

Is Target-Based Drug Discovery Efficient? Discovery and “Off-Target” Mechanisms of All Drugs

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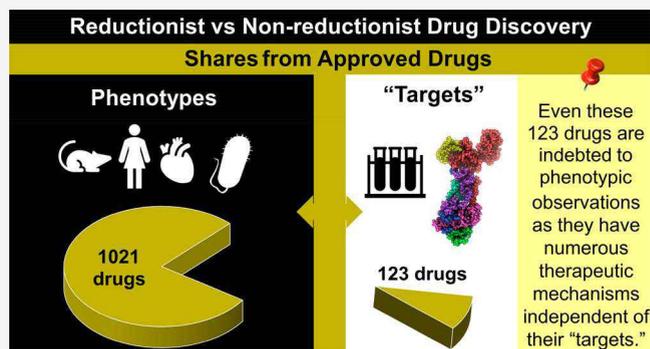


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ABSTRACT: Target-based drug discovery is the dominant paradigm of drug discovery; however, a comprehensive evaluation of its real-world efficiency is lacking. Here, a manual systematic review of about 32000 articles and patents dating back to 150 years ago demonstrates its apparent inefficiency. Analyzing the origins of all approved drugs reveals that, despite several decades of dominance, only 9.4% of small-molecule drugs have been discovered through “target-based” assays. Moreover, the therapeutic effects of even this minimal share cannot be solely attributed and reduced to their purported targets, as they depend on numerous off-target mechanisms unconsciously incorporated by phenotypic observations. The data suggest that reductionist target-based drug discovery may be a cause of the productivity crisis in drug discovery. An evidence-based approach to enhance efficiency seems to be prioritizing, in selecting and optimizing molecules, higher-level phenotypic observations that are closer to the sought-after therapeutic effects using tools like artificial intelligence and machine learning.



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■ SIGNIFICANCE

- This is the first systematic and comprehensive assessment of the real-world efficiency of target-based drug discovery.
- Merely 9.4% of approved small-molecule drugs have been discovered by this approach.
- Even these supposedly target-based drugs depend on numerous off-target mechanisms for their therapeutic effects.
- Reductionist target-based drug discovery has thus far been inefficient and maybe a cause of the productivity crisis.
- Approaches that prioritize higher-level observations are potentially more efficient based on both observational and theoretical evidence.

1. INTRODUCTION

1.1. Contemporary Drug Discovery Has Some Serious Problems. Drug discovery lies at an integral intersection where innovations and developments of diverse scientific fields and industries conjoin to translate into the ultimate purpose of improving health. However, the efficiency of discovering new drugs is so low that it would probably astonish researchers and practitioners in other domains.^{1,2} The ratio of the drug candidates that gain approval to those that enter clinical studies is about 13% but can be as low as 0.4% for more complex CNS disorders and cancers.^{3,4} Estimated research costs of introducing a new therapeutic to the market have soared up to 6.4 billion

dollars with a mean of 1.3 billion dollars.⁵ The translation of basic scientific research to clinical real-world impact has been denigrated as the “valley of death”.⁶ Such challenges have compelled many pharmaceutical companies, including Pfizer, Merck, GSK, AstraZeneca, and Amgen, to withdraw from neuroscience research at some point,⁷ although its related disorders are a primary cause of disability worldwide,^{8,9} impose immense societal costs,¹⁰ and many of them have no cure. Moreover, many approved drugs that have been considered to be successful have been the subject of criticism by experts and available evidence. A considerable number are suggested to exert minimal effects,^{11–18} offering almost no benefit compared to previously approved drugs,^{18–22} or have been approved only based on surrogate end points^{15,16,23–28} or flawed and limited evidence.^{15–18,22,26,29–38} Compared to placebo, many approved drugs probably offer at best only marginal benefit and may even lower a patient’s quality of life and survival.^{17,22–24,39–44}

Adding to the oddity of this low productivity is the observation that productivity has declined significantly from several decades ago despite significant technological advance-

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ments that have been developed and deployed in the most recent period. From 1950 to 2010, the number of drug approvals per billion dollars of research expenditure has halved every 9 years, a trend referred to as Eroom's Law.^{45,46} Although, as was predicted earlier,³⁴ it appears that the trend has been reversing in recent years,^{47,48} diagnosing the major causes of the low productivity of drug discovery and development is of paramount importance since it undermines the translation of all the progress we have made in advancing technology and enhancing biomedical knowledge into the ultimate goal of improving health.

1.2. Where Does the Problem Lie? Several factors have been proposed as causes of the productivity decline: exhaustion of "the more accessible and easily discoverable drugs" (the low-hanging fruit^{1,46,49}), the cumulative pressure to surpass previous blockbuster drugs (the "better than the Beatles" problem),¹ the decreased tolerance for risk by drug regulatory agencies (the "cautious regulator" problem), the increase in human and technological investments (the "throw money at it" tendency), and the overestimation of the positive impacts of the scientific and technological advances, such as molecular biology and high-throughput screening, which has led to hastily abandoning previous methodologies (the "basic research-brute force" bias⁴⁶). Many have also highlighted the reductionist tendency of the dominant methodology of drug discovery: target-based drug discovery.^{45,46,49–61} Interestingly, this methodology was born at roughly the same time as the onset of this decline and has now dominated drug discovery approaches for several decades.⁶⁰ Most target-based drug discovery investigations are reductionist in nature since they are based on reducing the therapeutic effects that emerge from interacting with complex networks of cellular and extracellular components and their intricate feedback loops to the modulation of either a single or few proteins.⁶² Notwithstanding, it is important to acknowledge that there have been attempts to move away from this extreme reductionism in target-based drug discovery by adopting polypharmacological approaches. Let us explore the evolution of drug discovery in order to better assess the criticisms against the focus on reductionism.

1.3. The Evolution of Drug Discovery. Drug discovery started when our ancestors began to recognize patterns between the substances they came across and their effects on the phenotypes they observed. For example, *Piptoporus betulinus* is a fungus whose several constituent substances have now been observed to be potent immunomodulator and antimicrobial agents.^{63–67} Evidence, including an infected mummified human carrying this fungus, suggests its potential use in treating infectious diseases like trichuriasis around 5300 years ago^{68–71} (also see refs 72–74). Further evidence indicates that the possible intentional use of effective drugs stretches back even further to 60000 years ago.^{75–81} Even now, some of the most crucial drugs used in the clinic can be traced back to the therapeutics our ancestors discovered centuries ago, including morphine analogs (21 drugs), aspirin, digoxin, and many others (the historically used category of Figure 4 and Supporting Information 1).

After thousands of years and the cumulative growth of our knowledge and capabilities,⁷⁸ some pioneers of modern biomedical sciences, like François Magendie⁸² and Claude Bernard,⁸³ began to unravel how these substances exerted their effects on phenotypes, i.e., their mechanism of action. The continuation of such investigations by trailblazing scientists like Rudolf Buchheim and Oswald Schmiedeberg^{84,85} blossomed

into the scientific discipline of pharmacology⁸⁶ (Figure 1). Afterward, in the 20th century, several highly prolific scientists

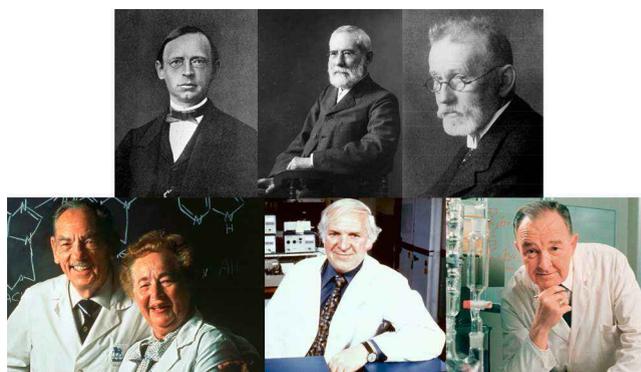


Figure 1. Some of the most important pioneers of pharmacology and rational drug discovery. Top row, from left to right: Rudolf Buchheim, Oswald Schmiedeberg, and Paul Ehrlich. Bottom row, from left to right: George Hitchings, Gertrude Elion, James Black, and Paul Janssen. The three images in the top row plus the photo of James Black in the bottom row are from Wikimedia Commons and are used under a CC BY 4.0 license. The images of George Hitchings and Gertrude Elion are from achievement.org/achiever/gertrude-elion. The image of Paul Janssen is from the Janssen Image Library, Janssen Global Services, LLC, used by permission.

