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Biotechnological Drug Development—The Role of Proteins, Genes, *In-Silico*, and Stem Cells in Designing Models for Enhanced Drug Discovery

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Abstract

The application of biotechnology in drug discovery has been discovered to be a promising and resourceful approach for the discovery of novel therapeutic candidates that comes with less time and cost than the traditional ways of drug discovery. This has additionally endowed researchers with the necessary understanding of diseases, which offers exceptional methods for treating patients. Additionally, diagnosis and treatment are becoming increasingly intertwined with the help of biotechnology. Today, researchers in biotechnology deal with the root of diseases and find solutions through therapeutic agents, hence, improving quality of life. The discovery of drugs in recent days is practically challenging without good modeling in biotechnology, this wonderful technique is now being adopted in the discovery of new and effective classes of drugs which include but are not limited to gene therapy, cancer vaccines, proteins, and even enzymes. In this current review, we review the efforts so far in the usage of this approach in drug discovery. The review targets the biotechnological application and design implementation in drug discovery. It explains the use of proteins, genes, *in-silico*, and stem cells in designing models for enhanced drug discovery, the chemical similarity network for drug discovery, and future recommendations on the integration of AI in biotechnology.

Subject Areas

Biomedical Sciences, Biotechnology, Computer Science

Keywords

Drug Discovery, Biotechnology, Diseases, Genes, Protein, *In-Silico*, Stem Cells, mRNA, DNA

1. Introduction

The word "biotechnology," which appears to have originated in the 1970s, is now widely used by researchers across different fields to signify different things based on their applications [1]. The relevant general definition of biotechnology is the use of organisms and their biological systems for practical and manufacturing processes [2]. Biotechnology can alternatively be defined as the fusion of biology and technology, thus for all intents and purposes implying the enclosure of all biological and related technologies in product alteration [3]. This further implies that biotechnology is a form of genetic engineering, specifically with cutting-edge molecular processes such as recombinant DNA, which use biological catalysts (enzymes) known as restriction endonuclease to cut and splice (or recombine) DNA fragments into large numbers of fragments [4]. Biotechnology is now recognized by biomedical science researchers as a front-line approach to solving most of the world's health challenges, including one-health, infectious, and non-infectious diseases [5], and scientists have used biotechnology knowledge for disease management over the last few decades [2]. The therapeutic yields of biotechnologies, known as biologics or biopharmaceuticals, are now at the forefront of delivering insights and advancements for the treatment of a wide range of human diseases, including microbial infections, diabetes, and malignancies. This has further demonstrated the usefulness of biotechnology in drug discovery over traditional methods [2].

Traditional drug discovery has been reported to be a costly and complex process requiring several billions of dollars, with thousands of chemicals failing before clinical trials representing 99% of the starting chemical compounds; of these chemical compounds assessed as part of drug discovery and preclinical testing, only a few made it to human clinical trials and were eventually accepted for commercial use by the Food and Drug Administration (FDA) [4]. Following these setbacks gave birth to a novel therapeutic development strategy based on genomic and proteomic know-how that has technologically progressed over the years in minimizing these challenges [5]. The genome that is, the full makeup of an organism's genetic information that includes both coding and non-coding nucleic acid sequences provides a framework for characterizing the proteome, which is a list of only the encoding nucleic acid regions that result in the biosynthesis of protein products [1]. The study of genes and proteins aids in the

discovery of new genes and proteins, as well as the evaluation of their levels in diseased cells, normal cells, and cells treated with a variety of chemicals with varying efficacy and toxicity [1]. As a result, they come in handy when it comes to identifying new therapeutic targets [5].

This review article discusses some of the techniques used in biotechnological drug discovery and development.

2. Overview and Design Implementation of Biotechnological Drug Discovery of Cancer Management

The use of a biotechnological approach to drug discovery has become prominent in research and development; biopharmaceuticals, which are products of the use of biotechnology in discovering new drug targets have generated revenues for several pharmaceutical companies, which is an indication of its importance in drug discovery [6] [7]. Over the years, biotechnological approaches such as whole-genome profiling and sequencing, proteomics, and microarray techniques have birthed positive innovations in discovering novel drug targets to cure certain diseases, most especially cancer [6]. The role of genomics and proteomics in achieving this cannot be over-emphasized.

