Resource Summary Report

Generated by dkNET on Aug 17, 2026

metaPocket

RRID:SCR_016653
Type: Tool

Proper Citation

metaPocket (RRID:SCR_016653)

Resource Information

URL: http://projects.biotec.tu-dresden.de/metapocket/

Proper Citation: metaPocket (RRID:SCR_016653)

Description: Software tool to identify pockets on protein surface to predict ligand-binding sites.

Synonyms: metaPocket, metaPocket 2.0

Resource Type: software application, simulation software, service resource, analysis service resource, software resource, production service resource

Defining Citation: PMID:19645590, PMID:21636590

Keywords: protein, surface, prediction, ligand, binding, site, identify, pocket

Funding: Ministry of Science and Technology (MOST) China ;
EU 7th Framework Marie Curie Actions of International Research Staff Exchange Scheme (IRSES)

Availability: Free for academic users, Freely available

Resource Name: metaPocket

Resource ID: SCR_016653

Alternate URLs: http://sysbio.zju.edu.cn/metapocket

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260817T040556+0000

Ratings and Alerts

No rating or validation information has been found for metaPocket.

No alerts have been found for metaPocket.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Merski M, et al. (2025) Molecular docking to homology models of human and Trypanosoma brucei ERK8 that identified ortholog-specific inhibitors. PLoS neglected tropical diseases, 19(9), e0013487.

Guerrero-Rodríguez SL, et al. (2025) Identification of New CD36 Antagonists by Structure-Based Virtual Screening. Chemical biology & drug design, 106(5), e70205.

Magwaza B, et al. (2024) Biochemical and in silico structural properties of a thermo-acid stable ?-glucosidase from Beauveria bassiana. Heliyon, 10(7), e28667.

Ugurlu SY, et al. (2024) Cobdock: an accurate and practical machine learning-based consensus blind docking method. Journal of cheminformatics, 16(1), 5.

Alshahrani M, et al. (2023) Comparative Analysis of Conformational Dynamics and Systematic Characterization of Cryptic Pockets in the SARS-CoV-2 Omicron BA.2, BA.2.75 and XBB.1 Spike Complexes with the ACE2 Host Receptor: Confluence of Binding and Structural Plasticity in Mediating Networks of Conserved Allosteric Sites. Viruses, 15(10).

Ogun OJ, et al. (2023) An In Silico Functional Analysis of Non-Synonymous Single-Nucleotide Polymorphisms of Bovine CMAH Gene and Potential Implication in Pathogenesis. Pathogens (Basel, Switzerland), 12(4).

C S, et al. (2022) Molecular docking, validation, dynamics simulations, and pharmacokinetic prediction of natural compounds against the SARS-CoV-2 main-protease. Journal of biomolecular structure & dynamics, 40(2), 585.

Mishra A, et al. (2022) Deciphering the anti-filarial potential of bioactive compounds from Ocimum sanctum: a combined experimental and computational study. Pharmaceutical biology, 60(1), 2237.

Barge S, et al. (2021) In-silico screening for identification of potential inhibitors against SARS-CoV-2 transmembrane serine protease 2 (TMPRSS2). European journal of pharmaceutical sciences : official journal of the European Federation for Pharmaceutical Sciences, 162, 105820.

Mwangi HN, et al. (2021) Methods for Identifying Microbial Natural Product Compounds that Target Kinetoplastid RNA Structural Motifs by Homology and De Novo Modeled 18S rRNA. International journal of molecular sciences, 22(9).

Jade D, et al. (2021) Virtual high throughput screening: Potential inhibitors for SARS-CoV-2 PLPRO and 3CLPRO proteases. European journal of pharmacology, 901, 174082.

Maiyo F, et al. (2020) Polymerized Selenium Nanoparticles for Folate-Receptor-Targeted Delivery of Anti-Luc-siRNA: Potential for Gene Silencing. Biomedicines, 8(4).

Kirubhanand C, et al. (2020) Molecular docking analysis of Bcl-2 with phyto-compounds. Bioinformation, 16(6), 468.

De Donato M, et al. (2020) KLF7: a new candidate biomarker and therapeutic target for high-grade serous ovarian cancer. Journal of experimental & clinical cancer research : CR, 39(1), 265.

Bhanu P, et al. (2020) Comparative molecular docking analysis of the SARS CoV-2 Spike glycoprotein with the human ACE-2 receptors and thrombin. Bioinformation, 16(7), 532.

Fernández-Juárez V, et al. (2020) "The Good, the Bad and the Double-Sword" Effects of Microplastics and Their Organic Additives in Marine Bacteria. Frontiers in microbiology, 11, 581118.

Shofiyah SS, et al. (2020) Isolation, expression, and characterization of raw starch degrading ?-amylase from a marine lake Bacillus megaterium NL3. Heliyon, 6(12), e05796.

Ragupathi NKD, et al. (2020) First hybrid complete genome of Aeromonas veronii reveals chromosome-mediated novel structural variant mcr-3.30 from a human clinical sample. Access microbiology, 2(4), acmi000103.

Farmer R, et al. (2019) Structure, function and dynamics in acyl carrier proteins. PloS one, 14(7), e0219435.

Kumar Sah R, et al. (2019) Phosphatidic acid homeostasis regulated by a type-2 phosphatidic acid phosphatase represents a novel druggable target in malaria intervention. Cell death discovery, 5, 107.