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Novel Drug Design

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Abstract: *One of the key forces influencing the advancement of the pharmaceutical, biotech, and pharmacology fields is the drug industry. Drug discovery is the method used to find and create new medications. The goal of the method is to locate a substance that can be used therapeutically to prevent and treat disease. The selection of candidates, synthesis, characterisation, screening, and therapeutic efficacy assays are all steps in the drug discovery process. A molecule will start the medication development process before clinical trials once it has proven useful in these testing. A new drug's development is a time-consuming and expensive process, and despite hopeful discoveries and multibillion-dollar investments, the industry is currently experiencing a crisis. Currently, only 400 different pharmacological targets are successfully targeted by all available therapies. According to estimates, Finding a therapeutically effective molecule for the treatment and cure of disease is the goal of drug discovery. The selection of candidates, synthesis, characterisation, validation, optimization, screening, and tests for therapeutic efficacy are all parts of this process. A molecule will start the medication development process prior to clinical trials once it has demonstrated its importance in these studies. A new drug must go through a number of stages of development in order to be produced that is both safe and efficient and meets all regulatory standards. One overarching theme of our article is that the procedure is sufficiently drawn out, expensive, and complex that numerous biological targets must be taken into account for every new drug that is eventually approved for clinical use. Additionally, new research tools may be required to examine each target.. From the time of discovery until the treatment is licenced, it takes roughly 12 to 15 years and costs about US $1 billion. A million molecules are typically tested, but only one is examined in advanced clinical trials and ultimately made available to patients. An overview of the procedures for discovering and developing novel drugs is given in this article.*

Keywords: Drug

I. INTRODUCTION

Drug design is a growing, integrated field that heralds the arrival of "tailored drugs." It entails the investigation of how biologically active substances interact with one another in terms of their molecular structure or other physico-chemical characteristics. It investigates the mechanisms by which a drug exerts its effects, how it interacts with the protoplasm to produce a specific pharmacological action or response, and how the organism modifies or detoxifies the drug before it is metabolised or eliminated.

The location, method, and strength of a drug's activity are largely determined by how It is disposed in each biosystem. In terms of drug design, the biological activity might be "positive" or "negative," as in toxicology. Therefore, either complete lead innovation or lead optimization is required in drug design. These ideas serve as the cornerstones on which the structure of drug design is constructed.

That drug is most frequently an organic small molecule that affects a biomolecule's ability to function, like a protein, either by activating it or by inhibiting it. This action benefits the patient's treatment. Drug design is essentially the process of creating tiny molecules that are complementary in form and charge to the biomolecular target they interact with and will attach to. Computer modelling methods are commonly but not always used in drug design. Computer-aided drug design is a common term used to describe this kind of modelling. Finally, drug design that is based on an understanding of the biomolecular target's three-dimensional structure is referred to as structure-based drug design. [1]

II. APPROACHES FOR DRUG DESIGNING

A few of the different methods utilised in drug design are listed here.

1. Random bioassay technique screening of artificial chemicals and natural items.

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2. The creation of novel compounds based on the lead skeleton, a naturally occurring material with biological activity that comes from both plants and animals.
3. Application of the bioisosteric principle, followed by the creation of lead structural analogues with increasing biological activity.

2.1 Drug Target

A critical molecule participating in a certain metabolic or signallingpathway that is linked to a particular disease condition or pathology, or to the infectivity or survival of a microbial pathogen, is known as a biomolecular target (most frequently a protein or a nucleic acid). Potential pharmacological targets must, by definition, be capable of treating or preventing disease. Small compounds may occasionally be made to either boost or inhibit the target function in a particular disease-modifying pathway.

Small compounds that are complementary to the target's binding site will be created, such as receptor agonists, antagonists, inverse agonists, or modulators; enzyme activators or inhibitors; or ion channel openers or blockers. Since medication interactions with off-target molecules may result in negative side effects, small molecules (drugs) can be created so as not to affect any other significant "off-target" molecules (commonly referred to as antitargets). Closely related targets discovered by sequence homology have the highest likelihood of cross reactivity and, thus, the biggest side effect potential because of similarity in binding sites. Drugs are typically organic small molecules made by chemical synthesis, however biopolymer-based medications (also called biopharmaceuticals) made through biological processes are more widespread. Additionally, therapeutic uses for mRNA-based gene silencing technologies are possible. [2]

A. Targets: Membrane Proteins

A biological pathway's contribution to the pathophysiology of a disease determines which targets make good drug targets. A target is "druggable" if its function and structural details are known.