2.1. Role of Genomics in Biotechnological Drug Discovery

Numerous diseases, such as diabetes, autoimmune disorders, neurological disorder, and cancer are caused because of dysregulation of a complex interplay of genes [8]. One of the most advanced and innovative techniques used by biotechnological researchers is genomics, which incorporates genomic sequence and human genome analysis. The knowledge of genomics has empowered researchers to adopt a more represented strategy in developing safe and effective drugs. Genome sequencing can predict the risk of developing diseases, the origin, traits, and response to drugs. With profound knowledge of genomic data, organizations are currently ready to develop drugs that affect pathogens or cancer cells, without causing any harm to healthy body cells [9]. In addition, vast knowledge in genomics can proffer further ideas into the mechanism of drug action, which contributes to discovering novel therapeutic agents [10]. Furthermore, dissimilarities in the genomic makeup in humans present a surplus opening for effective drug discovery [11], identification of target molecule, and evolving drug leads to the apt likelihood for preclinical and clinical studies [12]. The use of gene studies in the preclinical setting necessitates one to screen numerous compounds with negligible discrepancy. At the point when the target gene is isolated, the chemical that works best largely in contradiction of all its subtypes is picked for further studies [13].

Other sources which integrate genomic data at the notch of chromosomal DNA, disease-associated genes, mRNA transcript sum up of tissues, genetic difference data in humans, and animal and developmental modes applicable to disease all embrace genomic methods [14]. For illustration, if the disease target

implicates human endothelium, genomic data on the target organ context can be quarried with bioinformatics for the discovery process. The adoption of transcriptional arrays or DNA sequencing of a complementary DNA library of human endothelial cells provides a standpoint on gene transcription in the human endothelium. Likewise, proteomics can give an understanding of the useful protein in specific cells [14].

2.2. Proteomics Approach in Biotechnological Drug Discovery

Quite a lot of studies have proven that genomics aids majorly in the identification of drug-target processes since it is considered a high throughput screening of expressed genes. Also, the work of Zhang *et al.*, highlighted several works of literature to show that the analysis of the genome does not account for the post-translational process, which takes account of protein amendment and protein metabolism [15]. Genomics is positioned on genetic data, while proteomics considers genetic data of DNA or mRNA, as well as protein post-translational modification. Thus, the practices involved in the discovery of drugs moved from genomics to proteomics. Yet, the discovery of molecular targets for specific diseases requires the understanding and utilization of both genomic and proteomic methods at the biochemical and physiological levels [15].

Proteomics has attained a lot of consideration as a drug development platform [13], the skills adopted in proteomics can give a wide-ranging evaluation of countless activities in clinical research of numerous diseases [16]. As most drugs bind to proteins or nucleic acid (enzymes, ion channels, or receptors) [17], the proteomics model embroils trailing an unstable protein that is prompting a harmful effect, and subsequently, the application of a drug molecule to revise its effect [18]. The proteomics approach involves; 1) Target identification and validation, 2) Biomarker identification (Efficacy and safety) [19].

2.2.1. Target Identification and Validation

Target identification and validation make sure the protein (biological target) is druggable; the activity of the protein can be restrained and change the state of the disease (therapeutic effect), these proteins can then be employed to classify patients for clinical trials [20].

2.2.2. Biomarkers Identification

Biomarkers are customarily hired in each phase of drug discovery; the use of biomarkers has the potential to speed up the drug discovery process and approval procedures [21]. The ability of biomarkers is exploited during preclinical studies, to distinguish disease models, and investigate the consequence and mechanism of action of the lead drug candidates *in vivo* models [20]. In addition, the toxicity of biomarkers informs the presence or degree of toxicity, increasing confidence in safety, and the ability to forecast, detect and track drug-induced toxicity progression. The sum of the efficacy and impact of biomarkers toxicity in preclinical and clinical drug discovery will be strong-minded by their ability

to detect early toxicity, monitor onset, and reversibility, and succeed in adverse effects detected in the clinical studies [22]. **Table 1** highlights the major differences between genomics and proteomics approaches to drug discovery.

