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Review Article

A Review on Computer Aided Drug Design – In Silico

Pranali R. Bhujade*, Khemutai G. Shedame, Pooja R. Hatwar, Dr. Ravindra L. Bakal, Krushnali N. Nehar, Ankita Y.Gawai

Department of Pharmaceutics, Shri Swami Samarth Institute of Pharmacy, At Parsodi, Dhamangaon Rly, Dist - Amravati (444709) Maharashtra, India.

A B S T R A C T

The process of drug discovery takes a long time and costs a lot of money. Computer-Aided Drug Design (CADD) has become an important part of modern drug discovery because it speeds up the process and lowers prices. CADD includes many methods, such as Structure-Based Drug Design (SBDD) and Ligand-Based Drug Design (LBDD). These use computer programs to do things like molecular docking, virtual screening, QSAR, pharmacophore modeling, and molecular dynamics. LBDD is used when the shapes of receptors are unknown, while SBDD uses machine learning. This review provides a comprehensive overview of CADD methods, classification, principles, and uses in drug creation. The article discusses about how important it is to find targets, find lead compounds, and make things work better. It also talks about the role of computers in pharmaceutical chemistry and molecular biology. CADD has increased the speed and accuracy of drug finding, making it possible to find new medicines. The review shows how CADD could change the way drugs are made, help people who don't have access to proper medical care, and make patient results better. Researchers can speed up the process of finding new drugs by using CADD strategies. This review is a great resource for researchers, clinicians, and industry workers who want to use CADD in pharmaceutical research. Using CADD has changed the way drugs are found, and its continued growth could lead to better health for everyone.

Keyword: Computer-Aided Drug Design (CADD), Structure-Based Drug Design (SBDD), Ligand-Based Drug Design (LBDD), Molecular Docking, Virtual Screening, Pharmacophore Modeling.

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*Address for Correspondence:
Pranali R. Bhujade, Department of Pharmaceutics, Shri Swami Samarth Institute of Pharmacy, At Parsodi, Dhamangaon Rly, Dist -Amravati Maharashtra, India.

INTRODUCTION:

The drug discovery process is an extremely moneyand time-consuming process, which is necessary to guarantee the safety and the quality of novel therapeutical entities entering the market (1). The different steps needed to get a new small molecule from target review to regulatory approval can take up to 14 years and cost more than a billion dollars (2). Conventional drug development methodologies commence with target identification, followed by the identification of lead compounds, execution of preclinical and clinical trials, and ultimately, market introduction, each necessitating substantial time and resources(3). Although documentation for open access materials exists, publicly accessible educational platforms for concepts and applications in CADD are scarce (4). A drug candidate is identified and partially approved for the treatment of a specific disease, and the process for drug approval is known as computer-aided drug design (CADD)(5).

The advent of computer methods in pharmaceutical chemistry and molecular biology over the 20th century has transformed drug development processes(6). CADD can be broadly categorized into two types: STRUCTURE-BASED drug design (SBDD) and ligand-based drug design

(LBDD).Imaging clinical trials aim at answering specific scientific questions regarding the value of imaging technologies and procedures for detecting, diagnosing, guiding, or monitoring the treatment of disease. In silico drug designing is a form of computer-based modelling whose technologies are applied in drug discovery processes (7). Drug targets are biomolecules that are causally linked to disease occurrence within cells or contribute to disease progression, and can be addressed by pharmacological interventions for therapeutic purposes(8).

The identification of new active molecules is a complex endeavour that necessitates expertise in various disciplines, including chemistry and biology (9). A crucial question in drug discovery is the identification and validation of molecular targets with clinical application (10). The biological origin of a disease under lies the modern treatment of specific health conditions(11). The computer-aided drug design (CADD) fields encompass a wide range of computational approaches for small molecules and macromolecules, as well as for analysing and predicting protein-ligand interactions(12). The introduction of computational techniques in pharmaceutical chemistry and molecular biology over the 20th century changed drug development processes(6). CADD is defined all computer-assisted techniques employed for the identification, design, and optimization of molecules with specific structures and features (13). The evaluation of novel imaging technologies typically required a significant clinical trial to demonstrated advantages over the standard of care (14).