not only significantly contributed to the development of the science of pharmacology⁸⁷ but also applied the knowledge of how molecules exert their effects on phenotypes to designing better drugs (Figure 1). Among these are Paul Ehrlich, who devised concepts like the magic bullet, chemotherapy, and chemoreceptor⁸⁸ and discovered salvarsan and neosalvarsan,⁸⁹ George Hitchings and Gertrude Elion, who used knowledge on metabolism pathways to discover mercaptopurine,⁹⁰ thioguanine,⁹¹ azathioprine,⁹¹ pyrimethamine,⁹² allopurinol,⁹¹ cotrimoxazole,⁹³ acyclovir,⁹⁴ and nelarabine,⁹⁵ James Black, who applied receptor theory⁹⁶ to discover the first-in-class medicines propranolol and cimetidine,⁹⁷ and Paul Janssen who discovered diphenoxylate,⁹⁸ difenoxin,⁹⁹ haloperidol,¹⁰⁰ droperidol,¹⁰⁰ fentanyl,¹⁰¹ loperamide,¹⁰² etomidate,¹⁰³ pimozide, sufentanil, alfentanil, mebendazole, miconazole, terconazole, and ketocanazole.⁹⁹

This approach which attempted to use the available scientific knowledge, including pharmacological, pathological, and physiological aspects, to guide and focus the empirical screening of random substances and correlate with observations on their effects on phenotypes came to be known as *rational drug discovery*. Target-based drug discovery can be considered as a subsequent iteration of rational drug discovery that was born contemporaneously with the revolution of molecular biology and the development of technologies like X-ray crystallography, nuclear magnetic resonance imaging, computational chemistry, biotechnology, DNA sequencing, combinatorial chemistry, and high-throughput screening, that enabled the ever-finer dissection of biological processes to the point of the binding of molecules to a single protein.

Currently, target-based drug discovery heavily dominates drug discovery approaches in both academia and the pharmaceutical industry.^{104–115} Drug candidates for complex disorders like OCD, depression, and Alzheimer's disease are being screened, selected, and optimized primarily based on their binding affinity for a single protein that is hypothesized to be

fundamentally related to the development of the disease.¹¹⁶ Observing the therapeutic effects of molecules is primarily used for terminal filtering.⁶²

1.4. Reductionism and Antireductionism. Reductionism has been a dominant attitude in sciences since the Scientific Revolution and the Industrial Revolution.¹¹⁷ This approach gained further momentum in the later years of the 20th century and the initial years of this century¹¹⁸ because of the technological progress that facilitated it.

In parallel with the dominance of reductionism over the past 70 years, antireductionism, which was even advocated by Aristotle,¹¹⁹ has been spurred in diverse fields.^{120–131} This has been driven by the disillusionment resulting from the failures of reductionism in unraveling complexity, such as the unfulfilled promises of the Human Genome Project.^{118,130,132} Complex systems science has flourished^{133–135} with dedicated institutions specializing in it, including the Santa Fe Institute,¹³⁶ the New England Complex Systems Institute, and Complexity Science Hub Vienna.¹³⁷ Recognition of the importance of complexity science was also reflected by awarding the 2021 Nobel Prize in Physics “for groundbreaking contributions to our understanding of complex systems”.¹³⁸ Systems biology has also bloomed trying to pay more attention to the comprehensiveness of the components being studied and their interactions using computational and mathematical tools.^{139,140} In drug discovery, antireductionism has grown in several approaches including systems pharmacology, network pharmacology,^{141,142} and polypharmacology¹⁴³ and was given additional momentum after Swinney and Anthony showed that, despite the disproportionate dominance of reductionist target-based drug discovery, most of the first-in-class drugs approved between 1999 and 2008 were discovered by phenotypic approaches.⁵⁴ This could have inaugurated a rejuvenation of phenotypic drug discovery; alas, it is still being sidelined by a focus on target-based drug discovery^{144,145} and is viewed merely as a complementary approach for discovering novel mechanisms of action and first-in-class drugs.^{54,146}

1.5. Hypothesis: Target-Based Drug Discovery Is Inefficient. What is the relationship between the affinity of a molecule for a specific protein and its therapeutic effects on, for example, depressive disorders?¹⁴⁷ Can the tight binding of a molecule to a protein free the human body from such complex disorders? This question is the fundamental core of the criticisms that have been raised against the reductionism associated with target-based drug discovery. Besides the fact that plenty of these hypothesized “targets” may not even be relevant to the phenotypes they are attributed to,^{116,148} most disorders and desired therapeutic effects seem to be too complex to be reducible to modulating the behavior of single proteins, except maybe monogenetic Mendelian disorders.⁶⁰ Moreover, it is established that our knowledge of the underlying pathology of many disorders is dwarfed by our ignorance about them.¹⁴⁹ This knowledge gap further hampers the feasibility of pinpointing a single protein to target in an attempt to counteract a specific pathology.

Despite the numerous criticisms that have been advanced against target-based drug discovery,^{45,46,49–61} there is an absence of a comprehensive and systematic study that would be able to provide a relatively firm answer to the question: *Is target-based drug discovery an efficient, optimal, and rational approach?* Here, I attempt to provide an answer by examining the methodology of target-based drug discovery from several perspectives:

- How many of the currently approved drugs are indebted to reductionist target-based drug discovery in contrast to less-reductionist approaches?
- Even for the drugs discovered based on reductionist target-based drug discovery, can the therapeutic effects be reduced to the binding and modulation of the select proteins?
- How does the binding of drugs to “therapeutic targets” with high affinity correlate with their therapeutic effects?
- Does the methodology of target-based drug discovery stand on a sound theoretical foundation based on the available scientific knowledge?

2. EVIDENCE ON THE EFFICIENCY OF TARGET-BASED DRUG DISCOVERY

2.1. Contribution of Observing Therapeutic Effects vs Effects on Proteins to the Discovery of Approved Drugs.

2.1.1. Rationale. I hypothesized that a fundamental cause of drug discovery’s decline is the transition to the reductionist methodology of target-based drug discovery that selects and optimizes structures primarily based on their binding to a few hypothetically relevant “target” proteins and usually uses *in vivo* and human data only as terminal filters. On the other hand, traditional drug discovery inevitably was a more empirical approach primarily relying on selecting and optimizing molecules based on their therapeutic effects on humans and other organisms like nonhuman animals (hereinafter referred to as animals), fungi, and bacteria because of the absence of the tools needed for reductionism that would enable directly assessing the effects of drugs at the lower levels associated with individual proteins.

While the aforementioned analysis conducted by Swinney and Anthony was seminal in revitalizing phenotypic drug discovery, the period they analyzed (1999–2008) was so limited that their conclusions, apart from being restricted to the suggestion that phenotypic drug discovery may be more efficient for discovering first-in-class drugs, were subsequently challenged by an analysis that had assessed a longer time frame.¹⁵⁰ Moreover, Swinney and Anthony’s analysis did not cover the golden period of traditional drug discovery at all; thus, it is not suitable for comparing the real-world contributions of traditional and target-based drug discovery. Consequently, I expanded the analysis of Swinney and Anthony to include all approved drugs and tried to increase the accuracy and objectivity of the analysis.

2.1.2. Methods. I manually (not by automated methods like natural language processing) investigated the discovery origins of all drugs approved by the US FDA by the end of 2020, the list of which I had compiled using three databases: National Center for Advancing Translational Sciences (NCATS) Inxight Drugs (drugs.ncats.io),¹⁵¹ Drugs@FDA (accessdata.fda.gov/scripts/cder/daf/index.cfm), and the Orange Book (fda.gov/drugs/drug-approvals-and-databases/approved-drug-products-therapeutic-equivalence-evaluations-orange-book). In querying Inxight Drugs, I chose “US Approved OTC” OR “US Approved Rx” for the development status, “Approved” for the highest phase, “Principal Form” for substance form, and excluded treatment modalities of “Secondary,” “Inactive Ingredient,” “Diagnostic.” From Drugs@FDA, I retrieved drugs with type 1 (New Molecular Entity) and type 7 (“Previously Marketed but Without an Approved NDA”) applications among “Original NDA and Original BLA Approvals” and excluded the discontinued ones. I also added the nondiscontinued drugs

taken from the Orange Book if they were not already included. All of the retrieved drugs are listed in [Supporting Information 1](#), yet I did not investigate the discovery origins of the following groups of drugs: diagnostic agents like contrast agents; nutrients, vitamins, and nutrient inorganic ions; secondary agents without therapeutic activity themselves, like mesna; antidotes; enantiopure or racemic formulations of previously approved drugs; prodrugs of previously approved drugs; excipients; drugs whose therapeutic effects depend more on the physical properties of molecules; e.g., surfactants, chelating agents, radiopharmaceuticals, photochemotherapeutics, and osmotic diuretics.