2.3. Design Implementation of Biotechnological Drug Discovery

The use of biotechnology in drug discovery is a broad area and yet growing and famous field [27]. Effective quality and design are implemented in biotechnological drug discovery to allow persistent drug delivery and increase drug performance [28]. In support, biotechnological production is irreversible, very luxurious, and encompasses a lot of critical parameters throughout the process. Quality control tests applied to the intermediate and final product become inefficacious; therefore, sustaining predefined quality is vibrant [27]. The quality and design implementation in biotechnological drug discovery follows four key stages: 1) define a target; 2) design the product; 3) identify potential risk, and 4) develop a control strategy [27] [29].

Table 1. Major differences between genomics and proteomics approaches to drug discovery.

Parameters	Genomics	Proteomics
Definition	The study of an organism's entire genome, including genes, regulatory regions, and non-coding regions	The study of an organism's entire set of proteins, including their structure, function, and interactions
Focus	Identification of genes and their function	Identification of proteins and their function
Key Techniques	DNA sequencing, genome-wide association studies, transcriptomics	Mass spectrometry, protein microarrays, protein-protein interaction analysis
Output	Identification of potential drug targets based on genetic variants and gene expression patterns	Identification of potential drug targets based on protein expression patterns and protein-protein interactions
Advantages	Provides a comprehensive view of an organism's genetic makeup and potential drug targets	Identifies proteins that are actively involved in disease processes and may be more relevant drug targets than genes
Limitations	Identifying relevant genes and their functions can be challenging, as many genes have multiple functions and interact with each other	Protein identification and analysis can be complex and expensive, and it may be difficult to identify relevant proteins among the vast number of proteins in a cell or tissue
References	[23] [24]	[25] [26]

2.3.1. Define a Target Product Profile/Goals

To design quality into a product, the product design and performance stipulations must be well understood at the beginning of the design phase [27]. The profile of a target product is an exceptional and vigorous synopsis of the quality features of a drug product that supremely will be realized to facilitate the desired quality, safety, and efficacy of a drug product is succeeded [29] [30]. Significant target product profile takes account of dosage form and route of administration, dosage form strength(s), therapeutic moiety release, and pharmacokinetic characteristics suitable to the drug product dosage form being developed and drug product quality appropriate for the desired marketed product [31].

2.3.2. Design Product

For the innovation of a novel pharmaceutical product, the following system is followed by rub in the enactment of quality by design practically [31] [32] [33] [34]: 1) The product's preferred performance is defined by ascertaining the quality of the target product profile; 2) Serious quality traits identification; 3) Recognition of credible critical process factors and critical material elements; 4) Connotation of design of experiment with critical substantial characteristics and serious process factors to critical quality elements to obtain adequate data and how these variables quality target product profile. Thus, describe the design space, prominent to a product with a desired quality target product profile. The design product must satisfy predefined objectives.

2.3.3. Risk Assessment

An exact problem sketch or risk question is the inauguration of a quality risk assessment. If the risk in question is well structured, a proper risk-controlling tool and the types of data necessary to attend to the risk question will be more enthusiastically dogged [27]. A proficient quality risk evaluation should be used in any biotechnological drug practice [28]. Contained by the drug discovery phase, the risk management approach ought to concentrate on hazard awareness, avoidance, and reduction. Input into the scheme and choice of compounds will be mandatory to reduce their potential to form reactive metabolites and exhibit proof of objectionable safety parameters [35]. This will consist of the use of machinery that can detect shortages of compounds and can be embraced repeatedly while having the aptitudes necessary in the design and analysis phase [35].

2.3.4. Control Strategy

The control approach is a series of strategic controls, ascending from invention and process thoughtful that licenses procedure performance and product quality. The controls can entail parameters and elements and it is alarmed with the medicinal material and drug product materials and components, facility and kit operating settings, and the obligatory approaches and density of reflection and audit, comparability tests and strength testing [27] [36]. The likelihood of a harmful impact on product efficacy can be reduced by an all-inclusive method to the control strategy. A control strategy for a product object to offer that signifi-

cant controls are in domicile to hunt the risks associated with the product at an acceptable limit. Hence, the understanding of risk management and control strategy are momentously connected and the use of risk evaluation in creating the control strategy is exclusive to the quality design approach [27]. A well-established control strategy will diminish risk but does not change the criticality of qualities. The control strategy plays a fundamental role in guaranteeing that the serious process parameters are met, and therefore the quality target product profiles are apprehended [27]. **Figure 1** shows the steps involved in the design implementation of biotechnological drug discovery.