Membrane proteins that include transporters, ion channels, and receptors

Are important controllers of cellular activity.

Up to two thirds of known pharmacological molecules are composed of membrane proteins.

Targets that show they can be "druggable"

B. Targets: DNA

Important molecular targets for cancer, viral, and microbial treatment include DNA, mRNA, and rRNA.

Drugs that bind to these targets prevent mRNA from being translated into proteins, DNA replication, and mRNA transcription.

How structure-based methods have been used to study the rational mind

Binding substances for DNA grooves that can identify a particular nucleotide.

How this creates a chance for the creation of gene-specific Agents that prevent transcription.

C. Targets: RNA

DNA-binding compounds that prevent certain genes from being transcribed; compounds that block certain mRNA to prevent certain genes from being expressed; at the translational level.

Example: The application of siRNAs, or tiny inhibitory RNAs, in Gene silencing after transcription.

D. Targets: Enzymes

Numerous disease processes can therefore be slowed down or stopped by modifying the activity of particular enzymes. Many cellular processes involved in disease are mediated or controlled by the specific action of enzymes.There are several instances of how certain medications manifest their By interacting with these enzymes, therapeutic effects [3]

Rational drug discovery

Contrary to conventional approaches to drug discovery (known as forward pharmacology), which start with the notion that modulating a particular biological target might be useful for therapeutic purposes, rational drug design (also known

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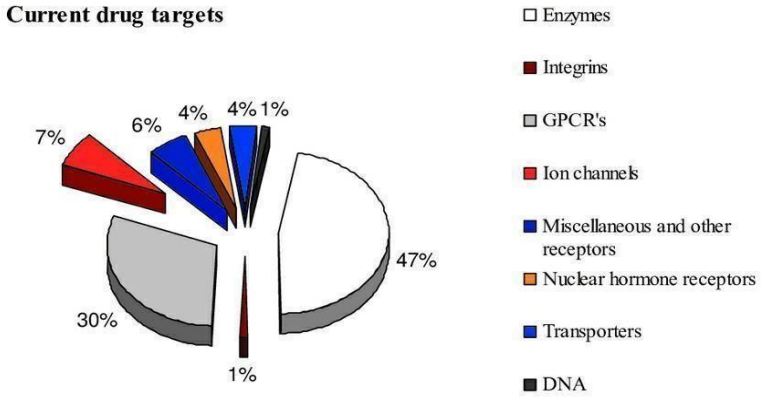
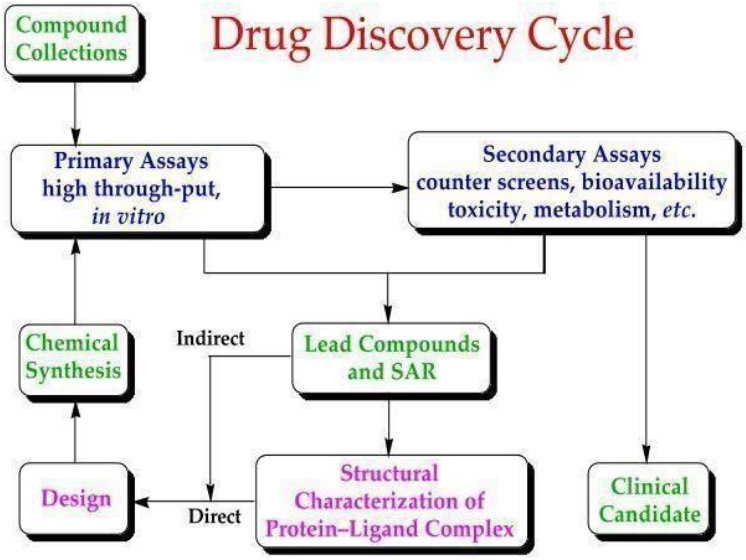
as reverse pharmacology) starts with a hypothesis that modulation of a particular biological target may have therapeutic value. Two key pieces of knowledge are necessary in order to choose a biomolecule as a therapeutic target. The first is proof that the target can be modulated to treat disease. This information could, for instance, come from disease linkage studies that demonstrate a connection between specific disease states and mutations in the biological target. The target is "druggable," which is the second factor. This implies that it has the ability to bind to a tiny molecule and that the small molecule has the ability to influence its activity.



Once an appropriate target has been found, it is typically synthesised, purified, and cloned. The screening test is then created using the purified protein. The target's three-dimensional structure can also be discovered.



