



Revolutionizing Drug Delivery: A Comprehensive Review of Computer- Aided Design and Development

Shivkumar M. Sontakke¹, Prajakta A. Kakade², Indrajeet D. Gonjari³, Avinash H. Hosmani⁴

1 Research Scholar, Department of Pharmaceutics, Government College of Pharmacy, Karad, India.

2 Research Scholar, Department of Pharmaceutics, Government College of Pharmacy, Karad, India.

3 Associate Professor, Department of Pharmaceutics, Government College of Pharmacy, Karad, India.

4 Associate Professor, Department of Pharmaceutics, Government College of Pharmacy, Karad, India.

Received: 2025-2-22

Revised: 2025-3-7

Accepted: 2025-3-12

ABSTRACT:

The scientific field of computer-aided drug design (CADD) is continuously growing and has a number of characteristics. Numerous areas of fundamental and applied research connect and inspire one another in the exciting and diverse subject of computer-aided drug design (CADD). CADD is theoretically based on quantum mechanics and molecular modeling research, including structure-based and ligand-based drug design, database searching, and binding affinity based on a biological target. We'll examine how CADD technology could support the drug development procedure in this review. Computer-aided drug design software uses mathematical equations to estimate the value and composition of characteristics from known, unidentified stable, and molecular species. Molecular docking research employ a variety of approaches, including molecular modeling, molecular mechanics, molecular docking, quantum mechanics, hybrid QM/MM, and QSAR. From lead identification to clinical trials, a normal drug discovery cycle should take about a year. Research and development expenses for pharmaceuticals could be reduced by 50% if computer-aided drug design technology is incorporated into a company's R&D procedures. Computer-Aided Drug Design (CADD) is emerging as a revolutionary force in the dynamic environment of drug development, bridging the gaps between biology and technology. This study provides an overview of CADD's historical history, classification into structure-based as well as ligand-based approaches, and critical significance in analyzing and accelerating drug discovery. As CADD improves, it becomes increasingly important to include different biological data while still protecting data privacy. Challenges continue, requiring algorithm optimization and strong ethical frameworks.

Keywords: Computer aided drug design, Finding new drug, Biological target

INTRODUCTION:

The expense of drug research and development is reduced by computer-aided drug design (CADD), which offers a variety of tools and methodologies to help in different stages of drug design. Drug research and development is a time-consuming, challenging, costly, and risky procedure with few commercial equivalents. This is because (CADD) techniques are commonly employed in the pharma sector to speed up the procedure. There is a substantial cost benefit to using computational methods in the early optimization stage of medication development. Pharmacological research laboratories devote a significant amount of money and effort in the various stages of drug development, beginning with the identification of therapeutic targets [1,2], Candidate drug development and optimization via preclinical and large clinical trials to examine the safety and effectiveness of newly created medications. The big pharmaceutical corporations have spent considerably in the regular ultra-High Throughput Screening (uHTS) of large quantity of drug-like compounds [3,4]. At the same time, computers are being used more and more for virtual screening in medication development and optimization [5-7]. New developments in DNA microarray research examine hundreds of genes linked to an illness, which can be used to learn more about the disease targets, metabolic pathways, and toxicity of medications [8].

Quantum mechanics, statistical mechanics, and empirical molecular mechanics are examples of theoretical approaches. The addition of explicit solvent effects has been made possible by this recent development. The availability of excellent computer graphics, which is primarily funded by workstations, is the reason for all of this labor [9].

1. History of Computer Aided Drug Delivery:

Table 1: History of Computer Aided Drug Delivery

Time Period	Key Developments	References
1960s-1970s	➤ Introduction of computer simulations in pharmaceutical research focusing on ADME	[10]
1980s-1990s	➤ Advancements in computational power. ➤ Modeling techniques, including CFD and population pharmacokinetic models	[11,12]
2000s-2010s	➤ Integration of artificial intelligence (AI). ➤ Machine learning (ML) in CADDs, including deep learning and GANs	[13, 14]
2020-2024	➤ Improved predictive modeling. ➤ Increased use of virtual reality, and growing emphasis on personalized medicine reality, and growing emphasis on personalized medicine	[15, 16, 17]

