

#### International Journal of Advanced Research in Science, Communication and Technology

International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal



Volume 5, Issue 1, August 2025

# A Review on Drug Design: Strategies, Advances, and Future Directions

Santosh Bayaji Kodalkar, Samadhan Gulab Parase, Kiran Ramchandra Gorad Rushal Vijay Shirkule, Saurabh Abasaheb Khuspe

Mandesh Institute of Pharmaceutical Science and Research Center, Mhaswad

Abstract: Drug design represents a cornerstone of modern pharmaceutical research, aiming to identify and optimize bioactive molecules that can modulate specific biological targets associated with disease. Over the past decades, drug discovery has transitioned from serendipitous findings and trial-and-error screening to rational, data-driven approaches guided by molecular biology, structural chemistry, and computational tools. This review provides an in-depth examination of traditional and contemporary drug design strategies, including structure-based drug design (SBDD), ligand-based drug design (LBDD), phenotypic screening, combinatorial chemistry, and novel modalities such as targeted covalent inhibitors, molecular glues, RNA therapeutics, and nanomedicine. The increasing role of artificial intelligence (AI) and machine learning (ML) in predictive modeling, virtual screening, and de novo molecular generation is discussed, alongside challenges in data quality, regulatory acceptance, and translational success. Finally, the paper outlines future perspectives, emphasizing the integration of multi-omics, explainable AI, and emerging chemical spaces to enhance the efficiency and success rate of drug discovery.

**Keywords**: drug design, structure-based drug design, ligand-based drug design, molecular docking, artificial intelligence, molecular glues, combinatorial chemistry, nanomedicine

## I. INTRODUCTION

Drug design is the process of identifying molecular entities that can modulate the function of a biological target to produce therapeutic benefit. This discipline lies at the interface of medicinal chemistry, structural biology, pharmacology, and computational science. Historically, early drug discoveries were largely empirical, arising from the observation of bioactive natural products (e.g., morphine from opium) or accidental findings (e.g., penicillin) [1]. Over time, the availability of detailed biochemical knowledge and technological advances have shifted drug design from a **phenotypic-first** to a **target-first** paradigm.

The central goals of modern drug design are to:

- Identify disease-relevant targets.
- Understand their structural and mechanistic properties.
- Develop chemical entities with high potency, selectivity, and favorable pharmacokinetics.

While the average cost of bringing a drug to market exceeds USD 2 billion and can take more than a decade [2], computational methods and AI have opened new possibilities for accelerating early-stage discovery. Nevertheless, challenges such as high attrition rates, off-target toxicity, and resistance mechanisms remain significant obstacles.

#### II. TRADITIONAL AND MODERN DRUG DESIGN APPROACHES

## 2.1 Structure-Based Drug Design (SBDD)

SBDD uses the 3D structural information of a biological target, typically obtained from X-ray crystallography, cryoelectron microscopy, or nuclear magnetic resonance (NMR) spectroscopy [3]. Key steps include:

- Determining the target's 3D conformation.
- Identifying active or allosteric sites.
- Performing virtual screening via molecular docking tools (e.g., AutoDock, Glide).
- Refining lead compounds using molecular dynamics (MD) simulations.

Copyright to IJARSCT www.ijarsct.co.in



DOI: 10.48175/IJARSCT-28653





## International Journal of Advanced Research in Science, Communication and Technology

International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal



Volume 5, Issue 1, August 2025

Case Example: Development of HIV protease inhibitors relied heavily on crystallographic data of the viral enzyme, enabling precise fitting of inhibitors into the active site [4].

Figure suggestion: A schematic showing the workflow of SBDD from target structure acquisition to lead optimization.

#### 2.2 Ligand-Based Drug Design (LBDD)

When the target structure is unavailable, LBDD uses data from known ligands to infer molecular features associated with activity. Approaches include:

- Quantitative Structure–Activity Relationship (QSAR) models [5].
- Pharmacophore modeling, defining the spatial arrangement of features required for activity.
- Similarity searching within chemical databases.

LBDD is particularly useful in identifying "scaffold hops" to circumvent patent barriers or improve properties.

#### 2.3 Phenotypic versus Target-Based Screening

**Phenotypic screening** identifies compounds based on observable changes in a biological system, without prior knowledge of the molecular target [6].

Target-based screening focuses on compounds that modulate a predefined biomolecule.

Recent trends indicate a revival of phenotypic screening, especially for complex diseases like cancer, neurodegeneration, and infectious diseases, where the disease biology is incompletely understood.

#### 2.4 Combinatorial and Dynamic Combinatorial Chemistry

Combinatorial chemistry accelerates library generation by systematically combining sets of building blocks [7].

- Click chemistry enables rapid assembly of stable, bioorthogonal molecules [8].
- **Dynamic combinatorial chemistry** allows equilibrium-driven selection of high-affinity binders in the presence of the target [9].

**Table suggestion:** Comparison of click chemistry vs. dynamic combinatorial chemistry, including speed, diversity, and target adaptability.

## III. NOVEL MODALITIES IN DRUG DESIGN

#### 3.1 Targeted Covalent Inhibitors (TCIs)

TCIs form irreversible or reversible covalent bonds with specific residues in the target protein, providing prolonged target engagement [10].

Examples:

- **Ibrutinib**: covalently binds to BTK in B-cell malignancies.
- **Sotorasib**: targets KRAS^G12C^ mutation in lung cancer.