Screening libraries of prospective therapeutic compounds is the first step in the search for small molecules that bind to the target. A "wet screen"—the screening assay—can be used to accomplish this. Additionally, a virtual screen of potential medications can be carried out provided the target's structural information is available. The ideal candidate drug molecules would have "druglike" qualities, such as appropriate chemical and metabolic stability, low adverse effects, and oral bioavailability. There are several ways to gauge druglikeness, including Lipinski's Rule of Five and a variety of scoring techniques like lipophilic efficiency. In the scientific literature, a number of techniques for forecasting drug metabolism have also been put forth. Multi-objective optimization approaches are occasionally used due to the numerous drug attributes that must be simultaneously addressed during the design process. Finally, drug design is still heavily dependent on serendipity and bounded rationality due to the shortcomings in the current approaches for activity prediction. [4]

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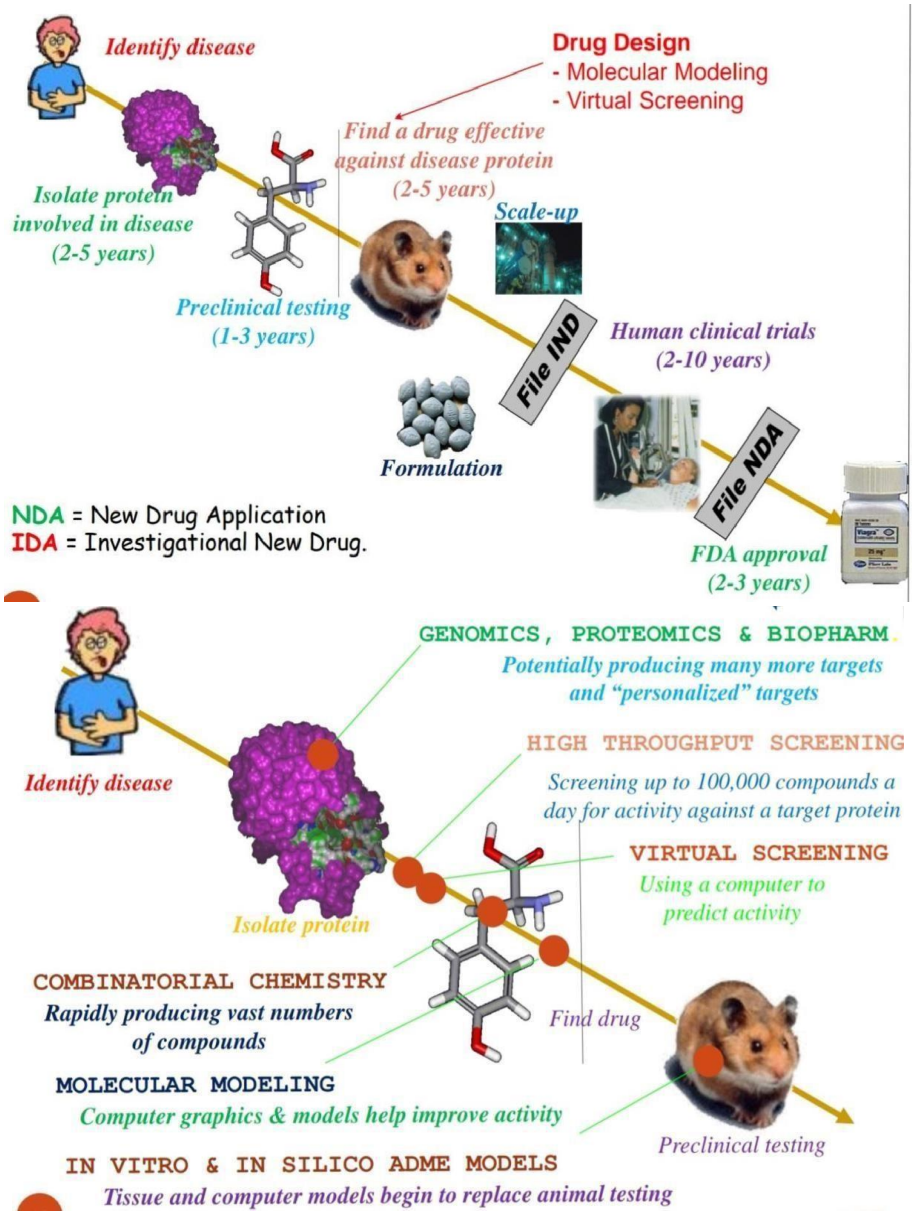
III. DRUG DISCOVERY AND DEVELOPMENT



3.1 Technology is Impact on these Process

A. Combinatoral Chemistry

Combinatorial chemistry is the systematic, repetitive, and covalent linking of multiple "building blocks" to produce a huge collection of structurally diverse molecules, referred to as a chemical library. Once ready, the chemical library's constituents can all be simultaneously checked for potential interactions with relevant biological targets. After that, positive substances can be found directly (in position-addressable libraries) or through decoding (using genetic or chemical means).