CLASSIFICATION: (15)

(Computer-assisted Drug Design)

1. Structure-Based Drug Design:
   - A. Structural Prediction
     - a) Homology Modeling
     - b) Ab initio structural prediction
     - c) Validation of Protein Models
   - B. Docking-Based Virtual Screening
     - a) Binding site identification
     - b) Ligand flexibility
     - c) Protein flexibility
     - d) Scoring function
2. Ligand-Based Drug Design
   - A. Similarity search
   - B. Quantitative Structure-Activity Relationship
   - C. Pharmacophore
   - D. Scaffold Hopping
3. Hierarchical Virtual Screening
4. De Novo and Fragment-Based Drug Design
5. MM-GBSA
6. Molecular Dynamics
7. QM/MM and DFT Approaches

Structure-Based Drug Design:

The potential use of crystallographic and NMR methods is currently being extended beyond structural determination into novel approaches for lead discovery (16). The accessibility of the three-dimensional structures of therapeutic target proteins and the investigation of the binding site cavity provides the foundation of structure-based drug design (SBDD) (17). Every technique based on this type of data belongs to the "structure-based drug design" (SBDD) family, which is by far the most popular method in computational drug discovery (18). The incorporation of machine learning techniques into structure-based drug design methodologies has improved performance (19). Structure-based virtual high-through put screening (SB-v HTS) is the tool used in silico to classify supposed hits of a huge library of compounds to targets of known structure, relies on comparing the small molecule's 3D structure with the putative binding pocket (20).

Ligand-Based Drug Design:

Ligand-based drug design is a prevalent method in computer-aided drug design, utilized when the three-dimensional structure of the target receptor is unavailable (21). The principle of ligand-based Drug Design is that structurally similar substances are likely to exhibit similar behaviours. A crucial stage in LBDD is to acquire and prepare small molecule libraries (22). These methods utilize a collection of reference structures derived from substances recognized to interact with the target of interest and examine their 2D or 3D configurations (23).The chemical structures of identified pharmaceuticals were obtained from the PubChem compound database, accessible at NCBI (24).

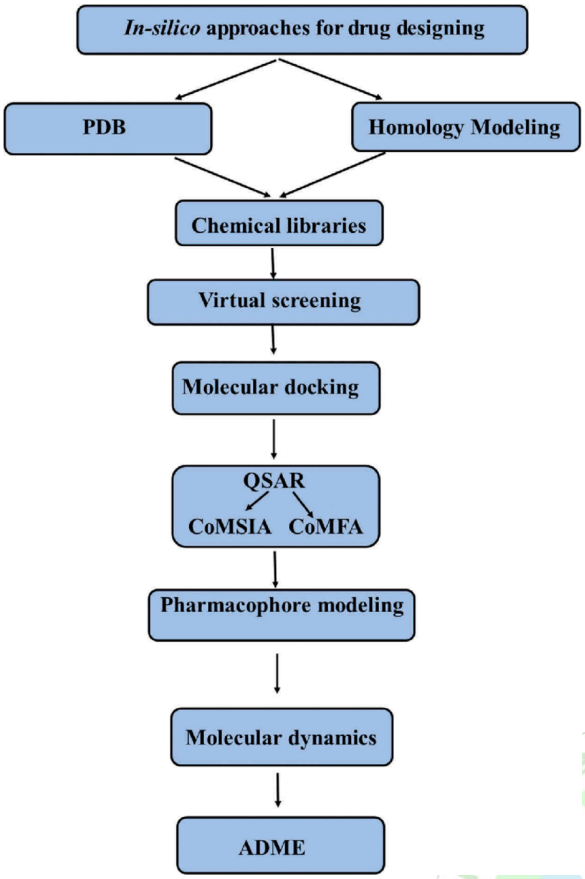

Figure 1: In silico methodologies for pharmaceutical design (25)

Homology modelling:

The HHpred web server was utilized for the homology modeling of all targeted HIV proteins. HHpred employed MODELLER subsequent to the PIR alignment of the target sequence with the template(s) exhibiting the highest sequence similarity and identity (26).Despite the current revolution in structural investigations, particularly the recent advancements in cryo-electron microscopy, the intricate structures of several proteins, notably membrane proteinswhich are disproportionately represented among therapeutic targetsremain undetermined (27). The initial phase of structure-based drug design (SBDD) involves selecting a target structure and identifying the binding site of interest (28).