To maximize objectivity, it is important to settle upon simple and unambiguous definitions ([Table 1](#)). *Discovery origin* was

Table 1. Concepts Used for Assessing the Contribution of Observing Therapeutic Effects vs Observing Effects on Proteins to the Discovery of Approved Drugs

concept	definition
Therapeutic class	A group of analogs along with their respective lead molecules which guided their discovery
Discovery origin	The first observation that has related a therapeutic class to its therapeutic effect
Target-based	Therapeutic classes whose discovery origin was observing the effects of molecules on proteins
Phenotype-based	Therapeutic classes whose discovery origin was observing the effects of molecules on phenotypes

defined as “the first observation that has related a therapeutic class to the therapeutic effect” and *therapeutic class* was defined as “a group of analogs (chemical and/or pharmacological¹⁵²) along with their respective lead molecules which guided their discovery.”¹⁵³ Drugs whose “discovery origin was observing the effects of molecules on proteins” were assigned to *target-based* and those whose “discovery origin was observing the effects of molecules on phenotypes” were assigned to *phenotype-based*. An example of the application of these definitions can be helpful in order to better gauge the objectivity of the conclusions. Captopril is known by many as one of the early drugs discovered “rationally.” To objectively assign its discovery origin to phenotype-based or target-based, the definitions of these terms given above were followed exactly. In [Supporting Information 1](#), these quotes from the discoverers of captopril themselves have been cited: “In 1968, Dr. Y.S. Bakhle demonstrated that dog lung ACE was inhibited by a mixture of peptides from the venom of the Brazilian viper *Bothrops jararaca*. [...] This exercise was not completely in vain; it showed how rare, indeed, were specific inhibitors of ACE, it also demonstrated that these, whether designed or stumbled upon, could be readily identified using a simple guinea pig ileum test system developed by Dr. Rubin and his colleagues. Success in this simple *in vitro* test was also highly predictive of activity *in vivo*, including antihypertensive activity. [...] The key result with this prototype compound, however, came in Dr. Rubin’s guinea pig ileum test. Unlike the 2000 or so random compounds that we had previously tested, succinyl-L-proline had the properties of a specific ACE inhibitor: it inhibited contractile actions of angiotensin I and potentiated those of bradykinin, without having any effects on contractile actions of angiotensin II or those of several other smooth muscle agonists¹⁵⁴ (emphases added).” As is evident in the quote, although the discovery took place with a “target” protein in mind, the selections and “the first observation that has related a therapeutic class to the therapeutic

effect” were completely based on “observing the effects of molecules on phenotypes.”

It is worth noting that, according to the definitions provided above for therapeutic class and discovery origin, the discovery origins of all approved analog drugs are attributed to the discovery origin of their respective first-in-class drugs. While this may be subject to debate, by definition, analog and “me-too” drugs are based on the structure of their respective first-in-class drugs, and total dismissal of this would have led to an unfair comparison of the real-world contributions of target-based and phenotype-based drug discovery. Nonetheless, as is acknowledged later in the article, target-based drug discovery plays a key role in analog-based drug discovery. To identify a set of chemicals as analogs objectively, I used and cited the published literature (e.g., ref 152) and calculated feature trees as the molecular similarity measure using FTrees 6.3.¹⁵⁵

Like Swinney and Anthony,⁵⁴ I counted biopharmaceuticals as a separate group, but I also further categorized them based on whether they are endogenous-based or not. I compared the share of phenotype-based and target-based categories among all the approved drugs and those approved after 1995, the approval year of the first “target-based” drug, saquinavir. I also further categorized the phenotype-based discovery origins into these: observing nonhuman or *ex vivo* phenotypes, observing phenotypes of humans, observing phenotypic effects of endogenous molecules, historically used compounds, sagaciously observed nonhuman or *ex vivo* phenotypes, mechanism of action-informed phenotypic observations.

In investigating the discovery origins, I highly prioritized the accounts of the initial reporting discovery papers (denoted as “From the discovery paper”:) and afterward, other narrations from the discoverer(s) themselves (denoted as “From the discoverer(s)”). I tried to quote with the highest fidelity, exactly transferring styles and even incorrect spellings; except for most in-between-commas details and in-text citations (I have kept a few in case they would be informative).

In summation, in the analysis of the discovery origins, I tried to maximize objectivity, precision, and accuracy through several measures:

- (1) Analyzing all drugs, not just drugs associated with a specific period.
- (2) Entirely manual, rather than automated analysis.
- (3) Basing decisions on simple definitions of discovery origin, therapeutic class, target-based, and phenotype-based.
- (4) Referencing verbatim accounts of the original discovery papers and the discoverer(s) themselves.
- (5) In cases where (4) was infeasible, referencing the published literature for the discovery process.
- (6) Basing decisions of therapeutic classes on the published literature and FTrees.
- (7) Detailed documentation of the paths followed to identify and assign each discovery origin.

2.1.3. Results and Discussion. Out of the 1310 US FDA-approved drugs, 69 were endogenous-based biopharmaceuticals and 97 were other biologic drugs. Out of the 1144 remaining small-molecule drugs, 123 (10.75%) were discovered by target-based drug discovery and 1021 (89.25%) by phenotype-based approaches. Despite the dominance of small-molecule target-based drug discovery in the last 40 years, it represents a meager share of the currently used drugs (123 drugs (9.39%)), in contrast to phenotype-based approaches (1021 (77.94%) vs) ([Figure 2a](#)). This disproportionate disparity holds up even when

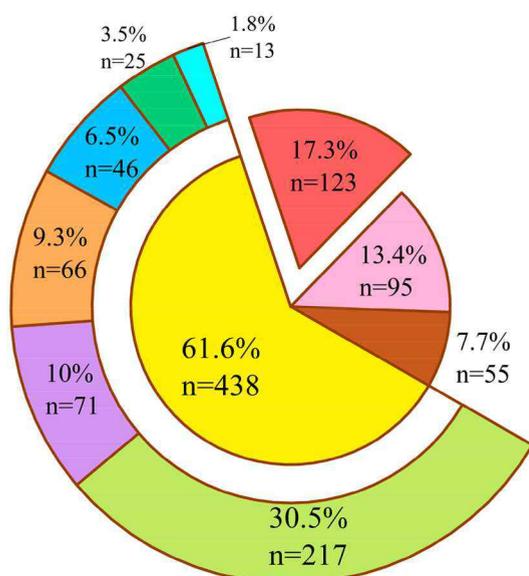
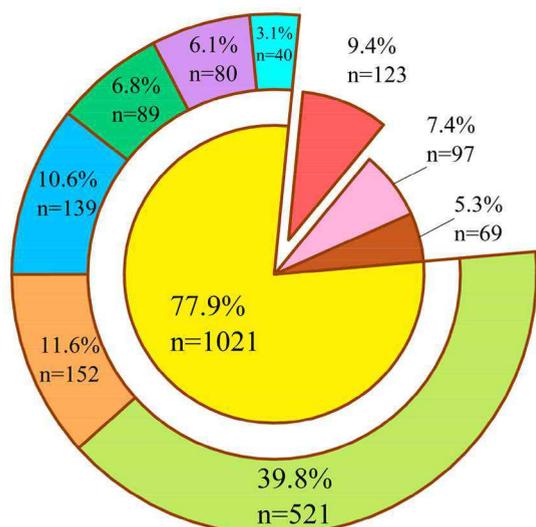
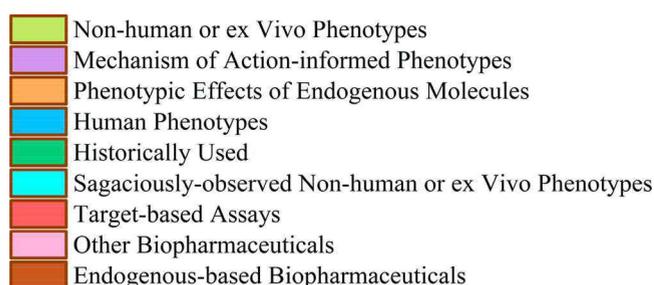


Figure 2. Shares of different approaches from the discovery origins of drugs. (a) All approved drugs; (b) drugs approved after 1995. All the drugs in each category are listed in Figure 4, and their detailed and manually extracted discovery origins are available in Supporting Information 1.

only the drugs approved after 1995 are taken into account (123 (17.30%) vs 438 (61.60%)) (Figure 2b). Although the share of target-based drug discovery from the drugs approved each year seems to have grown over time, there has not been a single year in which it was not surpassed by the share of phenotypic drug discovery (Figure 3).

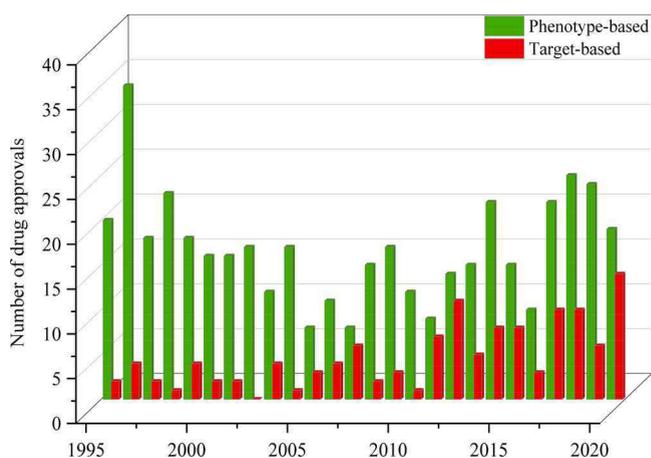


Figure 3. Number of drugs discovered by target-based or phenotype-based approaches and approved each year since 1995 (the approval year of the first target-based drug, saquinavir).