3. The Role of Proteins, Genes, Stem Cells, and *In-Silico* in Drug Discovery

Isolating protein targets of biologically active compounds is a resourceful way to discover unidentified protein functions, and molecular mechanisms of drug action [37]. Within the worldwide pharmaceutical industry, protein-based drugs have been reported to reveal the firmest growth in recent years and presently have matchless credit for their potential as a practicable treatment choice for numerous diseases [1]. According to [38], over 100 original proteins and an associated number of boosted proteins are approved for therapeutic clinical use in Europe and the USA, with 2010 sales of US$108 billion [38] [39]. In this group, monoclonal antibodies represent almost half (48%) of the sales. Protein therapeutics are used in the management of many major diseases including cancers, immune disorders, and infections [39].

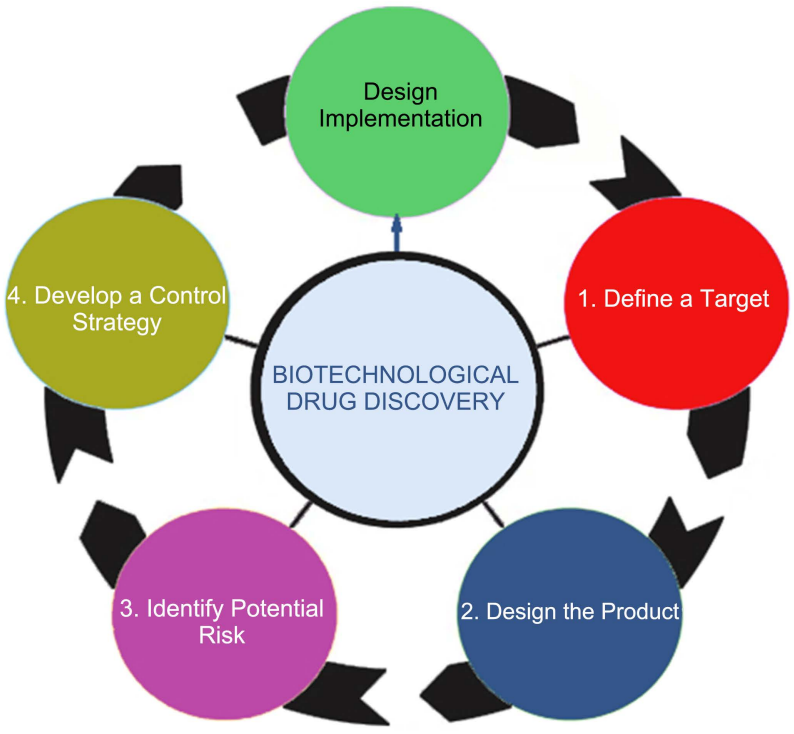

Figure 1. Design implementation of biotechnological drug discovery.

3.1. Protein Kinases as a Target for Drug Discovery

Protein kinases are at present one of the most detected classes of drug targets as established by the multiple kinase inhibitors that have arrived in clinical trials in recent years [37] [40]. Imatinib, a tyrosine kinase inhibitor, is a drug that is now approved by the food and drug administration (FDA) for the treatment of specific types of cancer. As there are over 500 known human protein kinases and most of them engage in adenosine triphosphate binding pocket which is extremely sealed, selectivity is a crucial issue [37]. The main use of protein for the advances of drug compounds is to identify the structure of a protein in a complex with a tool compound such as a lead inhibitor to give a new chemical postulate to enrich inhibitor affinity by signifying new chemical reforms [41].

3.2. Genome Sequences as a Foundation for Modern Drug Discovery

The importance of complete genome sequences for modern approaches to drug discovery can never be underestimated. Researchers now understand the full match of proteins encoded by the human genome, and most human proteins can be allocated into structurally and mechanistically allied folks based on sequence homology [42]. The study of gene purpose from high throughput studies of protein-protein collaborations can be divided into networks and pathways using bioinformatics data combination tools [43]. The sequence of the genome has given a comprehensive parts list elucidating all the proteins available in the human body, and high throughput screening techniques give podia for exposing these proteins to millions of small molecules [41]. Therefore, the role of protein and genome sequences cannot be overemphasized in today's drug discovery.