With Geysen's multi-pin technology and Houghten's tea-bag technology to simultaneously synthesis hundreds of thousands of peptides on solid support, the idea of combinatorial chemistry was created in the middle of the 1980s. One-bead, one-compound (OBOC) combinatorial peptide libraries were first developed by Lam et al. in 1991, while solution-phase mixtures of combinatorial peptide libraries were characterised by Houghten et al. Bunin and Ellman published the first instance of a tiny molecule in 1992. [5]

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B. Molecular Modeling

Today's science is increasingly dependent on computer experiments. High-performance computer has made it possible to conduct virtual experiments in silico as a tool for extrapolating between laboratory data and theory. In order to describe the role of computational simulations in enhancing experimental research when direct measurements are not possible, Schulten coined the phrase "computational microscope." He thought that computational biophysics had advanced to the point that it now provides a realistic perspective of intracellular components, frequently at a resolution not possible with lab equipment, reaching atomic or even electronic levels.

In 1964, Feynman made a foresightful observation: "Certainly no subject or field is making more progress on so many fronts at the present time than biology, and if we were to name the most powerful assumption of all, which leads one on and on in an attempt to understand life, it is that everything that living things do can be explained in terms of the jiggling and wiggling of atoms." An essential computational tool for comprehending the physical underpinnings of the structure, the dynamic evolution of the system, and the function of biological macromolecules is molecular dynamics (MD). [6]

IV. IN VITRO AND IN VIVO SILICO ADME MODELS

The subject of ADME prediction is quite difficult since many of the characteristics we attempt to predict are the outcome of many physiological processes. The amount of compounds that must be synthesised to achieve the desired biochemical/physico-chemical profile is minimised in this review by taking into account how in-silico predictions of ADME processes can be utilised to help bias medicinal chemistry into more optimal parts of property space. Although such models are not realistic enough to replace in-vivo or in-vitro approaches, they can nevertheless be used to understand the underlying physico-chemical relationships of the various ADME features and provide ideas for how to improve them. There have been numerous reports in the literature of global in-silico ADME models that were produced using sizable, varied datasets. In this article, we explore a few examples from each unique class and talk about how useful each one is for finding new drugs. To highlight the current state of the art, we restrict our discussion of each ADME parameter to the most recent, most accurate, or most insightful cases in the literature. The various models that are available for each parameter (such as simple rules, physico-chemical, and 3D based QSAR predictions), their general correctness, and the underlying SAR are all briefly summarised in each case. We also go through the models' usefulness in terms of the discovery research's lead generating and optimization phases. (7)

4.1 Computer-Aided Drug Design

Predicting whether and how strongly a given chemical will attach to a target is the primary objective of drug design. The most popular method for determining the intensity of the intermolecular interaction between the small molecule and its biological target is molecular mechanics or molecular dynamics. These techniques are also utilised to model potential conformational changes in the target that might take place when the small molecule binds to it as well as to forecast the conformation of the small molecule. Affinity Density functional theory, ab initio quantum chemistry, or semi-empirical methods are frequently used to provide optimised parameters for the molecular mechanics calculations as well as an estimation of the electronic properties of the drug candidate (electrostatic potential, polarizability, etc.) that will affect binding affinity. The binding affinity can also be semi-quantitatively predicted using Molecular Mechanics methods. Additionally, estimations of binding affinity may be provided using a knowledge-based scoring function. These techniques produce prediction binding affinity equations by fitting experimental affinities to computationally computed interaction energies between the small molecule and the target using linear regression, machine learning, neural nets, or other statistical techniques.A single chemical might theoretically be synthesised, saving a tonne of time and money, if the computational technique can predict affinity before a molecule is created. The truth is that current computational techniques are inefficient and can only produce estimates of affinity that are, at best, qualitatively accurate. In reality, finding the best drug still requires a number of design, synthesis, and testing iterations. By requiring fewer iterations, computational approaches have sped up discovery and frequently produced unique structures.