Reviewing the discovery origins provided in Supporting Information 1 demonstrates that, contrary to the textbook procedure of drug discovery which has been the standard of the past few decades,⁶² a significant portion of the most important drugs used in the clinic have originated from approaches that many drug hunters nowadays would consider “otherworldly”¹⁵⁶ and “taken place on another planet”.^{156–158} Most of the approved drugs have originated from emphasizing and using highly predictive phenotypic models, like predictive animal models, *ex vivo* systems, or cultures of bacteria, fungi, and protozoa (about 700 drugs including most of the drugs in these categories: observing nonhuman or *ex vivo* phenotypes, mechanism of action-informed phenotypic observations, and observing phenotypic effects of endogenous molecules). This is evident in the discovery origins of many drugs including isoproterenol,¹⁵⁹ propranolol,⁹⁷ cimetidine,⁹⁷ ethosuximide,¹⁶⁰ purine analogs,⁹¹ cyclosporine,¹⁶¹ pentamidine,^{162–165} omeprazole,^{166,167} propofol,^{168–170} paclitaxel,¹⁷¹ topotecan,^{172,173} ivermectin,^{174,175} topiramate,^{176,177} leflunomide,¹⁷⁸ sirolimus,¹⁷⁹ ezetimibe,¹⁸⁰ cinacalcet,¹⁸¹ and tecovirimat.^{182,183}

Many antimicrobial agents that were discovered by observing infected animals or the cultures of the microbes themselves, even during screening uncharacterized mixtures like soil samples, are other notable examples in this regard, like tetracyclines,¹⁸⁴ penicillins,¹⁸⁵ cephalosporins,¹⁸⁶ pyrimethamine,⁹² chloroquine,¹⁸⁷ vancomycin,¹⁸⁸ rifampin,¹⁸⁹ clavulanic acid,¹⁹⁰ pretomanid,¹⁹¹ retapamulin and lefamulin,^{192,193} spinosad,¹⁹⁴ and bedaquiline.^{195,196}

This attention to the predictivity of models was so high that in many cases, drug hunters used themselves as models and self-experimented with molecules, exemplified by lidocaine,¹⁹⁷ amphetamine,¹⁹⁸ cromolyn,¹⁹⁹ bisacodyl,²⁰⁰ ingenol mebutate,²⁰¹ and bromelanotide.²⁰²

The drugs discovered based on serendipity and sagaciously observing nonhuman or *ex vivo* phenotypes can also be considered to be indebted to this attention toward predictive models, including bacitracin,^{203,204} ticlopidine,²⁰⁵ valproic acid,²⁰⁶ warfarin,²⁰⁷ meprobamate,²⁰⁸ vinca alkaloids,²⁰⁹ dipyrindamole,²¹⁰ diazoxide,²¹¹ cisplatin,^{212,213} etomidate,¹⁰³ naftifine,²¹⁴ glatiramer acetate,^{215,216} imiquimod,^{217,218} thiazolidinediones,^{219,220} levetiracetam and piracetam,²²¹ and dapagliflozin and empagliflozin.²²² Such serendipitous discoveries would be impossible in target-based drug discovery’s biochemistry affinity

