Resource Summary Report

Generated by dkNET on Aug 16, 2026

Protein.Plus

RRID:SCR_019044
Type: Tool

Proper Citation

Protein.Plus (RRID:SCR_019044)

Resource Information

URL: https://proteins.plus/

Proper Citation: Protein.Plus (RRID:SCR_019044)

Description: Web server is focused on protein ligand interactions. Provides support for initial steps when dealing with protein structures, namely structure search, quality assessment, and preprocessing. Furthermore, advanced options, such as protein pocket detection, ensemble generation or prediction of metal coordinations are supported.

Resource Type: data access protocol, software resource, web service

Keywords: Protein ligand interaction, protein structure, quality assessment, protein pocket detection, ensemble generation, metal coordinations prediction

Availability: Free, Freely available

Resource Name: Protein.Plus

Resource ID: SCR_019044

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260815T182601+0000

Ratings and Alerts

No rating or validation information has been found for Protein.Plus.

No alerts have been found for Protein.Plus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Agbebi EA, et al. (2025) Uvarinol and Dichamanetin Derived from Uvaria chamae as Potential Dual-Site Inhibitors Against PBP2a in Methicillin Resistant Staphylococcus aureus: An In Silico Study. Pharmaceuticals (Basel, Switzerland), 18(4).

Xu Z, et al. (2023) Rethinking Biosynthesis of Aclacinomycin A. Molecules (Basel, Switzerland), 28(6).

Park S, et al. (2023) Association of Polygenic Variants Involved in Immunity and Inflammation with Duodenal Ulcer Risk and Their Interaction with Irregular Eating Habits. Nutrients, 15(2).

Shan S, et al. (2023) A female-biased odorant receptor tuned to the lepidopteran sex pheromone in parasitoid Microplitis mediator guiding habitat of host insects. Journal of advanced research, 43, 1.

Fatoki TH, et al. (2023) In Silico Exploration of Metabolically Active Peptides as Potential Therapeutic Agents against Amyotrophic Lateral Sclerosis. International journal of molecular sciences, 24(6).

Mirza Z, et al. (2023) Structure-Based Profiling of Potential Phytomolecules with AKT1 a Key Cancer Drug Target. Molecules (Basel, Switzerland), 28(6).

Vázquez-Jiménez LK, et al. (2023) Virtual Screening of Benzimidazole Derivatives as Potential Triose Phosphate Isomerase Inhibitors with Biological Activity against Leishmania mexicana. Pharmaceuticals (Basel, Switzerland), 16(3).

Khandazhinskaya A, et al. (2023) Design and Synthesis of New Modified Flexible Purine Bases as Potential Inhibitors of Human PNP. Molecules (Basel, Switzerland), 28(3).

Zhao Y, et al. (2023) Exploring the components and mechanisms of Shen-qi-wang-mo granule in the treatment of retinal vein occlusion by UPLC-Triple TOF MS/MS and network pharmacology. Scientific reports, 13(1), 5330.

Senra MVX, et al. (2023) In silico characterization of cysteine-stabilized ?? defensins from neglected unicellular microeukaryotes. BMC microbiology, 23(1), 82.

Meng JR, et al. (2023) Anti-Entry Activity of Natural Flavonoids against SARS-CoV-2 by Targeting Spike RBD. Viruses, 15(1).

Afzal M, et al. (2023) Genomic landscape of the emerging XDR Salmonella Typhi for mining druggable targets clpP, hisH, folP and gpmI and screening of novel TCM inhibitors, molecular docking and simulation analyses. BMC microbiology, 23(1), 25.

Dakpa G, et al. (2023) Antcin-B, a phytosterol-like compound from Taiwanofungus camphoratus inhibits SARS-CoV-2 3-chymotrypsin-like protease (3CLPro) activity in silico and in vitro. Scientific reports, 13(1), 17106.

Li C, et al. (2022) An integrated approach for identifying the efficacy and potential mechanisms of TCM against atherosclerosis-Wu-Zhu-Yu decoction as a case study. Journal of ethnopharmacology, 296, 115436.

Mutlu O, et al. (2022) Targeting SARS-CoV-2 Nsp12/Nsp8 interaction interface with approved and investigational drugs: an in silico structure-based approach. Journal of biomolecular structure & dynamics, 40(2), 918.

Srivastava A, et al. (2022) Exploring nature's bounty: identification of Withania somnifera as a promising source of therapeutic agents against COVID-19 by virtual screening and in silico evaluation. Journal of biomolecular structure & dynamics, 40(4), 1858.

Parker MI, et al. (2022) Delineating the RAS Conformational Landscape. Cancer research, 82(13), 2485.

Zhang Y, et al. (2022) Cotton flower metabolites inhibit SARS-CoV-2 main protease. FEBS open bio, 12(10), 1886.

Zhang L, et al. (2022) Isoorientin protects lipopolysaccharide-induced acute lung injury in mice via modulating Keap1/Nrf2-HO-1 and NLRP3 inflammasome pathways. European journal of pharmacology, 917, 174748.

Hassan SS, et al. (2022) Subtractive sequence analysis aided druggable targets mining in Burkholderia cepacia complex and finding inhibitors through bioinformatics approach. Molecular diversity, 1.