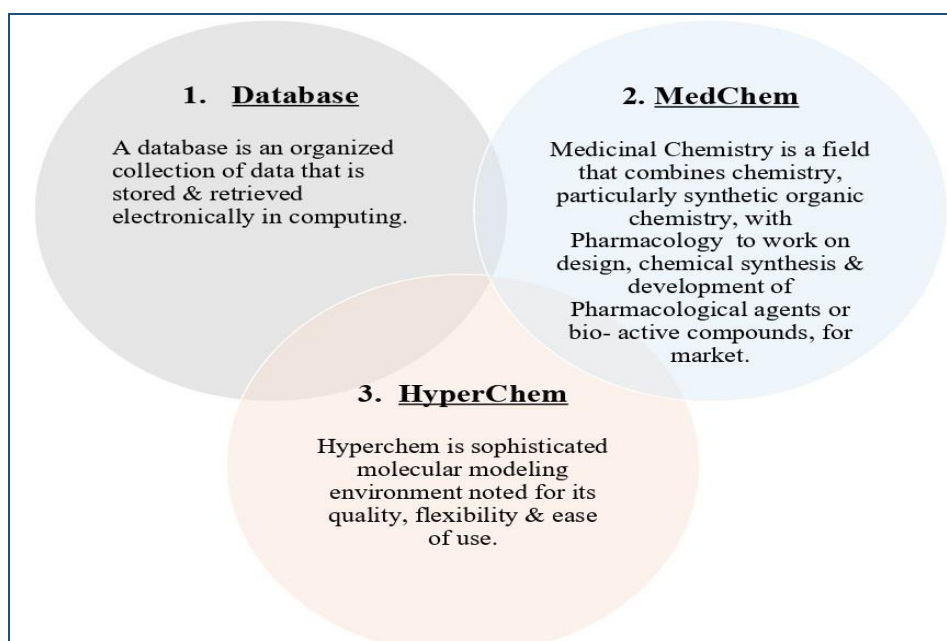


Figure 1: Computational tool for drug designing

The growth of CADD coincides with a paradigm change in drug discovery, which saw the process change from primarily empiric to more focused and rational [18]. However, like with any scientific process, computer aided drug designing has limitations. When forecasting the the way biological systems behave exclusively through computer simulations, it is critical to recognize the inherent flaws. Think about the fictitious situation in which a computer simulation precisely represents the molecular interactions among a receptor as well as its target. But if the simulation doesn't incorporate critical real-world data on external surroundings or unanticipated biological reactions, the projections may differ dramatically from the actual results [19,20]. Lastly, CADD is an example of the harmonious fusion of biology and technology with the goal of speeding up drug discovery. Although the science has advanced significantly, its full potential has not yet been reached as more computational tools and a deeper comprehension of biological systems become available.

2. OBJECTIVES, ADVANTAGES & DISADVANTAGES of CADD:

- To switch from



- 1) Randomly checking for disease tests
- 2) Screening specifically for disease tests
- 3) Natural versus synthetic chemicals
- To
 - 1) Creation and evaluation of rational medicine
 - 2) Accelerate the screening procedure.
 - 3) Boost the screening's effectiveness
 - 4) Create from the ground up
 - 5) Incorporating testing into the design process
 - 6) Rapidly fail drugs

BENEFITS:

- a) Saving money
- b) Time-to-market, but the forecasting power of CADD helps identify potential lead candidates, reducing time lost on unproductive pursuits.
- c) Enables scientists to concentrate only on the most promising molecules, saving time and money on both synthetic and biological testing.

DRAWBACKS:

- a) Intended systems are rapidly cleansed.
- b) Intravenous administration of carrier systems to induce immune response.
- c) Certain processes within tumor cells are not adequately targeted.
- d) Redistribution and dispersion of drug releases
- e) Formulation calls for very sophisticated technology.
- f) Skills in producing, storing, and administration are crucial.
- g) Medications can accumulate at the target site and create toxicity symptoms.
- h) It is challenging to keep the dosage form constant. [21]

3. DIFFERENT KINDS OF COMPUTER-AIDED DRUG DESIGN

Drug design -

A Ligand base

B Structural base

A. Ligand-based drug design:

Developing drugs with ligands By developing appropriate analogs based on structure-activity correlations (SAR), potency and other crucial characteristics are improved. Research on ligand-based drugs starts with a single molecule or a collection of

compounds that have been shown to be efficient against a particular target. Designs can be made using the Topliss technique or a straightforward analog layout that utilizes similarities in structure or features. In cases when the target structure is unknown but the structures of its closest homologues are known, the experimental coordinates of the closest homologue's structure can be used to construct a homology-based model. If the homology model is adequate, a structure-based design approach can be applied [22].