Non-Human or ex Vivo Phenotypes

CHLORDIAZEPOXIDE	FLUOROURACIL	CEFALEXIN	INDOMETHACIN	CAPTOPRIL	DIPHENHYDRAMINE	PROPRANOLOL	RIBAVIRIN	Standalone Drugs	Standalone Drugs
DIAZEPAM	CYTARABINE	CEFAZOLIN	TOLMETIN	ENALAPRILAT	PHENINDAMINE	TIMOLOL	ZIDOVUDINE	KETAMINE	METHYLPHENIDATE
OXAZEPAM	FLOXURIDINE	CEFOXITIN	SULINDAC	LISINAPRIL	PHENIRAMINE	METOPROLOL	DIDANOSINE	SPINOSAD	FOSFOMYCIN
FLURAZEPAM	FLUCYTOSINE	CEFADROXIL	DICLOFENAC	RAMIPRILAT	PYRILAMINE	NADOLOL	FLUDARABINE	BEDAQUILINE	TOPIRAMATE
CLORAZEPIC ACID	VIDARABINE	CEFACLOR	ETODOLAC	QUINAPRILAT	THONZYLAMINE	ATENOLOL	PENTOSTATIN	OMACETAXINE	NATAMYCIN
CLONAZEPAM	TRIFLURIDINE	CEFOTAXIME	BROMFENAC	BENAZEPRILAT	DOXYLAMINE	PINDOLOL	CLADRIBINE	MERTANSINE	ZILEUTON
LORAZEPAM	GEMCITABINE	CEFUROXIME	CELECOXIB	FOSINOPRILAT	CHLORPHENIRAMINE	LABELTALOL	STAVUDINE	PIRFENIDONE	GLATIRAMER
TEMAZEPAM	5'-DEOXY-5—	CEFTRIAZONE	NEPAFENAC	PERINDOPRILAT	CHLORCYCLIZINE	ACEBUTOLOL	LAMIVUDINE	BRETYLIUM	IMIQUIMOD
ALPRAZOLAM	FLUOROCYTIDINE	CEFOTETAN	IBUPROFEN	MOEXIPRILAT	PROMETHAZINE	BETAXOLOL	ABACAVIR	DOBUTAMINE	FENOLDOPAM
TRIAZOLAM	CAPECITABINE	CEFTAZIDIME	NAPROXEN	TRANDOLAPRILAT	CARBINOXAMINE	LEVOBUNOLOL	SOFOSBUVIR	DACARBAZINE	MODAFINIL
MIDAZOLAM	EMTRICITABINE	CEFIXIME	FENOPROFEN	PERINDOPRIL—	FUMARATE	ESMOLOL	DASABUVIR	MITOMYCIN	LEFLUNOMIDE
QUAZEPAM	AZACTIDINE	CEFPODOXIME	FLURBIPROFEN	ARGININE	CYCLIZINE	CARTEOLOL	BROMOCRIPTINE	DOXAPRAM	CLOSTAZOL
ESTAZOLAM	CLOFARABINE	CEFEPIME	KETOPROFEN	RIFAMPIN	MECLIZINE	SOTALOL	CABERGOLINE	GUANFACINE	DOCOSANOL
CLOBAZAM	NELARABINE	CEFDINIR	KETOROLAC	RIFABUTIN	HYDROXYZINE	BISOPROLOL	PANCURONIUM	TRIMETHOPRIM	ZONISAMIDE
REMIMAZOLAM	DECITABINE	CEFTAROLINE	OXAPROZIN	RIFAPENTINE	BROMPHENIRAMINE	IBUTILIDE	VECURONIUM	CAPREOMYCIN	GALANTAMINE
SULFANILAMIDE	REMDESIVIR	CEFTOLOZANE	STREPTOMYCIN	RIFAXIMIN	ORPHENADRINE	CARVEDILOL	Standalone Drugs	PYRANTEL	NITISINONE
SULFADIAZINE	METRONIDAZOLE	CEFIDEROCOL	NEOMYCIN	RIFAMYCIN	TRIPROLDINE	DOFETILIDE	WARFARIN	CYCLOSERINE	NITAZOXANIDE
SULFACETAMIDE	TINIDAZOLE	NAFTIFINE	GENTAMICIN	BENZOCAINE	CHLOPHEDIANOL	NEBIVOLOL	LITHIUM	MITOTANE	EZETIMIBE
MAFENIDE	BENZNIDAZOLE	TERBINAFINE	TOBRAMYCIN	TETRACAINE	CYPROHEPTADINE	CIMETIDINE	RESORCINOL	ETHAMBUTOL	FULVESTRANT
SULFAMETHOXAZOLE	SECNIDAZOLE	BUTENAFINE	AMIKACIN	BENZONATATE	CLEMASTINE	RANITIDINE	PYRITHIONE	HYDROXYUREA	DAPTOMYCIN
PENTOBARBITAL	CLAVULANIC ACID	IMPENEM	PLAZOMICIN	PRAMOXYNE	LORATADINE	FAMOTIDINE	PYRIMETHAMINE	METHYLENE BLUE	ZICONOTIDE
BUTALBITAL	SULBACTAM	MEROPENEM	CASPOFUNGIN	BENOXINATE	ACRIVASTINE	NIZATIDINE	GRISEOFULVIN	DICYCLOMINE	VARENICLINE
SECOBARBITAL	TAZOACTAM	ERTAPENEM	MICAFUNGIN	DYCLONINE	CETIRIZINE	OMEPRAZOLE	TRIAMTERENE	LINDANE	RANOLAZINE
PRIMIDONE	AVIBACTAM	LOPERAMIDE	ANIDULAFUNGIN	PROPARACAINE	OLOPATADINE	LANSOPRAZOLE	DACTINOMYCIN	PROGUANIL	SINECATECHINS
METHOHEXITAL	RELEBACTAM	ELUXADOLINE	ZOLPIDEM	ISONIAZID	FEXOFENADINE	RABEPRAZOLE	TOLNAFTATE	BUSULFAN	IXABEPILONE
NAPHAZOLINE	VABORBACTAM	RILUZOLE	ZALEPLON	PYRAZINAMIDE	AZELASTINE	PANTOPRAZOLE	MOLINDONE	THIOTEPA	RETAPAMULIN
TETRAHYDROZOLINE	LEVETIRACETAM	EDARAVONE	ESZOPICLONE	ETHIONAMIDE	KETOTIFEN	METHOTREXATE	VERAPAMIL	CU UNDECYLENATE	LACOSAMIDE
XYLOMETAZOLINE	BRIVARACETAM	AMIODARONE	LETROZOLE	IVERMECTIN	EPINASTINE	LEVOLEUCOVORIN	AMILORIDE	ATOMOXETINE	PLERIXAFOR
OXYMETAZOLINE	ERYTHROMYCIN	DRONEDARONE	ANASTROZOLE	MOXIDECTIN	BEPOTASTINE	PEMETREXED	POVIDONE-IODINE	DALFOPIRISTIN-	LUMEFANTRINE
CHLOROQUINE	CLARITHROMYCIN	TIOFIBAN	TOPOTECAN	POLYMYXIN B	ALCAFTADINE	PRALATREXATE	CYCLOSPORINE	QUINUPRISTIN	ERIBULIN
PRIMAQUINE	AZITHROMYCIN	EPTIFIBATIDE	IRINOTECAN	COLISTIN	CLONIDINE	LOSARTAN	BUSPIRONE	OZOGAMICIN	NIFURTIMOX
HYDROXYCHLOROQUINE	BELINOSTAT	PRAZOSIN	DERUXTECAN	LINCOMYCIN	APRACLONIDINE	VALSARTAN	MUPIROCIN	CENOBAMATE	FIDAXOMICIN
METOCLOPRAMIDE	PANOBINOSTAT	TERAZOSIN	SN-38	CLINDAMYCIN	BRIMONIDINE	IRBESARTAN	CISATRACURIUM	AMINOSALICYLATE	PITOLISANT
PRUCALOPRIDE	METHSUXIMIDE	DOXAZOSIN	MEPERIDINE	PACLITAXEL	TIZANIDINE	TELMISARTAN	TEMOZOLOMIDE	CHLORAMPHENICOL	CHLORHEXIDINE
AMISULPRIDE	ETHOSUXIMIDE	ALFUZOSIN	METHADONE	DOCETAXEL	DEXMEDETOMIDINE	CANDESARTAN	PRETOMANID	MIDOSTAURIN	FOSCARNET
ACYCLOVIR	NIFEDIPINE	PIROXICAM	ALVIMOPAN	CABAZITAXEL	LOFEXIDINE	OLMESARTAN	OSILODROSTAT	NABUMETONE	RUFINAMIDE
VALACYCLOVIR	AMLODIPINE	MELOXICAM	ROSIGLITAZONE	TAMOXIFEN	SIROLIMUS	AZILSARTAN	ETELCALCETIDE	INAMRINONE	LEFAMULIN
GANCICLOVIR	NIMODIPINE	LINEZOLID	PIOGLITAZONE	TOREMIFENE	TACROLIMUS	DAUNORUBICIN	TECOVIRIMAT	BUPROPION	CLIOQUINOL
VALGANCICLOVIR	NICARDIPINE	TEDIZOLID	ISOFLURANE	RALOXIFENE	PIMECROLIMUS	VALRUBICIN	AMIFAMPRIDINE	AURANOFIN	ALLANTOIN
CIDOFOVIR	ISRADIPINE	PHENYTOIN	DESFLURANE	BAZEDOXIFENE	TEMSIROLIMUS	MITOXANTRONE	ISTRADEFYLLINE	AZTREONAM	HALOPROGIN
PENCICLOVIR	FELODIPINE	ETHOTOIN	SEVOFLURANE	OSPEMIFENE	EVEROLIMUS	IDARUBICIN	LAMOTRIGINE	PERMETHRIN	FLAVOXATE
ADEFOVIR	NISOLDIPINE	DIMETHYL FUMARATE	MEFENAMIC ACID	TRABECTEDIN	TRABECTEDIN	EPIRUBICIN	LETERMIVIR	ETOPOSIDE	ATOVAQUONE
ENTECAVIR	CLEVIDIPINE	DIROXIMEL FUMARATE	MECLOFENAMIC ACID	LURBINECTEDIN	ALLOPURINOL	HEXACHLOROPHENE	PENTAMIDINE	STIRIPENTOL	
SALBUTAMOL	FLUTAMIDE	MONOMETHYL AURISTATIN E	CHLORTETRACYCLINE		FEBUXOSTAT	CROTAMITON	TRANEXAMIC ACID	TAVABOROLE	
TERBUTALINE	BICALUTAMIDE	MONOMETHYL AURISTATIN-F	OXYTETRACYCLINE	DOXORUBICIN	LOMUSTINE	MECAMYLAMINE	LIXISENATIDE	IVABRADINE	
SALMETEROL	APALUTAMIDE	PROPYLTHIOURACIL	TETRACYCLINE	TIGECYCLINE	STREPTOZOCIN	TRIMETHOENZAMIDE	PROPOFOL	CICLOPIROX	
FORMOTEROL	NILUTAMIDE	METHIMAZOLE	DEMECLOCYCLINE	ERAVACYCLINE	MEBENDAZOLE	BEMPEDOIC ACID	BACLOFEN	PRAZIQUANTEL	
VILANTEROL	ENZALUTAMIDE	PHENTOLAMINE	DOXYCYCLINE	OMADACYCLINE	ALBENDAZOLE	NITROFURANTOIN	AMPHOTERICIN B	MILTEFOSINE	
OLODATEROL	DARLUTAMIDE	PHENOXYBENZAMINE	MINOCYCLINE	SARECYCLINE	TRICLABENDAZOLE	DANTROLENE	DAPSONE	DILTIAZEM	

