

Resource Summary Report

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metaPocket

RRID:SCR_016653

Type: Tool

Proper Citation

metaPocket (RRID:SCR_016653)

Resource Information

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

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

Synonyms: metaPocket, metaPocket 2.0

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

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: 20260801T042800+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 [kravitz2](#) .

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 α -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).

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.

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.

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).

- 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.
- 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.
- 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.
- 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.
- 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 α -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.