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Computer-aided drug design can be applied at any of the following stages of drug discovery:

1. Hit recognition through virtual screening (structure- or ligand-based design)
2. Hit-to-lead affinity and selectivity optimization (structure-based design, QSAR, etc.) 3)

Lead optimization for additional drug attributes while preserving affinity [8]

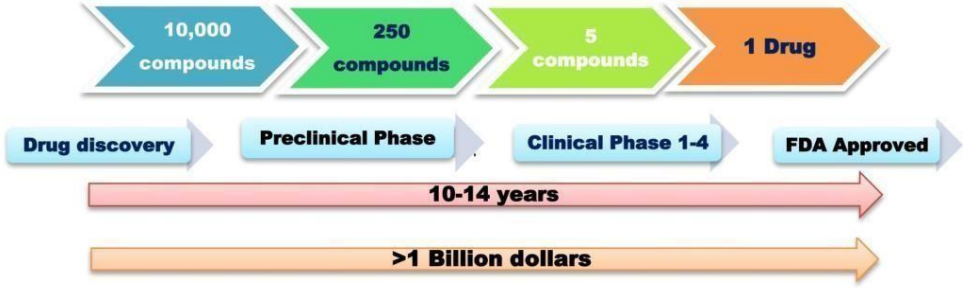

Figure 1: Traditional process of drug discovery and development.

4.2 Types

Highlighting both ligand-based (indirect) and structure-based (direct) drug design methodologies in the drug discovery cycle

The two main categories of drug design are as follows. Both are known as structure-based drug design and ligand-based drug design, respectively.

A. Structure-Based Drug Design

When using SBDD, the target protein's structure is known as well as the interactions or bioaffinities of every investigated chemical. Calculate the results of the docking process in order to create a new drug compound with improved protein interaction. [9]

Overview of the process involved in SBDD

Before the Optimized lead enters clinical trials, SBDD goes through several cycles. The target protein is isolated, purified, and its structure is determined using one of three key techniques, such as X-ray crystallography, homology modelling, or NMR, in the first cycle. Compounds that have been chosen through virtual screening of several databases are inserted into the protein's active site. Based on their steric, hydrophobic, and electrostatic interactions with the target protein's active site, these compounds are graded and ranked. Biochemical assays are used to evaluate top-ranked compounds. The second cycle includes the determination of the protein's structure in association with the first cycle's most promising lead, the one with the least amount of in vitro micro-molar inhibition, and it reveals the spots of the compound that can be improved for additional increases in potency. After a number of further cycles, such as the production of lead and further lead optimization through complex protein structures including lead molecule, the optimised compounds typically exhibit a noticeable increase in the binding affinity and target specificity.

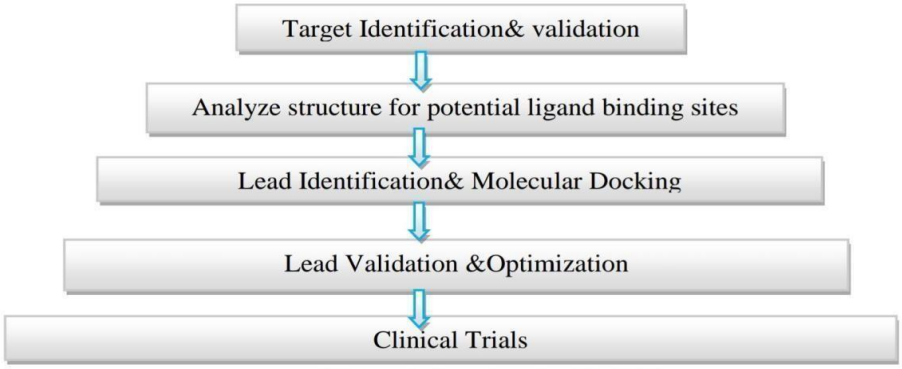

Figure 5: Steps involved in SBDD.

[10]

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B. Ligand-Based Drug Design

In LBDD, the target protein's three-dimensional structure is unknown, but it is known which ligands bind to the desired Target site. These ligands can be used to create molecules or pharmacophore models that have all the structural characteristics needed to bind to a target active site.

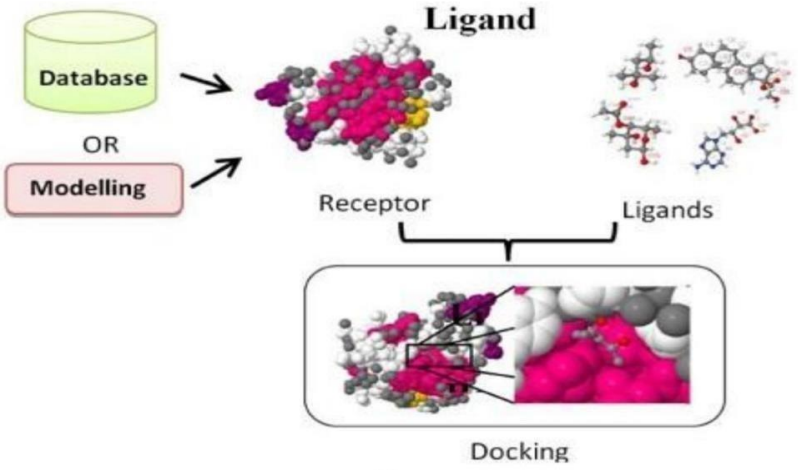

Figure 6: Outline of process involved in LBDD [7].