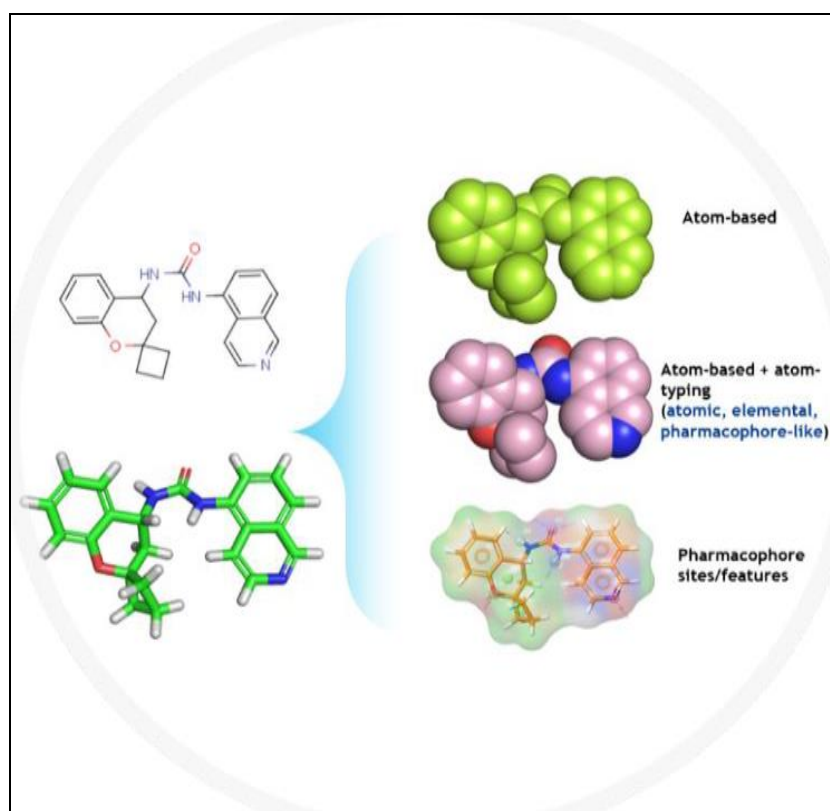


Figure 1: Ligand-based drug design [23]

- 1) Structure-activity relationship on a quantitative scale (QSAR)
- 2) CoMFA
- 3) CoMSIA (Commonwealth of Massachusetts Institute of Technology)

1) **QUANTITATIVE STRUCTURE-ACTIVITY Link** - Statistical and analytical tools are used to investigate the link between ligand structures and their associated effects. On the basis of structural features, mathematical models are created to characterize. Although 3D-QSAR has been accepted, 2D-QSAR was used in the past. The three-dimensional QSAR methods are CoMFA and CoMSIA.

2) **Comparative molecular field analysis (CoMFA)** The molecular fields that surround a molecule (steric and electrostatic) impact its biological activity. Has several difficulties.

3) **Comparative molecular similarity index analysis (CoMSIA)** Other features of the field are included. Hydrophobic, steric, electrostatic, and hydrogen bond donor and acceptor A more accurate structural-activity relationship can be obtained than with CoMFA [24].

B. Structure-based drug design:

Requires knowledge of the three-dimensional structure of the biological target, which can be achieved via:

1. X-ray crystallography is one type of x-ray crystallography.
2. Spectroscopy using Nuclear Magnetic Resonance (NMR).

A material's structure is determined by X-ray crystallography, whereas its chemical composition is determined using NMR spectroscopy. Homology modeling, also known as comparative modeling of proteins (the "template"), is the process of creating an atomic-resolution model of the "target" and an experimental three-dimensional structure of a similar homologous protein. A medicinal chemist's knowledge and interactive visualizations can be used to create potential medications with a high affinity and selectivity for the biological target. To find new medication candidates, a variety of automated computer procedures can be employed [25].

