

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, data processing software, software application, data analysis 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: 20260804T043708+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 75 mentions in open access literature.

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

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.

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.

Aganja RP, et al. (2025) Expression and delivery of HA1-M2e antigen using an innovative attenuated *Salmonella*-mediated delivery system confers promising protection against H9N2 avian influenza challenge. *Poultry science*, 104(1), 104602.

Ullah S, et al. (2025) GCMS analysis and acaricidal activity of *Ailanthus altissima* extract against cattle tick *Rhipicephalus (Boophilus) microplus* and *Hyalomma anatolicum*: in vitro and in silico approach. *Scientific reports*, 15(1), 19814.

Basharat Z, et al. (2025) Proteome mining of *Yersinia Enterocolitica* for drug targets and computational inhibitor identification with ADMET, anti-inflammation potential and formulation characteristics. *BioData mining*, 18(1), 68.

Ghaly HKF, et al. (2025) Phytochemical and antibacterial properties of calyces *Hibiscus sabdariffa* L.: an in vitro and in silico multitarget-mediated antibacterial study. *BMC complementary medicine and therapies*, 25(1), 62.

Mishra AP, et al. (2025) Integrative in silico and Petra/Osiris/Molinspiration (POM) analysis of baicalein: identification of therapeutically relevant pharmacophores against keloid pathology. *Drug target insights*, 19, 49.

Khatooni Z, et al. (2025) Combined immunoinformatic approaches with computational biochemistry for development of subunit-based vaccine against *Lawsonia intracellularis*. *PloS one*, 20(2), e0314254.

Martiz RM, et al. (2025) Identification and 3D modeling of bioactive peptides from *Lactobacillus brevis* RAMULAB49 protein hydrolysate with in silico ERK1 phosphorylation inhibition activity targeting diabetic nephropathy. *PloS one*, 20(9), e0331192.

Vieira Alves M, et al. (2025) Intratype variants and high genotypic diversity of human papillomavirus with polymorphisms in the antigenic hypervariable loops of the L1 protein from women living with human immunodeficiency virus in Northeastern Brazil. *Journal of medical microbiology*, 74(3).

Lian K, et al. (2025) Identification and expression of a novel antimicrobial peptide Gloverin and its antibacterial effect against *Staphylococcus aureus*. *BMC microbiology*, 25(1), 554.

Almowallad S, et al. (2024) Berberine modulates cardiovascular diseases as a multitarget-mediated alkaloid with insights into its downstream signals using in silico prospective screening approaches. *Saudi journal of biological sciences*, 31(5), 103977.

Oladipo EK, et al. (2024) Exploring computational approaches to design mRNA Vaccine against vaccinia and Mpox viruses. *Immunity, inflammation and disease*, 12(8), e1360.

Floch A, et al. (2024) Molecular dynamics of the human RhD and RhAG blood group proteins. *Frontiers in chemistry*, 12, 1360392.

Andrade-Pavón D, et al. (2024) Review and Current Perspectives on DNA Topoisomerase I and II Enzymes of Fungi as Study Models for the Development of New Antifungal Drugs. *Journal of fungi (Basel, Switzerland)*, 10(9).

Pourhajibagher M, et al. (2024) Bioinformatics analysis of photoexcited natural flavonoid glycosides as the inhibitors for oropharyngeal HPV oncoproteins. *AMB Express*, 14(1), 29.

Shoaib R, et al. (2024) Prefoldins are novel regulators of the unfolded protein response in artemisinin resistant *Plasmodium falciparum* malaria. *The Journal of biological chemistry*, 300(8), 107496.