3.3. Stem Cells as Vitriol Models for Drug Discovery

The use of *in vitro* models in drug development has been a foremost enhancement, not only in the innovation of essential chemical compounds, but also in providing relevant information on their pharmacodynamics *i.e.* "absorption, distribution, metabolism, and excretion" (ADME) features [44]. The advance of several *in vitro* pharmacodynamics models has prepared a resilient influence on the pathway in the route of transforming and accelerating drug discovery and development. For example, engineered tumour eternalized cells obtained from humans or animals have remained the finest acknowledged *in vitro* approach used by the biotechnology and pharmaceutical industries [45] [46]. Though these cell lines own the aids of aptness and scalability of the selection process, they elucidate extraordinary patchiness in their advance, strange genotype, and biological reaction to pharmaceutical formulations. However, the irregularities associated with these eternalized cells edged the rate and figure of prime molecules for drug development. Another example is the practice of dedicated basic culture approaches such as hepatocytes, human umbilical endothelial cells, and keratinocytes delivered fractional practice owing to their synchronized expanda-

bility [47]. In this case, the obligation for an enriched and constant physiological reaction, typical genotype, and development configuration has redirected drug innovation determinations near the understanding of stem cells. Furthermore, the prospect of detaching stem cells from a huge continuum of tissues [48] and evolving them *in vitro*, as well as their competence to ghettoize into several proficient cell types, has delivered an instrumental means for drug/target sighting and endorsement [49]. This implies that the application of stem cells does not only diminish the cost of pharmaceutical drug discovery but also upsurges the prospect of spotting primes with a target or pathway noteworthy to the disease diagnosis.

It is also important to note that stem cells from different biological components are not alike [50], and *in vitro* breeding where the stem cells are delivered with growing features is different from the small environment in which stem cells exist in the living system [51]. This means that stem cells have a more lethargic cell progression than their precursor cells *in vivo*, so the grade of the warmth of details resultant in a test tube or dish may vary from that of the living system [52].

3.4. *In Silico* Approach in Drug Discovery and Design

The use of the principle of mathematics and computer science application in biology has proven effective over the years, thereby triggering the expansion of the use of *in silico* approach. *In silico* (commonly called bioinformatics) denotes the use of computers or computer simulations to perform biological findings. Its practicality in biomedical sciences has additional worth to drug discovery study at the biotic level [53] [54]. Consequently, the computer approach is significant in cogent drug formulation, which principally depends on the prevailing biotic and pharmaceutical properties of ligands [55]. A sequence of ligands by such assets is vetted for the variety of the most feasible candidates. *In silico* approach is computer-based on the *in vivo* technique and their understanding is based on both mathematics and computations. In these techniques, mathematical means can be adopted to outline the integer of drug recipes in data screening, this will diminish the amount of pilot investigation in the order of tens of thousands of likely alignments. The result may perhaps be subjugated to the proof of identity of a prosperous drove-out drug amalgamation and the foremost syndrome subsidizing pathways. Computational scrutiny can now examine the amalgamated structures accompanying the host mechanisms, consistently the pathological pathways, to reserve therapeutic methods using equivalent models. A simulation is then run to definite considerations such as competencies, toxicities, and other side effects of the drugs in the handling of diseases from a system perception [56].

Typical illustrations are selection models called medicinal algorithmic combinational screens, and measurable confirmation action affiliation of herbal formulae. In this method, the network-constructed biological computational ap-

proach is smeared by mathematical models demonstrating the biological pathways which govern the sophisticated level of cellular special effects in multi- target drugs. Also, the unified network target-based identification of the multi-component synergy model, which relates drugs to their molecular targets [57], emphasizes its presentation as a data-modeling practice.

The efficacy of the *in-silico* techniques has auxiliary enriched the recognition of the hazardous properties of drug substances [58]. The *in silico* system has also lengthy the prospects of drug repurposing by combined networks [59] [60]. This routine scrutinizes the genomic dissimilarities that give to different reactions to drugs for precision medicine use and the forecast of disease proneness [61].

There are different approaches to *in silico* model of drug discovery, among which are genomics, proteomics, metabolomics, and much more with the most prominent one being molecular docking. Molecular docking is the use of the computational model for the prediction of ligands-target confirmation; of which ligands can be a small molecule or peptide synthesis from either plant, microbes, or animal while the target can be a protein or nucleic acid whose activity is paramount for the survival of a disease with having beneficial effect to the host or not evenly distributed throughout the living system. Although, because of the advances *in silico* analysis of drugs, several web servers are employed for the prediction of pharmacokinetics and drug-likeness proprietaries of a potential therapeutic agent. Also, a process called molecular dynamic stimulation is also employed to determine the selectivity and absorption potential of a promising drug candidate. Figure 2 denotes the process involved in molecular docking, and Table 2 gives a general overview of these techniques and their applications in drug discovery.