Pharmacophore-based approaches and quantitative-structure activity connections are the most common ligand-based methodologies (QSARs). In LBDD, it is presummated that substances with structural similarities also share the same biological effects and interactions with the target protein [11].

Virtual screening

Nowadays, using knowledge of the protein target or known active ligands, virtual screening has been used as a very practical approach to identify the best bioactive compounds. Virtual screening is today regarded as a revolutionary substitute for high-throughput screening, particularly in terms of cost efficiency and the likelihood of discovering the most suitable unique hit by filtering the vast libraries of compounds. [12] Virtual screening often comes in two flavours. Structure-based virtual screening (SBVS) and ligand-based virtual screening (LBVS) are two methods. The former relies on the target protein's active site structure, while the latter relies on an estimate of the similarity between known active and compound compounds from databases.

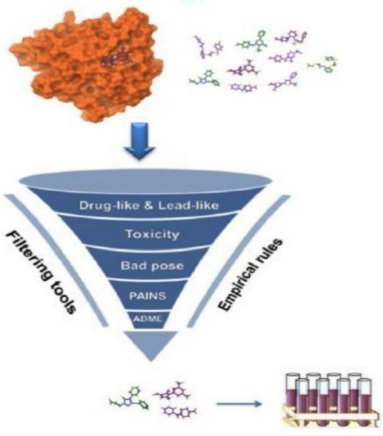

Figure 7: Overview of Virtual screening process [10].

Molecular Docking

Molecular docking is an in-silico technique that forecasts where tiny molecules or ligands will bind to their target proteins (receptor). It is primarily used to determine the most advantageous binding modes and bio-affinities of ligands with their receptors. At the moment, it is widely used in virtual screening to improve lead compounds Molecular

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docking technology primarily consists of three interconnected goals, such as virtual screening, bio affinity, and binding pose prediction. The search algorithm and scoring algorithms used in the molecular docking approach are the fundamental Tools for creating and assessing ligand conformations. [13]

Current Rational Design Approaches, Including Docking

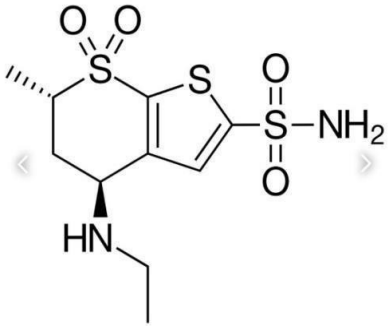
It is well known that molecular docking has applications in the drug discovery process [3, 5, 7, 18, 47, 49, 50, 63]. However, docking has inherent restrictions that reduce the accuracy of its predictions; the most significant of these were covered in the preceding section. Docking has traditionally been employed as a standalone method for drug design, but it is increasingly frequently incorporated into workflows that also use ligand-based, structure-based, and AI approaches. This contributes to explaining some of the most important drawbacks of this structure-based approach.

Examples

Utilizing three-dimensional data about biomolecules from methods like X-ray crystallography and NMR spectroscopy is one specific example of rational drug design. When a target protein is linked to a powerful ligand in a high-resolution structure, computer aided drug creation, in particular, becomes much more manageable. Structure-based drug design is another name for this method of drug discovery. The 1995 approval of the carbonic anhydrase inhibitor dorzolamide serves as the first concrete illustration of how structure based drug design might result in a successful medicine. (14/15)

Example: Dorzolamide

A drug called dorzolamide, also known by the brand name Trusopt, is used to treat high pressure inside the eye, including glaucoma instances. As an eye drop, it is employed. The effects start to take effect after three hours and remain for at least eight hours. It is additionally offered in combination with dorzolamide. [16]



Additional Examples Include:

Many of the atypical antipsychotics Selective COX-2 inhibitor NSAIDs Cimetidine, the original H2-receptor antagonist from which other members of the class were generated

A peptide HIV entrance inhibitor called enfuvirtideZopiclone and zolpidem are non-benzodiazepines.