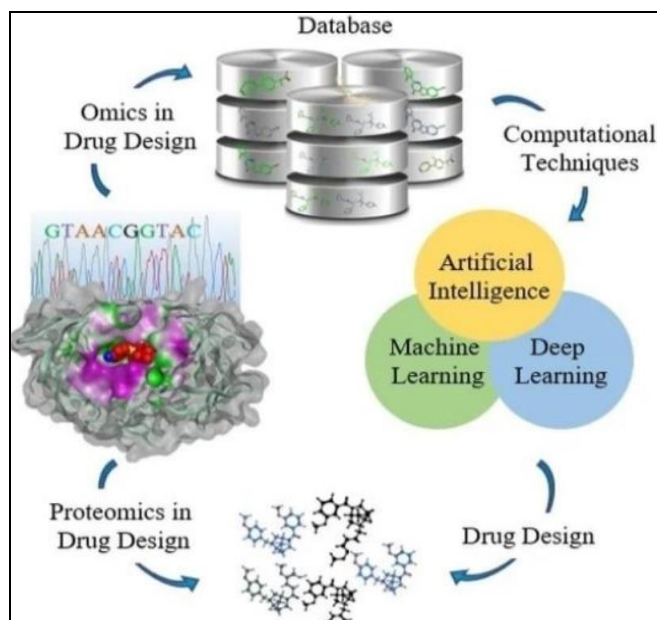


Figure 2: Drug design based on structure [23]

4. PROCESS OF DRUG DISCOVERY:

The process of finding therapeutic compounds that can effectively cure or regulate disease targets is known as drug discovery. To maximize disease targets, a lot of chemical substances are first screened. It is necessary to possess detailed information of the structure of the drug receptor in order to tailor the drug molecules to the specific binding site.

The drug development process begins with knowing the ailment for which the medicine will be created. It includes the following stages.

A. Candidate Drug Discovery

- Choosing a Treatment Target
- Lead Discovery
- Lead Optimization

B. Trials both preclinical and clinical to assess the medication's safety, effectiveness, and side effects

- Animal Studies
- Clinical Trials

C. Getting the newly discovered medicine approved by the FDA and releasing it for public usage

- Further post-marketing testing
- Additional medication development.