#### 3.2 Molecular Glues

Molecular glues induce or stabilize protein–protein interactions to drive degradation or activation of disease-relevant proteins [11]. This is distinct from traditional inhibitors, as the therapeutic effect arises from enforced proximity.

**Example:** Lenalidomide modulates cereblon to degrade specific transcription factors in multiple myeloma.

## 3.3 Retrometabolic Drug Design

Retrometabolic design involves creating drugs that are active only at the site of action and undergo predictable inactivation upon systemic circulation [12]. This reduces systemic toxicity.





## International Journal of Advanced Research in Science, Communication and Technology

International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal



Volume 5, Issue 1, August 2025

#### 3.4 Nanomedicine

Nanotechnology offers precise drug delivery, reduced off-target exposure, and improved solubility [13]. Lipid nanoparticles (LNPs) used in mRNA COVID-19 vaccines exemplify the integration of nanocarriers into modern therapeutics.

#### 3.5 RNA and Gene-Based Therapeutics

RNA-based drugs (siRNA, mRNA, antisense oligonucleotides) and CRISPR-Cas9 systems represent a paradigm shift toward programmable therapeutics [14].

#### IV. ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING IN DRUG DESIGN

## 4.1 Applications Across the Pipeline

AI and ML support:

- Target identification from omics datasets.
- Virtual screening for millions of compounds.
- ADMET (Absorption, Distribution, Metabolism, Excretion, Toxicity) prediction.
- **De novo design** of molecules [15].

#### 4.2 Graph Neural Networks (GNNs)

GNNs model molecules as graphs of atoms and bonds, improving property prediction and aiding generative design [16].

#### 4.3 Generative AI Models

Variational autoencoders (VAEs), generative adversarial networks (GANs), and reinforcement learning approaches are used to design novel compounds that satisfy specific activity and property constraints [17].

## 4.4 Explainable AI (XAI)

The lack of interpretability in AI models is a key barrier to regulatory acceptance [18]. XAI methods provide rationales for predictions, increasing trust in computationally designed drugs.

#### V. CHALLENGES IN DRUG DESIGN

- **High attrition rates**: More than 90% of candidates fail during clinical development [19].
- **Data limitations**: Incomplete or biased datasets compromise AI predictions.
- Regulatory hurdles: Limited frameworks for AI-generated molecules.
- **Resistance mechanisms**: Evolution of drug resistance in pathogens and cancer.
- Economic barriers: Rising R&D costs despite technological progress.

## VI. FUTURE DIRECTIONS

- **Hybrid design strategies** integrating SBDD, LBDD, and phenotypic screening.
- Multi-omics integration to better understand disease networks.
- Expansion into new chemical spaces such as macrocycles and degraders.
- AI-driven retrosynthetic planning to optimize synthesis routes.
- Regulatory adaptation for computational drug submissions.

#### VII. CONCLUSION

Drug design is undergoing a transformative era, moving from empirical trial-and-error toward a rational, technology-driven discipline. While traditional methods like SBDD and LBDD remain foundational, they are increasingly complemented by AI, molecular glues, RNA therapeutics, and nanomedicine. The integration of computational and

Copyright to IJARSCT www.ijarsct.co.in



DOI: 10.48175/IJARSCT-28653





#### International Journal of Advanced Research in Science, Communication and Technology



International Open-Access, Double-Blind, Peer-Reviewed, Refereed, Multidisciplinary Online Journal

Volume 5, Issue 1, August 2025

Impact Factor: 7.67

experimental tools, along with regulatory evolution, will be essential for addressing unmet medical needs in the coming decades.

#### REFERENCES

- [1]. Hughes JP, et al. Br J Pharmacol. 2011;162(6):1239–1249.
- [2]. DiMasi JA, et al. J Health Econ. 2016;47:20–33.
- [3]. Blundell TL, et al. Nat Rev Drug Discov. 2002;1(1):45–54.
- [4]. Wlodawer A, et al. Science. 1989;245:616–621.
- [5]. Cherkasov A, et al. J Med Chem. 2014;57(12):4977–5010.
- [6]. Moffat JG, et al. Nat Rev Drug Discov. 2014;13(8):588–602.
- [7]. Gordon EM, et al. J Med Chem. 1994;37(10):1385–1401.
- [8]. Kolb HC, et al. Angew Chem Int Ed. 2001;40:2004–2021.
- [9]. Lehn JM. Science. 2002;295:2400–2403.
- [10]. Singh J, et al. Nat Rev Drug Discov. 2011;10(4):307–317.
- [11]. Schreiber SL. Nature. 2021;594:170–177.
- [12]. Bodor N, Buchwald P. Adv Drug Deliv Rev. 2012;64:953–968.
- [13]. Patra JK, et al. J Nanobiotechnology. 2018;16:71.
- [14]. Sahin U, et al. Nat Rev Drug Discov. 2014;13(10):759–780.
- [15]. Vamathevan J, et al. Nat Rev Drug Discov. 2019;18:463–477.
- [16]. Wu Z, et al. IEEE Trans Neural Netw Learn Syst. 2021;32(1):4–24.
- [17]. Zhavoronkov A, et al. Nat Biotechnol. 2019;37:1038–1040.
- [18]. Molnar C. Interpretable Machine Learning. 2022.
- [19]. Waring MJ, et al. Nat Rev Drug Discov. 2015;14:475–486.