HIV integrase inhibitor raltegravir

Zanamivir is an antiviral medication of the SSRI (selective serotonin reuptake inhibitor) class of antidepressants.

Case Studies

Acetylcholine Receptor Agonists.

A substance known as a nicotinic agonist imitates the effects of acetylcholine (Ach) on nicotinic acetylcholine receptors (nAChRs). Because of its affinity for nicotine, the nAChR is thus termed.

Examples include nicotine (by definition), choline, lobeline, varenicline, acetylcholine (the endogenous agonist of nAChRs), epibatidine, and cytisine.

Angiotensin Receptor Antagonists

Angiotensin receptor blockers (ARBs), also known as sartans or angiotensin (AT1) receptor antagonists, are a class of antihypertensive medications that lower blood pressure by blocking the actions of the hormone angiotensin II (Ang II) in the body. Their structure is comparable to that of Ang II, and they act as inhibitors when they bind to Ang II receptors, such as [T24 from Rhys Healthcare].

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ARBs are frequently prescribed medications in the therapeutic context today, with their primary uses being the treatment of diabetic nephropathy, chronic heart failure, secondary stroke prevention, and mild to moderate hypertension. The identification of the various subtypes of Ang II receptors through the discovery and development of ARBs is an illustrative example of contemporary rational drug design and how design can be utilised to learn more about physiological systems. (17)

Proton pump inhibitors

Gastric hydrogen potassium ATPase (H+/K+ ATPase) is blocked by proton pump inhibitors (PPIs), which also prevent the secretion of gastric acid. Acid-related disorders such gastroesophageal reflux disease (GERD) and peptic ulcer disease are now commonly treated with these medications. PPIs are being used to reduce acid efflux from cancer cells and chemotherapy treatment resistance because they can bind to other forms of proton pumps, such as those found in cancer cells.

Non-nucleoside reverse transcriptase inhibitor

Antiretroviral medications known as non-nucleoside reverse- transcriptase inhibitors (NNRTIs) are used to treat human immunodeficiency virus (HIV). Reverse transcriptase (RT), an enzyme that regulates the replication of HIV's genetic material, is inhibited by NNRTIs. RT is one of the most well-liked targets in the realm of developing antiretroviral medications. [18]

In the late 1980s, NNRTIs were first discovered and developed[2]. By the end of 2009, four NNRTIs had received regulatory approval, and a number of others were in the clinical development stage. Drug resistance emerges quickly if NNRTIs are used as monotherapy, hence combination therapy—a highly effective antiretroviral therapy—is always used when NNRTIs are used. Reverse transcriptase inhibitors for nucleosides and nucleotides The AIDS crisis in Western cultures in the 1980s sparked the discovery and development of nucleoside and nucleotide reverse-transcriptase inhibitors (NRTIs and NtRTIs). RT, an enzyme that regulates the replication of the human immunodeficiency virus' genetic material, is inhibited by NRTIs (HIV). Zidovudine was the first NRTI, and its approval by the U.S. Food and Drug Administration (FDA) in 1987 marked the beginning of HIV treatment. One NtRTI has followed six NRTI agents. The endogenous 2'-deoxy-nucleoside and nucleotide are analogues of the NRTIs and NtRTI, respectively. The inevitable result of HIV-1 being exposed to antiHIV medications for an extended period of time is drug-resistant viruses.

V. HIV PROTEASE INHIBITOR

Regulation of proteolytic enzyme activity is crucial to many important physiological processes, and disruption of the equilibrium between an enzyme and its substrates can have severe repercussions. In this regard, the identification of small-molecule ligands that can control catalytic activities, such as protease inhibitors, has significant therapeutic implications. As a result, one of the most crucial therapeutic interventions for HIV infection is the inhibition of the HIV protease, and their creation is regarded as a key achievement in structure-based drug design. They have been a crucial part of anti-retroviral therapy for HIV/AIDS since the 1990s due to their strong effectiveness against HIV.

VI. SOURCES OF DRUGS

The process of creating a new medicine is difficult, expensive, and time-consuming. A new medicine typically takes 12 years to develop before it is available in clinics, with current investment levels exceeding $1 billion USD. The identification of new chemical entities (NCEs), possessing the necessary properties of druggability and medicinal chemistry, is essentially what new drug discovery entails. These NCEs can be obtained either chemically or by isolating them from natural materials. The first success stories in discovering novel drugs came from innovations in medicinal chemistry, which prompted the demand for the creation of more chemical libraries through combinatorial chemistry. However, it has been shown that this strategy has a lower overall success rate.There are several instances of novel medications being developed from plant sources.