Figure 4. continued

Non-Human or ex Vivo Phenotypes	Phenotypes of Humans			Phenotypic Effects of Endogenous Molecules			Historically Used	
MICONAZOLE	IMIPRAMINE	CHLORPROMAZINE	Standalone Drugs	CORTISONE	PROGESTERONE	LEUPROLIDE	MORPHINE	SCOPOLAMINE
CLOTRIMAZOLE	AMITRIPTYLINE	PROCHLORPERAZINE	ACETAMINOPHEN	HYDROCORTISONE	HYDROXYPROGESTERONE	GOSERELIN	CODEINE	PROPANTHELINE
KETOCONAZOLE	DESIPRAMINE	PERPHENAZINE	NITROUS OXIDE	PREDNISON	MEDROXYPROGESTERONE	HISTRELIN	HYDROCODONE	CLIDINIUM
ECONAZOLE	NORTRIPTYLINE	FLUPHENAZINE	MEMANTINE	PREDNISOLONE	ETHYNODIOL	GANIRELIX	OXYCODONE	METHSCOPOLAMINE
TIOCONAZOLE	PROTRIPTYLINE	TRIFLUOPERAZINE	BISMUTH	TRIAMCINOLONE	LEVONORGESTREL	CETRORELIX	LEVORPHANOL	IPRATROPIUM
BUTOCONAZOLE	DOXEPIN	THIORIDAZINE	METHENAMINE	NORETHINDRONE	MEGESTROL	DEGARELIX	DEXTROMETHORPHAN	TROSPIUM
SULCONAZOLE	CYCLOBENZAPRINE	THIOHIXENE	BENZYL ALCOHOL	METHYLPREDNISOLONE	DANAZOL	TESAMORELIN	DIHYDROCODEINE	SOLIFENACIN
TERCONAZOLE	TRIMIPRAMINE	LOXAPINE	SULFASALAZINE	DEXAMETHASONE	NORGESTIMATE	NAFARELIN	HYDROMORPHONE	TIOTROPIUM
OXICONAZOLE	MAPROTILINE	PIMOZIDE	PROBENECID	FLUOROMETHOLONE	DESOGESTREL	TRIPTORELIN	OXYMORPHONE	DARIFENACIN
FLUCONAZOLE	AMOXAPINE	CLOZAPINE	DISULFIRAM	FLUCINOLONE	MIFEPRISTONE	Standalone Drugs	NALBUPHINE	ACLIDINIUM
ITRACONAZOLE	FLUOXETINE	OLANZAPINE	HYDRALAZINE	FLURANDRENOLIDE	NORELGESTROMIN		OXYTOCIN	FENTANYL
VORICONAZOLE	CLOMIPRAMINE	QUETIAPINE	METHYLDOPA	BETAMETHASONE	ETONOGESTREL	GUANIDINE	PENTAZOCINE	REVEFENACIN
SERTAONAZOLE	SERTRALINE	ASENAPINE	BENZOYL PEROXIDE	FLUCINONIDE	DIENOGEST	UNDECYLENIC ACID	NALOXONE	ATROPINE
POSAONAZOLE	PAROXETINE	LURASIDONE	ANAGRELIDE	DESONIDE	ULIPRISTAL	CORTICOTROPIN	BUTORPHANOL	
LULICONAZOLE	VENLAFAXINE	HALOPERIDOL	HYDROQUINONE	HALCINONIDE	SEGESTERONE	LEVODOPA	BUPRENORPHINE	DICYLOMINE
EFINACONAZOLE	FLUVOXAMINE		DROPERIDOL	DEACETYLBISACODYL	DIFLORASONE	BREXANOLONE	DOPAMINE	NALTREXONE
ISAVUCONAZOLE	MIRTAZAPINE	ARIPRAZOLE	BREMELANOTIDE	CLOCORTOLONE	TESTOSTERONE	AMINOCAPROIC ACID	SUFENTANIL	GLYCOPYRROLATE
MECHLORETHAMINE	CITALOPRAM	RISPERIDONE	DIBUCAINE	DESOXIMETASONE		METHYLTESTOSTERONE	METYROSINE	ALFENTANIL
CHLORAMBUCIL	DULOXETINE	ZIPRASIDONE	MALATHION	AMCINONIDE	OXYMETHOLONE	URSODIOL	TRAMADOL	TOLTERODINE
4-HYDROXYCYCLOPHOSPHAMIDE	DESVENLAFAXINE	ARIPRAZOLE	FLIBANSERIN	FLUNISOLIDE	FLUOXYMESTERONE	PHENYLACETIC ACID	REMIFENTANIL	FESOTERODINE
MELPHALAN	ACETAZOLAMIDE	CARIPRAZINE	PROCAINAMIDE	ALCLOMETASONE	FINASTERIDE	EFLORNITHINE	TAPENTADOL	Standalone Drugs
CARMUSTINE	DICHLORPHENAMIDE	BREXIPRAZOLE	CHLOROPROCAINE	CLOBETASOL	EXEMESTANE	MIGLITOL	EPHEDRINE	
ESTRAMUSTINE	METHAZOLAMIDE	PIMAVANSERIN	MEPIVACAINE	BECLMETHASONE	DUTASTERIDE	TEGASEROD	AMPHETAMINE	COCAINE
IFOSFAMIDE	DORZOLAMIDE	LUMATEPERONE	PRILOCAINE	MOMETASONE	ABIRATERONE	GLUTAMINE	METHAMPHETAMINE	DIGOXIN
BENDAMUSTINE	BRINZOLAMIDE	THALIDOMIDE	BUPIVACAINE	FLUTICASONE	CLASCOTERONE	PRAMLINTIDE	PROPYLHEXEDRINE	KAOLIN
CIPROFLOXACIN	QUININE		LENALIDOMIDE	MEXILETINE	HALOBETASOL	EPINEPHRINE	SAPROPTERIN	PHENTERMINE
OFLOXACIN	MEFLOQUINE	POMALIDOMIDE	FLECAINIDE	PREDNICARBATE	PHENYLEPHRINE		ICATIBANT	DIETHYLPROPION
GATIFLOXACIN	TAFENOQUINE	APREMILAST	PROPAFENONE	BUDESONIDE	ISOPROTERENOL	AFAMELANOTIDE	BENZPHETAMINE	MENTHOL
MOXIFLOXACIN	NABILONE	ISOCARBOXAZID	ROPIVACAINE	LOTEPREDNOL	NOREPINEPHRINE	HEMIN	PHENDIMETRAZINE	PILOCARPINE
GEMIFLOXACIN	DRONABINOL	TRANLYCYPROMINE	ARTICAINE	CICLESONIDE	DROXIDOPA	MISOPROSTOL	PSEUDOEPHEDRINE	APOMORPHINE
BESIFLOXACIN	FUROSEMIDE	PHENELZINE	NITROGLYCERIN	FLUTICASONE FUROATE	METAPROTERENOL	SETMELANOTIDE	FENFLURAMINE	METHOXSALEN
DELAFLOXACIN	ETHACRYNIC ACID	SELEGILINE	ISOSORBIDE DINITRATE	DIFLUPREDNATE	MIDODRINE	OXIGLUTATIONE	THEOPHYLLINE	NICOTINE
OZENOXACIN	BUMETANIDE	RASAGILINE	NITROPRUSSIDE	²¹ DESACETYLDE-FLAZACORT	SOLIRIAMFETOL	SEMAGLUTIDE	PENTOXIFYLLINE	PODOFLOX
VANCOMYCIN	TORSEMIDE	SAFINAMIDE	NITROPRUSSIDE	DEOXYCHOLIC ACID	LINACLOTIDE	CALCIPOTRIENE	MILRINONE	METFORMIN
TELAVANCIN	DAPAGLIFLOZIN	TOLBUTAMIDE	ISOSORBIDE MONONITRATE	CHOLIC ACID	PLECANATIDE	GABAPENTIN	TETRABENAZINE	SUCCINYLCHOLINE
DALBAVANCIN	CANAGLIFLOZIN	GLYBURIDE	NITRATE	OBETICHOIC ACID	RAMELTEON		4, HYDROXYBUTANOTE	(+)-α, DIHYDROTETRA-BENZAZINE
ORITAVANCIN	EMPAGLIFLOZIN	GLIPIZIDE	SPIRONOLACTONE	ESTRADIOL	TASIMELTEON	PREGABALIN	VALBENZAZINE	BIVALIRUDIN
ROPINIROLE	ERTUGLIFLOZIN	GLIMEPIRIDE	DROSPIRENONE	ETHINYL ESTRADIOL	HEPARIN	ACAMPROSATE	SALICYLIC ACID	INGENOL MEBUTATE
ROTIGOTINE	QUINIDINE	TRAZODONE	EPLERENONE	PRASTERONE	ENOXAPARIN	VIGABATRIN	ASPIRIN	CANNABIDIOL
AMANTADINE	DISOPYRAMIDE	NEFAZODONE	GEMFIBROZIL	DINOPROSTONE	PENTOSAN POLYSULFATE	TRETINOIN	DIFLUNISAL	METHYLERGONOVINE
RIMANTADINE	CHLOROTHIAZIDE	VILAZODONE	FENOFIBRIC ACID	CARBOPROST	FONDAPARINUX	ADAPALENE	MESALAMINE	DIHYDROERGOTAMINE
MERCAPTOPYRINE	METOLAZONE	SILDENAFIL	FENOFIBRATE	ALPROSTADIL	LATANOPROST	ACITRETIN	OLSALAZINE	ERGOLIDS
THIOGUANINE	INDAPAMIDE	VARDEFANIL	CROMOLYN	BIMATOPROST	DOXERCALCIFEROL	TAZAROTENIC ACID	NEOSTIGMINE	ERGOLOIDS
AZATHIOPRINE	CHLOROTHALIDONE	TADALAFIL	NEDOCROMIL	TRAVOPROST	CALCIFEDIOL	BEXAROTENE	PYRIDOSTIGMINE	ARTEMETHER
REPAGLINIDE	HYDROCHLOROTHIAZIDE	AVANAFIL	LODOXAMIDE	TAFLUPROST	CALCITRIOL	TRIFAROTENE	RIVASTIGMINE	ARTESUNATE
NATEGLINIDE	BENDROFLUMETHIAZIDE			OCTREOTIDE	ACETYLCHOLINE	EPOPROSTENOL		
DIPHENOXYLATE				LANREOTIDE	BETHANECHOL	TREPROSTINIL		
DIFENOXIN				PASIREOTIDE	CARBAMOYLCHOLINE	ILOPROST		
				VASOPRESSIN	CARBACHOL	LEVOTHYROXINE		
				DESMOPRESSIN	CEVIMELINE	LIOTHYRONINE		