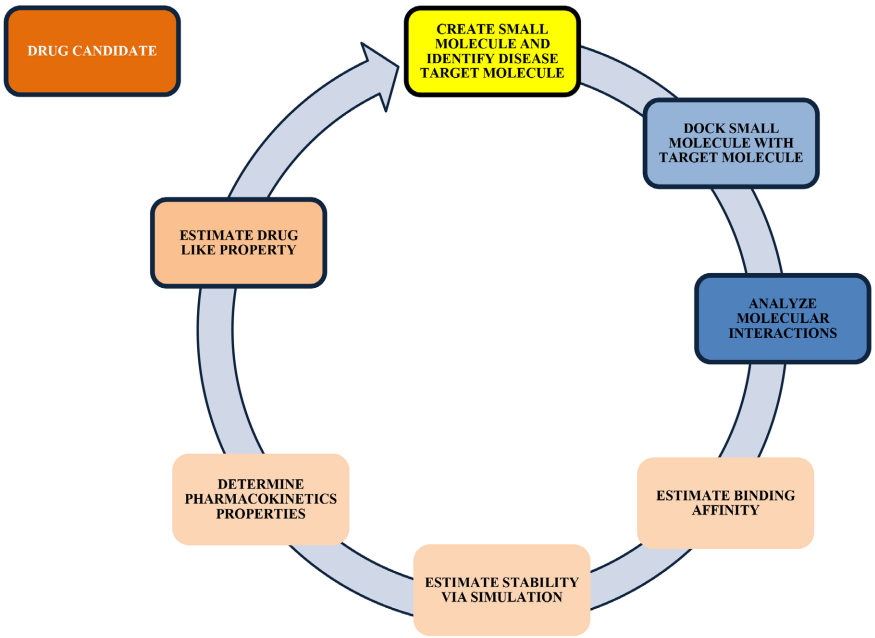

Figure 2. *In silico* process of drug discovery using molecular docking.

Table 2. General overview of the applications of these techniques including their pros and cons.

Parameters	Stem cells as vitro models	*In Silico* Approach
Definition	The use of stem cells *in vitro* to study drug responses and toxicity	The use of computer simulations to predict drug properties and interactions
Applications	Testing drug efficacy and toxicity, identifying drug targets and mechanisms of action, disease modeling, and drug screening	Predicting drug-target interactions, identifying drug candidates, optimizing drug properties, virtual screening, and molecular docking
Key Techniques	Differentiation of stem cells into specific cell types, microfluidics, gene editing, organoid culture, high-throughput screening, transcriptomics, and proteomics	Molecular docking, molecular dynamics simulation, virtual screening, ligand-based and structure-based drug design
Pros	More physiologically relevant models, potential for personalized medicine, and ability to model complex diseases	High throughput, cost-effective, allows for the exploration of large chemical space, no need for physical samples, and the ability to predict drug properties and interactions
Cons	Technical challenges and limitations, the potential for batch-to-batch variability, limited scalability and reproducibility, and ethical concerns related to the use of human embryos or fetal tissue	Limited accuracy and reliability, inability to account for all biological factors, lack of experimental validation, and inability to predict the toxicity and other adverse effects
References	[62]-[67]	[68] [69] [70] [71]

4. Target Identification, Chemical Similarity Network and AI Integration in Drug Discovery

One of the newest trends in drug discovery is target identification, which is built on the discovery that a drug can muddle with other drugs and change its purpose by binding to the target accountable for the activity [72]. High throughput screening (HTS) is a popular target-based technique in which a large sum of compounds is uncovered for disease and decisions are made based on the chemical's capacity to block the disease [73]. **Figure 3** shows an overview of the stages involved in drug development.