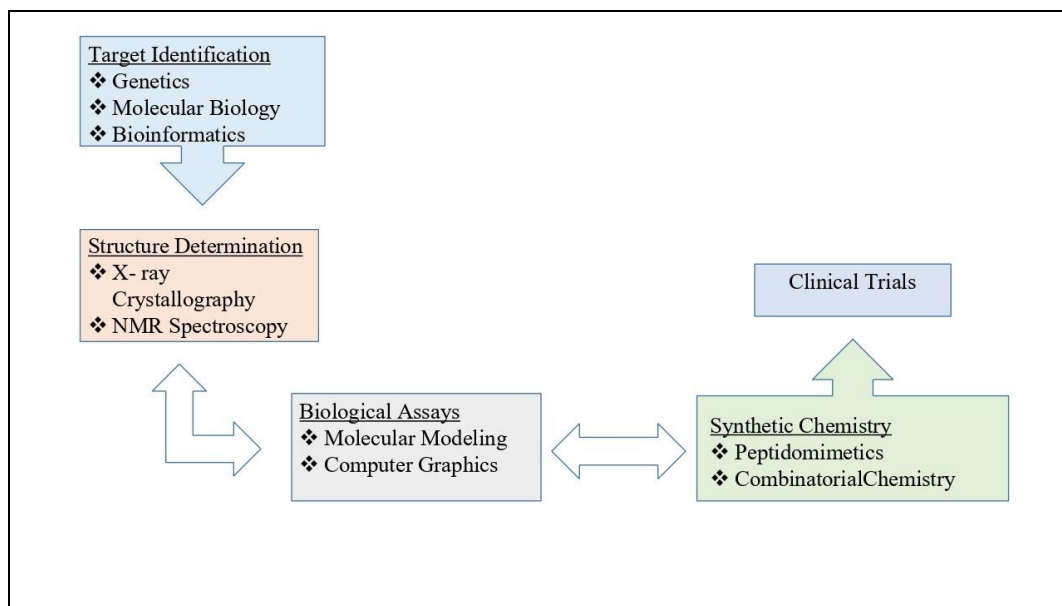


Figure 3: Working of CADD

Preclinical development and new medication research usually take three to six years. Before a product is put on the market, clinical research may take ten years or longer [26]. The development of a successful medication takes 12 to 15 years and costs more than 1.3 billion dollars [27]. Of the 5000–10,000 tested compounds, 250 are typically selected for preclinical research. Only one of them gets approved by the FDA after a comprehensive evaluation of the recently discovered medication, and only five make it to clinical trials.

5. The Use of CADD Techniques in Drug Discovery

The quantity of structural and extra information about the target (enzyme/receptor) and ligands that is available determines the different CADD strategies. There are currently two main modeling approaches used in the drug design process: direct design and indirect design. The structural characteristics of known active and inactive chemicals are compared as the foundation for the indirect design process. The target's three-dimensional characteristics (enzyme/receptor) are taken into consideration during direct design [28].

6. RESTRICTIONS AND DIFFICULTIES IN CADD:

1. Recognizing the Challenges: The Barriers in Computer-Aided Drug Development

While computer aided drug designing provides unique benefits in terms of speeding up and improving drug development, it is critical to acknowledge its inherent constraints. A significant challenge is a lack of AI/ML professionals in CADD. It is crucial to implement initiatives like targeted recruitment and specific training programs, such as in-silico medicine is leading the way in bridging this gap by cultivating a competent workforce capable of exploiting new computational approaches for drug development [29].

2. The precision of predictive models:

Assuring the accuracy of computational models is a critical issue in CADD because theoretical models provide the basis of docking scores, machine learning predictions, and molecular dynamics simulations. The intricacies of biological systems could not be adequately represented by these models. Understanding the intricacies of scoring algorithms is essential to increasing accuracy [30].

3. Quality and Quantity of data:

The accuracy of CADD tools' predictions is limited by the data on which they are taught. If there is little or low quality underlying data, the forecasts will most likely be wrong. One ongoing challenge is the lack of well selected, high-quality datasets, especially when it comes to machine learning in drug development [31].



Scoring systems in drug development are critical for estimating the binding affinity of compounds to their targets. It's crucial to actively lower the possibility of false positives and negatives in order to ensure their correctness. This calls for extensive scoring criteria calibration, the incorporation of several chemical descriptors, and continuous validation against experimental data. For instance, forecast reliability can be increased by thoroughly comparing docking results to known binding affinities. Researchers can increase their confidence in scoring systems and reduce the likelihood of errors in drug discovery prediction by balancing sensitivity and specificity [32-34].

4. Excessive dependence on computational forecasts:

Successful drug development requires balancing computational predictions with experimental evidence, and while CADD is a useful tool, depending only on its predictions without additional experimental validation could result in misdirected endeavors [35].

5. Computational Cost and Time:

Some advanced CADD techniques require a significant amount of computer power, especially those that call for intricate machine learning models or huge molecular dynamics simulations. The associated time and infrastructure costs may be too much for certain research organizations [36].

6. Signifying Molecular Adaptability:

Target proteins and possible medicinal compounds are among the many biological molecules with a high degree of flexibility. It can be challenging to accurately depict this flexibility, particularly when using methods like molecular docking, which can significantly impact the results of CADD investigations [37].

7. Ability of AI Models to Interpretate:

The more complex AI and machine learning models develop, the harder it is to comprehend their predictions. It can be challenging to understand why a certain molecule is expected to be effective or how its structure might be altered due to the "black-box" nature of AI models [38].

CONCLUSION

Researchers from a variety of fields, including pharmacology, medicine, and information technology, are drawn to the multidisciplinary field of computer-aided drug design (CADD) to develop new methods and tools or enhance preexisting ones that aid in the drug development process. These methodologies demonstrated to be beneficial at various phases of the drug discovery process, decreasing both the cost and time required to produce a medicine compared to traditional methods. These technologies may be utilized and developed to help with the various stages of drug development. The transition from previous discoveries to the current landscape emphasizes its critical role in accelerating drug development. But as CADD charts its future, new challenges appear that require constant optimization, ethical considerations, and the incorporation of diverse biological data. Success stories show how CADD may be used practically in clinical settings, and machine learning can improve prediction abilities and open up new possibilities. Global initiatives and cooperative networks democratize drug research while emphasizing the strength of solidarity. Although personalized medicine offers specific therapies, there are accessibility and ethical issues.