Figure 4. continued

Sagaciously-observed Non-human or ex Vivo Phenotypes	Mechanism of Action-Informed Phenotypes		Endogenous-based Biopharmaceuticals		Other Biopharmaceuticals	Target-based Assays			
PENICILLIN G	PRAVASTATIN	SUMATRIPTAN	ASPARAGINASE	PARATHYROID HORMONE	BOTULINUM TOXIN TYPE B	SAQUINAVIR	IMATINIB	Standalone Drugs	
PENICILLIN V	SIMVASTATIN	ZOLMITRIPTAN	PEGASPARGASE	PEGINTERFERON α -2A	BOTULINUM TOXIN TYPE A	RITONAVIR	DASATINIB	DONEPEZIL	
AMPICILLIN	FLUVESTATIN	NARATRIPTAN	SARGRAMOSTIM	PEGINTERFERON β -1A	IBRITUMOMAB TIUXETAN	INDINAVIR	NILOTINIB	ACARBOSE	
DICLOXACILLIN	ATORVASTATIN	RIZATRIPTAN	SOMATROPIN	INTERFERON α -2B	ATOLTIVIMAB;ODESIVIMAB;AFTIVIMAB	NELFINAVIR	BOSUTINIB	FOMEPIZOLE	
OXACILLIN	ROSUVASTATIN	ALMOTRIPTAN	TERIPARATIDE	INTERFERON α -N3	MOXETUMOMAB PASUDOTOX	AMPRENAVIR	PONATINIB	ORLISTAT	
NAFCILLIN	PITAVASTATIN	FROVATRIPTAN	FILGRASTIM	INTERFERON GAMMA-1B	CERTOLIZUMAB PEGOL	LOPNAVIR	PEXIDARTINIB	CONIVAPTAN	
AMOXICILLIN	ONDANSETRON	ELETRIPTAN	PEGFILGRASTIM	METHOXY POLYETH-	CAPROMAB PENDETIDE	ATAZANAVIR	RIPRETINIB	SUNITINIB	
PIPERACILLIN	GRANISETRON	FINGOLIMOD	BERACTANT	YLENE GLYCOL-EPOETIN β	BALOXAVIR MARBOXIL	TIPRANAVIR	SELPERCATINIB	MARAVIROC	
MEPROBAMATE	ALOSETRON	SIPONIMOD	ALDESLEUKIN	VELAGLUCERASE α	MARGETUXIMAB	DARUNAVIR	GEFITINIB	ALISKIREN	
METHOCARBAMOL	PALONOSETRON	OZANIMOD	DORNASE α	TALIGLUCERASE α	FREMANEZUMAB	OCRELIZUMAB	ZANAMIVIR	ERLOTINIB	TOLVAPTAN
GUAIFENESIN	PAMIDRONATE	LUMACAFTOR	IMIGLUCERASE	ELOSULFASE α	GALCANEZUMAB	DUPLUMAB	OSELTAMIVIR	LAPATINIB	ROFLUMILAST
CHLORZOXAZONE	ALENDRONATE	TEZACAFTOR	BECAPLERMIN	ASFOTASE α	TEPROTUMUMAB	CERLIPONASE α	PERAMIVIR	VANDETANIB	VEMURAFENIB
CARISOPRODOL	RISEDRONATE	ZAFIRLUKAST	ALBUMIN HUMAN	SEBELPASE α	NAXITAMAB	DURVALUMAB	RALTEGRAVIR	AFATINIB	LOMITAPIDE
METAXALONE	ZOLEDRONATE	MONTELUKAST	SACROSIDASE	ABALOPARATIDE	VILTOLARSEN	SARILUMAB	ELVITEGRAVIR	DACOMITINIB	NINTEDANIB
FELBAMATE	IBANDRONATE	Standalone Drugs	RETEPLASE	VESTRONIDASE α	LUMASIRAN	GUSELKUMAB	DOLUTEGRAVIR	OSIMERTINIB	VORAPAXAR
CARBAMAZEPINE	PARITAPREVIR	CYSTEAMINE	CALFACTANT	ELAPEGADEMASE	PEGAPTANIB	GEMTUZUMAB	BICTEGRAVIR	NERATINIB	ELIGLUSTAT
OXCARBAZEPINE	GRAZOPREVIR	MIGLUSTAT	ETANERCEPT	CHORIOGONADOTROPIN α	RESLIZUMAB	INOTUZUMAB	NEVIRAPINE	AVAPRITINIB	SACUBITRIL
ESLICARBAZEPINE	GLECAPREVIR	CINACALCET	COLLAGENASE	CALASPARGASE PEGOL	IXEKIZUMAB	BENRALIZUMAB	EFAVIRENZ	TUCATINIB	VENETOCLAX
TICLOPIDINE	VOXILAPREVIR	ROMIDEPSIN	LIRAGLUTIDE	CALCITONIN SALMON	DACLIZUMAB	EMICIZUMAB	ETRAVIRINE	SORAFENIB	LIFITEGRAST
CLOPIDOGREL	LEDIPASVIR	DALFAMPRIDINE	INSULIN LISPRO	CORTICORELIN OVTNE	OLARATUMAB	LANADELUMAB	RILPIVIRINE	AXITINIB	NETARSUDIL
PRASUGREL	ELBASVIR	IVACAFTOR	INSULIN ASPART	PORACTANT α	BEZLOTOXUMAB	PATISIRAN	DORAVIRINE	REGORAFENIB	TELOTRIPTAT
TICAGRELOR	VELPATASVIR	PERAMPANEL	INSULIN DEGLUDEC	DARBEPOETIN α	NUSINERSEN	ABCIXIMAB	BOSENTAN	LENVATINIB	ERDAFITINIB
CANGRELOR	OMBITASVIR	RIOCIGUAT	INSULIN GLULISINE	THYROTROPIN α	DEFIBROTIDE	RITUXIMAB	AMBRISENTAN	PAZOPANIB	TAFAMIDIS
VINBLASTINE	PIBRENTASVIR	SELEXIPAG	INSULIN DETEMIR	HYALURONIDASE	ETEPLIRSEN	BASILIXIMAB	MACITENTAN	CRIZOTINIB	BEROTRALSTAT
VINCRIStINE	TRAMETINIB	CRISABOROLE	INSULIN GLARGINE	ANGIOTENSIN II	BRODALUMAB	GIVOSIRAN	APREPITANT	CABOZANTINIB	TIRBANIBULIN
VINORELBINE	COBIMETINIB	CARGLUMATE	TENECTEPLASE	ERYTHROPOIETIN	RAXIBACUMAB	ISATUXIMAB	NETUPITANT	CERITINIB	PRALSETINIB
CISPLATIN	BINIMETINIB	FOSTAMATINIB	ANAKINRA	PALIVIZUMAB	OBINUTUZUMAB	EPTINEZUMAB	ROLAPITANT	ALECTINIB	TOFACTINIB
CARBOPLATIN	SELUMETINIB	MIGALASTAT	AGALSIDASE β	INFLIXIMAB	RAMUCIRUMAB	TAGRAXOFUSP	SITAGLIPTIN	BRIGATINIB	OLICERIDINE
OXALIPLATIN	RUXOLITINIB	SELINEXOR	LARONIDASE	TRASTUZUMAB	SILTUXIMAB	EMAPALUMAB	SAXAGLIPTIN	LAROTRECTINIB	BEROTRALSTAT
Standalone Drugs	BARICTINIB	VOXELOTOR	SOMAPACITAN	RASBURICASE	VEDOLIZUMAB	RAVULIZUMAB	LINAGLIPTIN	LORLATINIB	IBRUTINIB
BACITRACIN	UPADACITINIB	RISDIPLAM	ALBIGLUTIDE	ENFUVIRTIDE	PEMBROLIZUMAB	CAPLACIZUMAB	ALOGLIPTIN	ENTRECTINIB	ACALABRUTINIB
VALPROIC ACID	FEDRATINIB	TAZEMETOSTAT	METRELEPTIN	ADALIMUMAB	GOLODIRSEN	ROMOSUZUMAB	RIVAROXABAN	CAPMATINIB	ZANUBRUTINIB
DIPYRIDAMOLE	VISMODEGIB	FOSTEMSAVIR	RILONACEPT	OMALIZUMAB	DULAGLUTIDE	RISANKIZUMAB	APIXABAN	OLAPARIB	ELTROMBOPAG
PROCARBAZINE	SONIDEGIB	LONAFARNIB	ECALLANTIDE	BEVACIZUMAB	BLINATUMOMAB	POLATUZUMAB	EDOXABAN	RUCAPARIB	LUSUTROMBOPAG
DIAZOXIDE	GLASDEGIB	LUBIPROSTONE	BELATACEPT	CETUXIMAB	SECUKINUMAB	BROLUCIZUMAB	BETRIXABAN	NIRAPARIB	AVATROMBOPAG
ETOMIDATE	IDELALISIB	ABAMETAPIR	TEDUGLUTIDE	NATALIZUMAB	DINUTUXIMAB	LUSPATERCEPT	PALBOCICLIB	TALAZOPARIB	UBROGEPANT
MYCOPHENOLATE	COPANLISIB	ECHOTHIOPHATE	ABATACEPT	EXENATIDE	ALIROCUMAB	ENFORTUMAB	RIBOCICLIB	ELAGOLIX	RIMEGEPANT
DISODIUM	DUVELISIB	ACETOHYDROX-	PALIFERMIN	RANIBIZUMAB	EVOLOCUMAB	CRIZANLIZUMAB	ABEMACICLIB	RELUGOLIX	SUVOREXANT
AZELATE	ALPELISIB	AMIC ACID	IDURSULFASE	PANITUMUMAB	IDARUCIZUMAB	CEMPLIMAB	ARGATROBAN	BORTEZOMIB	LEMBOREXANT
PRAMIPEXOLE	DABRAFENIB	TAMSULOSIN	GALSULFASE	ECULIZUMAB	DARATUMUMAB	SACITUZUMAB	DABIGATRAN	CARFILZOMIB	MIRABEGRON
VORINOSTAT	ENCORAFENIB	SILODOSIN	MECASERMIN	CANAKINUMAB	NECITUMUMAB	INEBILIZUMAB	ENASIDENIB	IXAZOMIB	VIBEGRON
			PEGVISOMANT	PEGLOTICASE	ELOTUZUMAB	TAFASITAMAB	IVOSIDENIB		
			AFLIBERCEPT	IPILIMUMAB	OBILTOXAXIMAB	BELANTAMAB			
			OCRIPLASMIN	PERTUZUMAB	INOTERSEN	SATRALIZUMAB			

