

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

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: 20260808T190126+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 [SPARC SAWG](#) .

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).

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).

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.

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.

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.

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.

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.

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.

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.