Validation of YBX1 Inhibitors in Hepatocellular Carcinoma. *Biomedicines*, 14(3).

Czyrek AA, et al. (2026) Engineered fibroblast growth factor 1 variants uncouple glucose-lowering effects from mitogenic activity with therapeutic potential for type 2 diabetes. *Molecular biomedicine*, 7(1), 4.

Teimoori P, et al. (2026) Computational Design of an mRNA Vaccine Targeting LRP6 for Triple-Negative Breast Cancer Therapy. *Cancer reports (Hoboken, N.J.)*, 9(5), e70567.

Arriagada V, et al. (2025) In Silico Design and Characterization of a Multiepitope Vaccine Candidate Against *Brucella canis* Using a Reverse Vaccinology Approach. *Journal of immunology research*, 2025, 6348238.

Han Y, et al. (2025) Molecular Characterization of a Novel Alkaline Endo-Pectate Lyase from *Paenibacillus borealis* and Over-Production in Bioreactor Realized by Constructing the Tandem Expression Cassettes in Host Genome. *Molecules (Basel, Switzerland)*, 30(17).

Kasibhatla SM, et al. (2025) Construction of an immunoinformatics-based multi-epitope vaccine candidate targeting Kyasanur forest disease virus. *PeerJ*, 13, e18982.

Nahian M, et al. (2025) Immunoinformatic strategy for developing multi-epitope subunit vaccine against *Helicobacter pylori*. *PloS one*, 20(2), e0318750.

Farooq A, et al. (2025) Detection of probable phytochemical inhibitors targeting kallikrein related peptidase 7 (KLK7) in ovarian cancer through molecular dynamics and virtual screening approaches. *Scientific reports*, 15(1), 34749.