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, software resource, software application, data processing software

Defining Citation: DOI:10.1107/S0021889892009944

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

Funding:

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: 20250421T054306+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 62 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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).

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.

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

Arshad NF, et al. (2024) Engineering receptor-binding domain and heptad repeat domains towards the development of multi-epitopes oral vaccines against SARS-CoV-2 variants. PloS one, 19(8), e0306111.

Basu Mallick S, et al. (2024) Comprehensive in silico analyses of fifty-one uncharacterized proteins from Vibrio cholerae. PloS one, 19(10), e0311301.

Shetty S, et al. (2024) Immunoinformatics design of a multi-epitope vaccine for Chlamydia trachomatis major outer membrane proteins. Scientific reports, 14(1), 29919.

Zhang LJ, et al. (2024) Identification of lipid senolytics targeting senescent cells through ferroptosis induction. bioRxiv : the preprint server for biology.

Dueñas S, et al. (2023) Chimeric Peptides from Californiconus californicus and Heterodontus francisci with Antigen-Binding Capacity: A Conotoxin Scaffold to Create Non-Natural Antibodies (NoNaBodies). Toxins, 15(4).

Muscat S, et al. (2023) In silico investigation of cytochrome bc1 molecular inhibition mechanism against Trypanosoma cruzi. PLoS neglected tropical diseases, 17(1), e0010545.

Tasneem M, et al. (2023) In silico annotation of a hypothetical protein from Listeria monocytogenes EGD-e unfolds a toxin protein of the type II secretion system. Genomics & informatics, 21(1), e7.

Tasleem M, et al. (2023) An In Silico Bioremediation Study to Identify Essential Residues of Metallothionein Enhancing the Bioaccumulation of Heavy Metals in Pseudomonas aeruginosa. Microorganisms, 11(9).

Khater I, et al. (2023) A computational peptide model induces cancer cells' apoptosis by docking Kringle 5 to GRP78. BMC molecular and cell biology, 24(1), 25.

Waseem M, et al. (2023) Molecular Characterization of spa, hld, fmhA, and lukD Genes and Computational Modeling the Multidrug Resistance of Staphylococcus Species through Callindra harrisii Silver Nanoparticles. ACS omega, 8(23), 20920.

Chakma V, et al. (2023) In silico analysis of a novel hypothetical protein (YP_498675.1) from Staphylococcus aureus unravels the protein of tryptophan synthase beta superfamily (Try-synth-beta_ II). Journal, genetic engineering & biotechnology, 21(1), 135.

Shahzadi K, et al. (2023) Novel Coumarin Derivatives as Potential Urease Inhibitors for Kidney Stone Prevention and Antiulcer Therapy: From Synthesis to In Vivo Evaluation. Pharmaceuticals (Basel, Switzerland), 16(11).

Moin AT, et al. (2023) A computational approach to design a polyvalent vaccine against human respiratory syncytial virus. Scientific reports, 13(1), 9702.