ABBREVIATION:

CADD- Computer Aided Drug Design

QSAR- Quantitative Structure Activity Relationship

CoMFA- Comparative Molecular Field Analysis

CoMSIA- Comparative Molecular Similarity Index Analysis

NMR- Nuclear Magnetic Resonance



REFERENCES:

1. Whittaker. The role of bioinformatics in target validation. Drug Discovery To-Clinical trial registration: a statement from the International Committee of Medical Journal Editors. Medical Journal of Australia, 2004; 181: 293-4.
2. Lengauer. Bioinformatics. From Genomes to Drugs. Wiley- VCH, Weinheim, Germany, 2002.
3. Lipinski. Lead and drug-like compounds: the rule-of-five revolution. Drug Discovery Today: Technologies, 2004; 1(4): 337-341.
4. Leeson P D, Davis A M, Steele J. Drug-like properties: Guiding principles for design – or chemical prejudice? Drug Discovery Today: Technologies, 2004; 1(3): 189-195.
5. Hou T. Xu X. Recent development and Application of Virtual Screening in Drug Discovery: An Overview. Current Pharmaceutical Design, 2004; 10: 1011-1033.
6. Klebbe G. Lead Identification in Post-Genomics: Computers as a Complementary Alternative. Drug Discovery Today: Technologies, 2004; 1(3): 225-215.
7. Gisbert Schneider. Uli Fechner. Computer-based de novo design of drug-like molecules. Nature. Reviews. Drug Discovery, 2005; 4(8): 649-663.
8. Butte A. The use and analysis of microarray data. Nature Reviews Drug Discovery, 1(12): 951-960.
9. Richards W. G. Computer-Aided Drug Design. Pure and Applied Chemistry, 1994; 6(68): 1589-1596.
10. Gibaldi, M., & Feldman, S. (1970). Mathematical modeling of drug absorption and disposition. Journal of Pharmaceutical Sciences, 59(5), 579-589.
11. Ku, D. N., & Flannery, B. P. (1990). Computational fluid dynamics in pharmaceutical research. Pharmaceutical Research, 7(10), 1036-1042.
12. Ette, E. I., & Williams, P. J. (2004). Population pharmacokinetics II: Estimation methods. Annals of Pharmacotherapy, 38(11), 1907-1915.
13. Schneider, G. (2017). Automating drug discovery. Nature Reviews Drug Discovery, 16(1), 1-2.
14. Ekins, S., & Puhl, A. C. (2018). Artificial intelligence in drug discovery: A review. Journal of Medicinal Chemistry, 61(11), 4561-4575.
15. Chen, H., & Zhang, Y. (2020). Deep learning in drug discovery: A review. Journal of Pharmaceutical Sciences, 109(10), 3131-3141.
16. Lee, J., & Kim, B. (2020). Virtual reality in pharmaceutical research: A review. Journal of Controlled Release, 321, 137-146.
17. Singh, S., & Kumar, V. (2022). Personalized medicine using computer-aided drug delivery systems: A review. Journal of Pharmaceutical Sciences, 111(5), 1231-1241.
18. Kapoor, L.; Oprea, T.I. From empirical to rational drug discovery: The importance of CADD. Drug Des. Rev. 2018, 15, 345–356.
19. Fu, C.; Xiang, M.A.; Chen, S.; Dong, G.; Liu, Z.; Chen, C.; Liang, J.; Cao, Y.; Zhang, M.; Liu, Q. Molecular drug simulation and experimental validation of the CD36 receptor competitively binding to Long-Chain fatty acids by 7-Ketocholesteryl-9-carboxynonanoate. ACS Omega 2023, 8, 28277–28289. [CrossRef]
20. Schaduangrat, N.; Lampa, S.; Simeon, S.; Gleeson, M.P.; Spjuth, O.; Nantasenamat, C. Towards reproducible computational drug discovery. J. Cheminform. 2020, 12, 9.
21. Drug Development Strategies, Awanish Kumar Ph.D, Anubhuti Jha, in Anticandidal Agents, 2017.
22. Vaishnav Bhaskar, Krishnan Namboori, Leena K Pappachen. In Silico Discovery of Novel Ligands for Anti-Tubercular Targets using Computer Aided Drug Design. Research J. Pharm. and Tech. 2019; 12(11):5646-5650.
23. Darshana M. Nagare, Arti M. Jadhav. Review on “Computer Aided Drug Design”: 2022, International Journal of Research Publication and Reviews, Vol 3, no 1, pp 1009-1018.
24. Divya Jindam, Lokesh Ravi, Kannabiran Krishnan. Construction of Computational Protein Structure Data base by Homology Modeling for the Aquatic Pathogen Perkinsus marinus for Targeted Drug Design and Development. Research J. Pharm. and Tech 2018; 11(6): 2203-2208.
25. Structure based and ligand based drug designing, Vysakh Mohan M..
26. Kitchen D B. Decornez H. Furr J R. Bajorath J. Docking and scoring in virtual screening for drug discovery: methods and applications. Nature reviews in drug discovery, 2004; 3: 935-949.
27. DiMasi J A. Grabowski H G. The cost of biopharmaceutical R&D: is biotech different? Managerial and Decision Economics, 2007; 28: 469-479.
28. Fauman EB, Rai BK, and Huang ES. Structure-based druggability assessment-identifying suitable targets for small molecule therapeutics. Curr. Opin. Chem. Biol., 2011; 15: 463-468.
29. Jorgensen, W.L. The many roles of computation in drug discovery. Science 2004, 303, 1813–1818.
30. Warren, G.L.; Andrews, C.W.; Capelli, A.M.; Clarke, B.; LaLonde, J.; Lambert, M.H.; Murray, C.W. A critical assessment of docking programs and scoring functions. J. Med. Chem. 2006, 49, 5912–5931.
31. Aleksandrova, A. Machine-Learning Scoring Functions to Improve Structure-Based Binding Affinity Prediction and Virtual Screening. 2016. Available online: https://www.academia.edu/28830051/Machine_learning_scoring_functions_to_improve_structure_based_binding_affinity_prediction_and_virtual_screening (accessed on 10 November 2023).