Virtual Screening (VS)

Popular VS techniques emerged in the 1980s, however the inaugural publication on VS was released in 1997. Recently, the application of VS approaches has demonstrated to be a superior option to high-throughput screening, particularly regarding cost-effectiveness and the likelihood of identifying the most suitable outcome from an extensive virtual database (29).VS is a computational method employed in the drug discovery process. In VS, extensive datasets of molecular structures are systematically assessed by computational techniques (30). The virtual screening (VS) method has successfully enhanced high-throughput screening (HTS) for hit identification (31). It has become a highly convenient approach for identifying the most favourable bioactive compounds using information regarding protein targets or active ligands (32).

Molecular Docking:

Grid generation was accomplished utilizing the receptor grid to establish the docking platform via the GLIDE (Grid-based Ligand Docking with Energetics) module of the Schrödinger Suite, which identifies and delineates the active site location (33). Docking is the process of optimizing molecular configurations for optimal interaction with a receptor (34). A significant benefit of DNN compared to other ML methods is its capacity for representation learning (35). Molecular docking is used to determine and optimize drug candidates by analysing and modeling the interactions between ligands and target macromolecules (36).

QSAR(Quantitative Structure Activity Relationship):

The quantitative structure-activity relationship (QSAR) uses mathematical and statistical multivariate techniques to identify significant connections between a set of structures and their functions(37). Quantitative Structure-Activity Relationship (QSAR) is a crucial instrument in bioinformatics and chemical information, principally relying on data derived from molecular modeling and computational chemistry to forecast the toxicities of compounds (38). QSAR modeling investigates the correlation between molecular chemical structures and their biological functions (39).

Pharmacophore Modeling:

A pharmacophore model clarifies the spatial configuration of chemical characteristics in ligands necessary for interaction with the target receptor (26). Some Chemical characteristics utilized in pharmacophore modeling includes hydrogen bond donors, hydrogen bond acceptors, aromatic ring systems, hydrophobic regions, positively charged ionizable groups, and negatively charged ionizable groups (40).

A further method of CADD for identifying drug-like novel compounds within an extensive chemical space enables the discovery of new drugs by optimizing many pharmaceutical features essential for efficacy (41). Pharmacophores are collections of electronic and steric features necessary for a compound's recognition by a protein target (42).

Molecular Dynamics:

MD simulations of the novel molecule 1 were conducted using the YASARA software package, in conjunction with the apo form of Mpro. These simulations were conducted to examine the virtual stability of the ligand situated in the

binding pocket. A dynamic system comprised one copy of Mpro, one copy of the attached chemical, water molecules, and 0.9% NaCl at a temperature of 298K (43). Experimentally determined structures give significant insights for drug design, however they only capture a static representation of the complete conformational space inherent to the changeable nature of biological systems (44).

ADME (Adsorption, Distribution, Metabolism, Excretion):

They denote bidirectional interaction between drug effect and the human body, wherein drugs influence physiological processes through receptor inhibition, activation, and signal pathway obstruction, while the body processes drugs via absorption, distribution, metabolism, and excretion (45).

Methods and Materials

Study design: This systematic study assessed the computational in silico models employed to identify novel anti-COVID-19 drugs (46).

The development of a multi-epitope vaccination encompassed several technical procedures. Summarizes the overall methodology employed in the design of a multi-subunit vaccine and the associated pipeline for the present investigation (47).

Bibliographic Review and Lead Identification: To discover a possible therapy for L. amazonensis, we hypothesize that disrupting a critical metabolic route of the parasite might result in its demise and therefore alleviate the disease's consequences (48). Our study consists of a regression in-silico analysis and an in-vitro analysis. The in-silico study comprises data collection, preparation, validation, molecular docking, MM\GBSA, kinetic simulation, and ADMET analysis (49).

population, Concept, and Context: We employed the population-concept-context (PCC) mnemonic to direct the formulation of research questions, establish eligibility criteria, and conduct the literature search. The articles in this scoping review should concentrate on in silico methodologies for drug repurposing within the field of oncology research. We did not define a specific population as our focus was on the computational approaches employed in oncology research broadly, encompassing various study designs and populations (50).