About 200 years ago, opium made from chopped seed pods of the pappy plant (Papaver somniferum) was found to contain morphine. As a result of the discovery of penicillin, pharmaceutical research expanded after World War II to

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include extensive testing of microbes for novel antibiotics. Penicillin, tetracycline, erythromycin, antiparasitics (e.g., avermectin), antimalarials(e.g., quinine, artemisinin), lipid-controlling medications (e.g., lovastatin and analogues), immunosuppressants for organ transplants (e.g., cyclosporine, rapamycins), and anticancer medications are just a few examples (e.g. paclitaxel, irinotecan).There are various examples of development of new drugs from the plant sources.

Morphine was isolated from opium produced from cut seed pods of the poppy plant (Papaver somniferum) approximately 200 years ago. Pharmaceutical research expanded after the second world war to include massive screening of microorganisms for new antibiotics, inspired by the discovery of penicillin. Few drugs developed from natural sources have undoubtedly revolutionized medicine, like antibiotics (e.g. penicillin, tetracycline, erythromycin), antiparasitics (e.g. avermectin), antimalarials (e.g. quinine, artemisinin), lipid control agents (e.g. lovastatin and analogs), immuno suppressants for organ transplants (e.g. cyclosporine, rapamycins), and anticancer drugs (e.g. paclitaxel, irinotecan).

More than 100 medications derived from natural products are undergoing clinical trials, while at least 100 molecules or compounds are in the preclinical development stage. [1] The majority of these compounds in the pipeline for development are derived from leads found in plants and microorganisms. The drug discovery programme is based on natural products, and its two main therapeutic areas are cancer and infections. However, many other therapeutic areas are also covered, including neuro-pharmacological, cardiovascular, gastrointestinal, inflammatory, metabolic, etc. [1] There are about 108 projects based on plants among the many programmes in various therapeutic fields. A further classification of these initiatives shows that 2 are in the pre-registration stage, 14 are in phase I, 41 are in phase II, and 46 are in preclinical stage [19].

Drug Discovery from Natural Resources:

Advantages and Disadvantages

Usage of botanical sources as starting point in the drug development program is associated with few specific advantages:

Mostly, the selection of a candidate species for investigations can be done on the basis of long-term use by humans (ethnomedicine). This approach is based on an assumption that the active com-pounds isolated from such plants are likely to be safer than those derived from plant species with no history of human use. At certain time point afterward, one may attempt upon synthesis of active molecule and reduce pressure on the resource. Drug development from Rauwolfiaserpentina, Digitalis purpurea, etc. in the past fall under this category of approach. 2] Due to the intrinsic limits of the original molecule, such procedures occasionally result inthe development of unique molecules derived from the source. For example, toxicities that were dose-limiting were found in podophyllin, which was produced from Podophyllumhexandrum. These restrictions could be greatly reduced by semi-synthesis of etoposide, which is still employed in cancer treatment today. The same thing happened with camptothecin, which inspired the creation of brand-new anticancer molecules like topotecan and irinotecan after being first isolated from Camptotheca sp. And then Mappia sp.

Starting with natural resources holds the dual promise of producing the original isolate as a candidate or the production of a semi-synthetic molecule to get beyond any drawbacks of the original molecule.

On the other side, creating drugs from natural resources has a few drawbacks as well:

The development of new drugs and their eventual commercialization would frequently put great pressure on available resources and could have a negative impact on the environment. While it is possible to completely synthesise an active molecule, not all molecules are receptive to this process. As a result, there would still be some reliance on the lead resource. Since a complete synthesis is not achievable, anticancer compounds like etoposide, paclitaxel, docetaxel, topotecan, and irinotecan continue to rely on extremely susceptible plant resources for the starting material. However, it is predicted that by the end of this century, 25,000 plant species would no longer exist.

The protection of Intellectual property rights for natural products has been deteriorating over time. The leads are typically based on some connection to conventional usage. The procedure of gaining access to the primary resource, benefit sharing throughout the commercial phase, etc. got extremely complicated in many countries as more nations

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joined the Convention on Biological Diversity (CBD). Regardless of the issues that led to these processes, they have a tendency to slow down the discovery process at different stages. (20)

Selection of Candidate Plant Species for Screening

According to estimates, there are roughly 250,000 species of higher plants, which include angiosperms and gymnosperms. Only 6% of them have reportedly undergone biological activity screening, while 15% have undergone phytochemical activity screening. The initial listing of the candidate species for biological activity screening is a significant effort in and of itself. The following strategies have been employed thus far by researchers for this objective, according to Fabricant and Farnsworth.

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