32. Fujimoto, K.; Minami, S.; Yanai, T. Machine-Learning- and Knowledge-Based scoring functions incorporating ligand and protein fingerprints. *ACS Omega* 2022, 7, 19030–19039.
33. Guedes, I.A.; Barreto, A.; Marinho, D.; Krempser, E.; Kuenemann, M.A.; Spérandio, O.; Dardenne, L.E.; Miteva, M.A. New machine learning and physics-based scoring functions for drug discovery. *Sci. Rep.* 2021, 11, 3198.
34. Walters, W.P.; Murcko, M.A. Prediction of 'drug-likeness'. *Adv. Drug Deliv. Rev.* 2002, 54, 255–271.
35. Kitchen, D.B.; Decornez, H.; Furr, J.R.; Bajorath, J. Docking and scoring in virtual screening for drug discovery: Methods and applications. *Nat. Rev. Drug Discov.* 2004, 3, 935–949.
36. Dror, R.O.; Dirks, R.M.; Grossman, J.P.; Xu, H.; Shaw, D.E. Biomolecular simulation: A computational microscope for molecular biology. *Annu. Rev. Biophys.* 2012, 41, 429–452.
37. Teague, S.J. Implications of protein flexibility for drug discovery. *Nat. Rev. Drug Discov.* 2003, 2, 527–541.
38. Ching, T.; Himmelstein, D.S.; Beaulieu-Jones, B.K.; Kalinin, A.A.; Do, B.T.; Way, G.P.; Greene, C.S. Opportunities and obstacles for deep learning in biology and medicine. *J. R. Soc. Interface* 2018, 15, 20170387.

How to cite this article:

Shivkumar M. Sontakke¹ et al. *Jcpr.Human*, 2025; Vol. 21 (3): 13-21.

Conflict of Interest Statement:

The authors have no conflicts of interest to declare.

This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.