In Silico Hydrolysis of the Parent Protein: The Expasy online application was utilized to analyse the trypsin potential of parental proteins (19). Trypsin is a peptide chain endonuclease that selectively hydrolyses peptide chains containing arginine and lysine. The Exposé peptide cutter software provides an extensive array of enzymes, including trypsin. Upon inputting the protein sequence, the relative locations of the cleavage sites for various enzymes will be indicated on the specified protein. Upon selecting the target enzyme, the obtained protein fragments will be represented with greater accuracy (51).

Details regarding Drug-Drug Interactions (DDIs) and the formulation of Training Sets: We utilized DDIs data obtained from two informational sources. The secondary source of DDIs data was the Fujitsu ADME Database (52).

Features Based on Sequence: The independent version of the feature was employed to compute several characteristics from protein sequences in this investigation. Numerous features or descriptors of protein or peptide sequences can be computed with feature (53).

We utilized the composition-based function module of features to generate a vector including 8,968 features. In addition to these, we have also examined various composition features individually from the features in both datasets (54).

REFERENCE

1. Martin L, Hutchens M, Hawkins C. Clinical trial cycle times continue to increase despite industry efforts. Nat. Rev. Drug Discov. 2017; 16: 157.
2. Simoens S, Huys I. R&D Costs of New Medicines: A Landscape Analysis. Front. Med. 2021; 8: 760762.
3. Li H, Zou L, Kowah JAH, He D, Liu Z, Ding X, Wen H, Wang L, Yuan M, Liu X. A compact review of progress and prospects of deep learning in drug discovery. J Mol Model. 2023;29(4):117. doi: 10.1007/s00894-023-05492-w. PMID: 36976427.
4. Sydow D, Morger A, Driller M, et al. TeachOpenCADD: a teaching platform for computer-aided drug design using open source packages and data. J Cheminform. 2019; 11(29): 1-7. https://doi.org/10.1186/s13321-019-0351-x
5. Sharma A, Jangid L, Shaikh N and Bhangale J. Computer-Aided Drug Design Boon in Drug Discovery. Asian Journal of Organic & Medicinal Chemistry.2022;7(1):55-64
6. Gu R, Wu F, Huang Z. Role of Computer-Aided Drug Design in Drug Development. Molecules. 2023;28(20):7160. doi: 10.3390/molecules 28207160. PMID: 37894639; PMCID: PMC10609497.
7. Zhang X, Wu F, Yang N. et al. In silico Methods for Identification of Potential Therapeutic Targets. InterdiscipSci Comput Life Sci 14, 285–310 (2022). https://doi.org/10.1007/s12539-021-00491-y
8. Gao D, Chen Q, Zeng Y, Jiang M, Zhang Y. Applications of Machine Learning in Drug Target Discovery. Curr Drug Metab. 2020;21(10):790-803. doi: 10.2174/1567201817999200728142023. PMID: 32723266.
9. Santos Nascimento DJI, Aquino MT de and Silva-Júnior FE da. The New Era of Drug Discovery: The Power of Computer-aided Drug Design (CADD).Letters in Drug Design & Discovery. 2022(19)951-955.
10. Medina-Franco JL. Grand Challenges of Computer-Aided Drug Design: The Road Ahead. Front. Drug. Discov. 1:728551. doi: 10.3389/fddsv.2021.72855
11. Ece A. Computer-aided drug design (2023). 17:26 https://doi.org/10.1186/s13065-023-00939-w
12. Bajorath J. Deep Machine Learning for Computer-Aided Drug Design. Front. Drug. Discov. 2:829043. doi: 10.3389/fddsv.2022.829043
13. Zhenhui Wu, MScabc, Shupeng Chen, MScb, Yihao Wang, MDc,

Fangyang Li, BScc, Huanhua Xu,MDa, Maoxing Li, MDc, Yingjian Zeng, PhDb, Zhenfeng Wu, PhDa, Yue Gao, PhD ac, Current perspectives and trend of Computer-Aided drug design: a review and bibliometric International Journal of Surgery (2024) Published online19 March 2024.
http://dx.doi.org/10.1097/JS9.0000000000001289

14. BadanoA. In silico imaging clinical trials: cheaper, faster, better, safer, and more scalable. Trials 22, 64 (2021). https://doi.org/10.1186/s13063-020-05002-w

15. Chang Y, Hawkins BA, Du JJ, Groundwater PW, Hibbs DE, Lai F. A Guide to In Silico Drug Design. Pharmaceutics. 2022 Dec 23;15(1):49. doi: 10.3390/pharmaceutics15010049. PMID: 36678678; PMCID: PMC9867171.