4.1. Approach Used in Chemical Similarity Network for Drug Discovery

Chemical similarity is a key perception in drug development that is utilized to invent compounds with comparable bioactivities centered on structural resemblances between two ligands [74]. A drug designer can build a series of structural

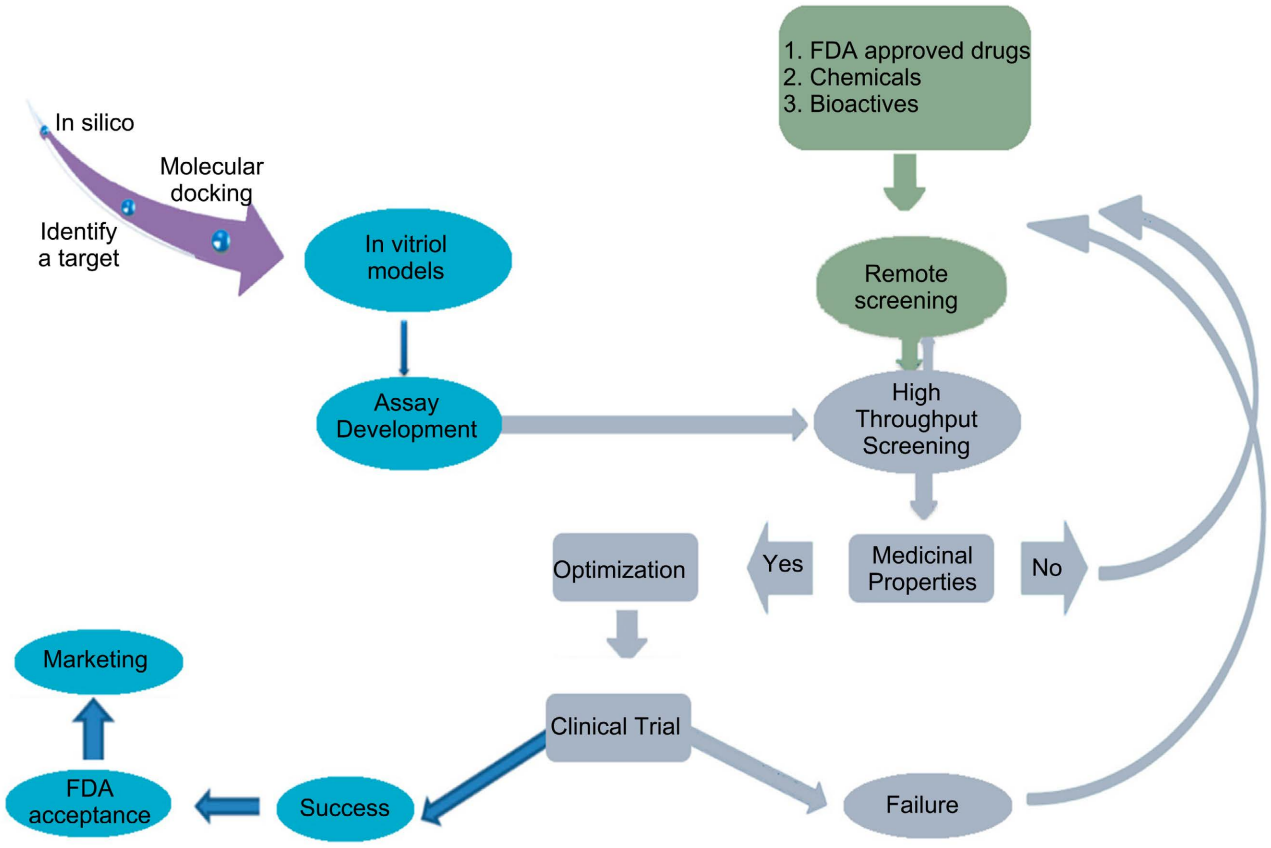

Figure 3. Overview of the stages involved in drug development.

equivalents with superior pharmacological characteristics when a prime compound is revealed using a chemical screen. The chemical correspondence concept, which holds that if two compounds have analogous structures, they are probable to have equivalent bioactivities, is at the core of similarity-based drug discovery. While there are exceptions, the relationship between chemical structure and compound activity in medicinal chemistry is well known [75]. Consequently, the causal structural similarity between two compounds is a prerequisite aimed at match-built drug discovery. A visual inspection can quickly determine the similarity between two ligands at a basic level by finding shared practical groups, structural motifs, or substructures. On the other hand, human involvement is frequently subjective and unsuitable for large-scale examination. Therefore, a successful drug discovery exertion necessitates the use of computational methods for unprejudiced chemical connection assessment and a thorough database [76].