16. Blundell TL, Jhoti H, Abell C. High-throughput crystallography for lead discovery in drug design. Nat Rev Drug Discov. 2002 Jan;1(1):45-54. doi: 10.1038/nrd706. PMID: 12119609.

17. Bassani D, Moro S. Past, Present, and Future Perspectives on Computer-Aided Drug Design Methodologies. Molecules. 2023; 28(9):3906. https://doi.org/10.3390/molecules28093906

18. Turzo SBA, Hantz ER, Lindert S. Applications of machine learning in computer-aided drug discovery. QRB Discov. 2022;3:e14. doi: 10.1017/qrd.2022.12. PMID: 37529294; PMCID: PMC10392679.

19. Purohit1D,MakhijaM,Pandey P,KumarS,Kumar S,DuttR,Kaushik D, Kumar P, Kumar S. Role of computer-aided drug design in the discovery and development of new medicinal agents. A review Journal of medical pharmaceutical and alliedsciences.11(3):4794 - 4801 doi: 10.55522/jmpas.V11I3.2300.

20. Macalino SJ, Gosu V, Hong S, Choi S. Role of computer-aided drug design in modern drug discovery. Arch Pharm Res. 2015;38(9):1686-701. doi: 10.1007/s12272-015-0640-5. Epub 2015 Jul 25. PMID: 26208641.

21. Gurung AB, Ali MA, Lee J, Farah MA, Al-Anazi KM. An Updated Review of Computer-Aided Drug Design and Its Application to COVID-19. Biomed Res Int. 2021 Jun 24;2021:8853056. doi: 10.1155/2021/8853056. PMID: 34258282; PMCID: PMC8241505

22. Sharma1 V, Wakode1 S, Kumar H. A review on Structure- and Ligand-based drugdesign:Concepts, approaches, And challenges ,Chemoinformatics and Bioinformatics in the Pharmaceutical Sciences, 2021;https://doi.org/10.1016/B978-0-12-821748-1.00004-X

23. Das PS and Saha P. A Review On Computer Aided Drug Design In Drug Discovery,World Journal of Pharmacy and Pharmaceutical Sciences. 2017; 6(7):279-291. DOI: 10.20959/wjpps 20177-9450

24. QidwaiT. QSAR modeling, docking and ADMET studies for exploration of potential anti-malarial compounds against Plasmodium falciparum. In Silico Pharmaco*l.* **5,** 6 (2017).

https://doi.org/10.1007/s40203-017-0026-0

25. Malathi K, Ramaiah S. Bioinformatics approaches for new drug discovery: a review. Biotechnology and Genetic Engineering Reviews. 34(2):243–260. https://doi.org/10.1080/02648725.2018.1502984

26. Elalouf A. In-silico Structural Modeling of Human Immunodeficiency Virus Proteins. Biomed Eng Comput Biol. 2023;14:11795972231154402. doi: 10.1177/11795972231154402. PMID: 36819710; PMCID: PMC9936402.

27. Salman MM, Al-Obaidi Z, Kitchen P, Loreto A, Bill RM, Wade-Martins R. Advances in Applying Computer-Aided Drug Design for Neurodegenerative Diseases. International Journal of Molecular Sciences. 2021; 22(9):4688. https://doi.org/10.3390/ijms22094688

28. Dorahy G, Chen JZ, Balle T. Computer-Aided Drug Design towards New Psychotropic and Neurological Drugs. Molecules. 2023;28(3):1324. doi:10.3390/molecules28031324. PMID: 36770990; PMCID: PMC9921936.

29. Maia EHB, Assis LC, de Oliveira TA, da Silva AM, Taranto AG. Structure-Based Virtual Screening: From Classical to Artificial Intelligence. Front Chem. 2020;8:343. doi:10.3389/fchem.2020.00343. PMID: 32411671; PMCID: PMC7200080.

30. Oliveira TAd, Silva MPd, Maia EHB, Silva AMd, Taranto AG. Virtual Screening Algorithms in Drug Discovery: A Review Focused on Machine and Deep Learning Methods. Drugs and Drug Candidates. 2023; 2(2):311-334. https://doi.org/10.3390/ddc2020017

31. Dar KB, Bhat AH, Amin S, Hamid R, Anees S, Anjum S, Reshi BA, Zargar MA, Masood A, Ganie SA. Modern Computational Strategies for Designing Drugs to Curb Human Diseases: A Prospect. Curr Top Med Chem. 2018;18(31):2702-2719. doi:10.2174/1568026619666190119150741. PMID: 30659543.

32. Chandershekar A, Bhaskar A,Mekkanti MR,Mathappan R. A review On Computer Aided Drug Design (CAAD) and It's Implications. In Drug Discovery And Development Process International Journal of Health Care and Biological Sciences. 2020; 1(1):27-33.

33. Sahu A, Pradhan D, Veer B, Kumar S, Singh R, Raza K, Rizvi MA, Jain AK, Verma S. In silico screening, synthesis, characterization and biological evaluation of novel anticancer agents as potential COX-2 inhibitors. Daru. 2023; 31(2):119-133. doi:10.1007/s40199-023-00467-x. Epub 2023 Jul 15. PMID: 37454036; PMCID: PMC10624798.

34. Raval K, Ganatra T. Basics, types and applications of molecular docking: A review. IP Int J Compr Adv Pharmacol. 2022;7(1):12-16.https://doi.org/10.18231/j.ijcaap.2022.0032581-5555/©2022

35. Dana D, Gadhiya SV, St Surin LG, Li D, Naaz F, Ali Q, Paka L, Yamin MA, Narayan M, Goldberg ID, Narayan P. Deep Learning in Drug Discovery and Medicine; Scratching the Surface. Molecules. 2018; 23(9):2384.doi:10.3390/molecules23092384. PMID: 30231499; PMCID: PMC6225282.

36. Wadood, Abdul et al. In-silico drug design: An approach which revolutionarised the drug discovery process. Drug design and delivery. (2013): DOI:10.13172/2054-4057-1-1-1119 Corpus ID: 5021463

37. Oselusi SO, Dube P, Odugbemi AI, Akinyede KA, Ilori TL,Egieyeh ES,Sibuyi NRS,MeyerM,Madiehe AM,Wyckoffe GJ, Egieyeh SA. The role and potential of computer-aided drug discovery strategies in the Discovery of novel antimicrobial, Computers in Biology and Medicine 2024;169:107927.https://doi.org/10.1016/j.compbiomed.2024.107927

38. Rim KT. In silico prediction of toxicity and its applications for chemicals at work. Toxicol Environ Health Sci. 2020;12(3):191-202. doi:10.1007/s13530-020-00056-4. Epub 2020 May 14. PMID: 32421081; PMCID: PMC7223298.

39. Niazi SK, Mariam Z. Computer-Aided Drug Design and Drug Discovery: A Prospective Analysis. Pharmaceuticals (Basel). 2023;17(1):22. doi:10.3390/ph17010022. PMID: 38256856; PMCID: PMC10819513.

40. Cerchia C, Lavecchia A. In Silico Drug Design and Discovery: Big Data for Small Molecule Design. Biomolecules. 2022; 13(1):44. doi:10.3390/biom13010044. PMID: 36671429; PMCID: PMC9855915.

41. Tiwari A, Singh S.Computational approaches in drug designing. Bioinformatics: Methods and Applications. 2021:207-217.https://doi.org/10.1016/B978-0-323-89775-4.00010-9

42. Buglak AA,Samokhvalov AV, Zherdev AV, Dzantiev BB. Methods and Applications of In Silico Aptamer Design and Modeling. International Journal of Molecular Sciences.2020; 21(22):8420. https://doi.org/10.3390/ijms21228420