More than a few computational chemical relationship search performances have been developed [74] [75] [76]. Chemical infrastructure impressions are the most often exploited method. By drawing common chemical motifs into twofold arrays known as structural keys, non-hashed structural fingerprints such as molecular access system (MACCS) keys or open babel fingerprints detect predetermined substructures or functional group patterns in a molecule. Each fragment

is turned into a dualistic sequence of 0 and 1, representing the existence or absence of a precise substructure, to relate chemical relationships between two molecules. Chemical-muddled patterns, such as daylight fingerprints on the other hand, utilize paths in their hashing [74].

The next step is to use a distance metric to measure chemical similarity when the chemical fingerprints have been resolute in a chemical hunt and the particles have been interpreted to acceptable data demonstrations. Some of the common distance measurements frequently used in chemoinformatics and bioinformatics to achieve this are Euclidean, and Mahalanobis metrics [77]. On the other hand, the Tanimoto index is the simplest and most direct distance metric in the instance of dual chemical impressions. In the range of 0 - 1, Tanimoto metrics compute the element of mutual bits among chemical prints. Even though there is no common Tanimoto index cutoff (Tc) for determining whether double fragments are satisfactorily alike, most chemical searches should begin with a Tc value of 0.7. Alternatively, depending on the total Tc score distribution, statistical metrics such as a Z-score can be generated [76].

In addition, 3-dimensional chemical similarities prints have been engendered in addition to 2D prints. For structural correspondence assessment, 3D chemical connection patterns use 3D structural evidence from ligands such as molecular shape, pharmacophore points, or molecular interaction fields [75]. Even if 3D chemical match evaluations may stereotypically capture fundamental characteristics important for protein-ligand interaction, 3D arrangement systems are computationally expensive and often demand considerable optimization techniques to augment the coincided volume. Nonalignment approaches established on chemical descriptors such as GETAWAY or 3D-MoRSE descriptors, on the other hand, can be employed [78]. The 3D chemical descriptor can capture 3D ligand properties from 2D data, potentially reducing computing time. To prove 3D structural similarity, however, extensive post-validation may be required [77].

4.2. Future Recommendation: Encouraging the Integration of Artificial Intelligence and Biotechnology in Enhanced Drug Discovery

In the era of big data, the integration of artificial intelligence (AI) with biotechnology in drug discovery holds great promise [79]. By harnessing AI, hidden or meaningful patterns and relationships within complex biological systems can be discovered [80]. This will facilitate the analysis of genomic and proteomic data, enabling the identification of new therapeutic targets and the design of more effective drugs [81]. Through AI-driven predictive modeling, machine learning (ML) algorithms can be leveraged to analyze existing data on drug-target interactions, chemical structures, and biological activities. AI algorithms can also be utilized in two key areas: natural language processing (NLP) and virtual screening. In the context of NLP, AI algorithms can process and extract information from vast databases [82]. Additionally, AI algorithms can be employed in virtual

screening to screen large databases of compounds [83]. This can help identify potential compounds that exhibit a high affinity for specific therapeutic targets. These analyses will help optimize drug design and the prediction of safe and therapeutically efficacious compounds. Embracing AI in biotechnology represents a transformative approach that accelerates the discovery of innovative therapeutic agents, providing researchers with powerful tools for precise and personalized treatment options.

5. Conclusion

Biotechnological models are a potent approach to drug discovery. Researchers are now using novel biotechnology models to discover new drugs for diseases. The discovery of new drugs involves the discovery of a protein that will improve and enhance treatment to better human lives. Some of the new drugs developed using this approach have proven to be effective and efficient in the treatment of some illnesses. The success of these drugs is a result of the novel technologies involved in their production. Thus, this novel technology and development will enable clinicians to administer various classes of drugs to attack the same illness. This review indicates that drug discovery in recent days is almost impossible without good modeling in biotechnology. Again, the integration of AI with biotechnology in drug discovery holds great promise. Therefore, biotechnological models for drug discovery and AI techniques should be encouraged and adopted by researchers and the drug manufacturing industries. Hence, the impact of biotechnological models in enhanced drug discovery cannot be overemphasized.

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Conflicts of Interest

The authors declare no conflicts of interest.

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