43. Zohora FT, Azam ATMZ, Ahmed S, Rahman KM, Halim MA, Anwar MR, Sohrab MH, Tabassum F, Hasan CM, Ahsan M. Isolation and In Silico Prediction of Potential Drug-like Compounds with a New Dimeric Prenylated Quinolone Alkaloid from Zanthoxylum rhetsa (Roxb.) Root Extracts Targeted against SARS-CoV-2 (Mpro). Molecules. 2022; 27(23):8191.

https://doi.org/10.3390/molecules27238191

44. Sydow D,Rodr´ıguez-GuerraJ,Kimber TB,SchallerD,Taylor CJ,Chen Y,LejaM,Misra S,Wichmann M, Ariamajd A and Volkamer A. Teach Open CADD, open source and FAIR Python Pipelines to assist in structural bioinformatics and Cheminformatics, research Nucleic Acids Research. 2022; 50:https://doi.org/10.1093/nar/gkac267

45. Wang Y, Xing J, Xu Y, Zhou N, Peng J, Xiong Z, Liu X, Luo X, Luo

C, Chen K, Zheng M, Jiang H. In silico ADME/T modelling for rational drug design. Q Rev Biophys. 2015;48(4):488-515. doi: 10.1017/S0033583515000190. Epub 2015 Sep 2. PMID: 26328949.

46. Onyango OH. In Silico Models for Anti-COVID-19 Drug Discovery: A Systematic Review, Advances in Pharmacological and Pharmaceutical Sciences. 2023:https://doi.org/10.1155/2023/4562974
47. Naz S, Aroosh A, Caner A, Şahar EA, Toz S, Ozbel Y, Abbasi SW. Immunoinformatics Approach to Design a Multi-Epitope Vaccine against Cutaneous Leishmaniasis. Vaccines (Basel). 2023;11(2):339. doi: 10.3390/vaccines11020339. PMID: 36851219; PMCID: PMC9967539.
48. Vicente-Barrueco A, Román ÁC, Ruiz-Téllez T, Centeno F. In Silico Research of New Therapeutics Rotenoids Derivatives against Leishmania amazonensis Infection. Biology (Basel). 2022 Jan 14;11(1):133. doi: 10.3390/biology11010133. PMID: 35053132; PMCID: PMC8772715.
49. Sahu A, Ahmad S, Imtiyaz K. et al. In-silico and in-vitro study reveals ziprasidone as a potential aromatase inhibitor against breast carcinoma. Sci Rep 13, 16545 (2023). https://doi.org/10.1038/s41598-023-43789-1
50. Cavalcante BRR, Freitas RD, Siquara da Rocha L d O, Santos R d SB D, Souza BSdF, Ramos PIP, Rocha GV and Gurgel Rocha CA. In silico approaches for drug repurposing in oncology: a scoping review. Front.Pharmacol. 15:1400029. doi: 10.3389/fphar.2024.1400029
51. Liu M, Lv J, Chen L, Li W, Han W. In Silico Discovery of Anticancer Peptides from Sanghuang. Int J Mol Sci. 2022;23(22):13682. doi: 10.3390/ijms232213682. PMID: 36430160; PMCID: PMC9693127.
52. Dmitriev AV, Rudik AV, Karasev DA, Pogodin PV, Lagunin AA, Filimonov DA, Poroikov VV. In Silico Prediction of Drug–Drug Interactions Mediated by Cytochrome P450 Isoforms. Pharmaceutics. 2021; 13(4):538. https://doi.org/10.3390/pharmaceutics13040538
53. Rahman MM, Islam MR, Akash S, Mim SA, Rahaman MS, Emran TB, Akkol EK, Sharma R, Alhumaydhi FA, Sweilam SH, Hossain ME, Ray TK, Sultana S, Ahmed M, Sobarzo-Sánchez E, Wilairatana P. Insilico investigation and potential therapeutic approaches of natural products for COVID-19: Computer-aided drug design perspective. Front Cell Infect Microbiol. 2022; 12:929430. doi:10.3389/fcimb.2022.929430. PMID: 36072227; PMCID: PMC9441699.
54. Kaur D, Patiyal S, Arora C, Singh R, Lodhi G, Raghava GPS. In-Silico Tool for Predicting, Scanning, and Designing Defensins. Front Immunol. 2021; 12:780610. doi:10.3389/fimmu.2021.780610. PMID: 34880873; PMCID:PMC8645896.