Figure 4. Discovery origins of all approved drugs. This is the detailed list of the drugs which have made up Figure 2a. Each rectangle represents a specific therapeutic class, and the color of each rectangle corresponds to the category as depicted in Figure 2 (which is also indicated in the headings above the therapeutic classes in this figure). Details of the discovery origins are available in Supporting Information 1.

assays where the output is merely the affinity of a molecule for a specific protein.

A minor portion of the discovery origins (the 10.6% human phenotypes plus the 6.8% historically used) can be traced back to serendipity and sagaciously observing the therapeutic effects

of substances in humans. Examples include chlorpromazine^{223–225} (the prototype of almost all antipsychotics), imipramine^{223,226,227} and iproniazide^{228,229} (the prototypes of almost all antidepressants), acetaminophen,²³⁰ corticosteroids,^{231,232} disulfiram,²³³ several diuretic²³⁴ and diabetes medications,^{211,235} methyl dopa,²³⁶ minoxidil,²³⁷ flibanserin,²³⁸ gemfibrozil,²³⁹ nabilone,^{240,241} anagrelide,²⁴² sildenafil,²⁴³ azelaic acid,²⁴⁴ hydroquinone,²⁴⁵ and memantine.²⁴⁶ It is fair to add to these cases the many drugs discovered based on historical observations, including metformin,²⁴⁷ digoxin,²⁴⁸ artemether,^{249,250} podofilox,²⁵¹ ingenol mebutate,²⁰¹ fingolimod,^{252,253} eribulin,^{254,255} and spinosad.¹⁹⁴ These cases highlight the importance of sagacity in clinical settings.

The discovery origins of drugs suggest that another aspect that has undergone a notable transition during the evolution of drug discovery since the last century is a transition in the structure and functioning of drug discovery teams.^{157,158} A few decades ago, drug discovery teams were small in number, comprising a few medicinal chemists and pharmacologists, all of whom were trying to answer the same question and who directly oversaw the relationships between chemical structures and modifications and their effects on phenotypes. Nowadays, drug discovery teams are significantly larger, and the goal of discovering a drug has been reduced and specialized into disconnected tasks.²⁵⁶ The not-too-much-specialized structure of yestercenury's drug discovery teams enabled seamless two-way reiterative translation of phenotypic observations to structural selections and optimizations and observing the phenotypic outcomes of these optimizations. On the other hand, the specialized and fragmented structure of current drug discovery teams lends itself to the scheme of reductionist target-based drug discovery: one-way serial filtering and funneling in which phenotypic observations are primarily used only as terminal filters (e.g., see Figure 6 of ref 62).^{46,56,57}

This insight can be inferred from the gleaned data that the “recent increase in productivity”^{47,48} can be traced back more to the adaptation of the pharmaceutical industry to its failures rather than addressing their fundamental causes. For example, efforts have been redirected from the unaddressed challenge of complex CNS disorders toward the more reducible rare and monogenic disorders^{7,48,49,257} or deriving analogs of drugs discovered decades ago, for example, sarecycline, eravacycline, omadacycline plazomicin, remimazolam, and lumateperone (Supporting Information 1). Even in some cases, drugs that were not brought forward to the market decades ago have been taken off the shelf and contribute to the apparent “increase in productivity.” For example, rifamycin was originally discovered in 1963 using a phenotypic screen but was not developed further in the US; rather, it was instead optimized to rifampin which the US FDA approved in 1971.¹⁸⁹ Anyhow, in 2018, rifamycin itself was approved by the US FDA, and the drug was introduced to the US market.²⁵⁸ Other similar examples include triclabendazole,²⁵⁹ artesunate,²⁵⁰ moxidectin,²⁶⁰ and tafenoquine.²⁶¹ The peculiarity of these cases of returning to decades-old structures and molecules can be illuminated by heeding that the drug-like chemical space is estimated to be so vast, up to 10⁶⁰ molecules,^{262–264} that novel structures ought not to be scarce.

It is also fair to add to the disproportionate contribution of phenotypic observations the numerous postapproval labeled and off-label indications that have been added for many approved drugs. In many cases, such repurposings and added indications have been based on phenotypic observations made by astute clinicians.^{265,266}

2.2. Are the Therapeutic Effects of “Target-Based” Drugs Reducible to Their Binding to a Single Protein?

2.2.1. Rationale. Although we have discovered that a disproportionate majority of the currently used drugs have been discovered by nonreductionist approaches that are now less prevalent, this is not definitive evidence that the reductionist approach of target-based drug discovery is inefficient because, as was cited earlier, this disparity may have been caused by other factors.

Another perspective from which we can assess target-based drug discovery is to question its role in the discovery of the drugs whose discovery origins we have identified as “target-based.” This helps to investigate if the therapeutic effects of such drugs can really be reduced to the modulation of single proteins. We know that a majority of the drugs do not survive clinical phases because of a lack of efficacy, although many of them that have been discovered based on target-based drug discovery bind their targets with high affinity.⁴ This implies that there may exist other variables that are consequential for the effectiveness of drugs, other than their binding to the targets with high affinity. One such variable is the degree of the relevance of the select target to the disorder. Interestingly, it has been shown that many of the supposed targets do not reliably relate to disorders.^{116,267} Another possibility is that the therapeutic effects of drugs may emerge from suitable manipulation of a multitude of components in addition to the target. It is well-established in pharmacology that the therapeutic effects of many drugs are mediated by a multitude of mechanisms (see Supporting Information 3).^{268–271} Moreover, it was recently shown that “off-target toxicity is a common mechanism of action of cancer drugs undergoing clinical trials”.^{272–274} Having put all of these alongside the fact that even in target-based drug discovery, assessments of therapeutic effects play some role as terminal filters, it can be hypothesized that even for the “target-based” drugs, the therapeutic effects might not be entirely attributable to the scheme of target-based drug discovery. Therapeutic “off-target” mechanisms can be unconsciously and fortuitously selected by the phenotypic terminal filters. This hypothesis is strengthened by heeding that plenty of the approved drugs that we use in contemporary clinical practice have very modest discovery origins. They were discovered by observing their effects in humans or in vivo models either serendipitously or among a few hundred screened molecules (Supporting Information 1) rather than by systematically screening large libraries.²⁷⁵

In other words, attributing the discovery of the “target-based” drugs we identified in the previous section to target-based drug discovery and their affinity for a single “target” can be considered a case of survival bias.⁴⁶ Survival bias is the logical fallacy of focusing on the entities that have made it past some selection step and overlooking those that have not, typically because of their lack of visibility. When most of the drugs designed for binding to a single “target” with high affinity fail the efficacy phase of clinical trials, the efficacy of those that happen to pass this test should not be simply attributed to their high binding affinity.

2.2.2. Methods. To test the hypothesis that the therapeutic effects of many of the drugs discovered by the “target-based” approach are indebted to “off-target” mechanisms, I performed a systematic review (as in evidence-based medicine²⁷⁶) for each of the “target-based” drugs which were identified in the previous section. I searched PubMed and Embase with these queries: “[Drug]/pharmacology”[Majr] for PubMed and “Drug”/exp/

Table 2. Counts of “Off-Target” Therapeutic Mechanisms of “Target-Based” Drugs^a

DONEPEZIL	40	BORTEZOMIB	69	ORLISTAT	10
ACARBOSE	14	CARFILZOMIB	2	RIMEGEPANT	1
ALISKIREN	12	EFAVIRENZ	2	ROFLUMILAST	9
RIVAROXABAN	7	NINTEDANIB	229	SACUBITRIL	2
EDOXABAN	1	GEFITINIB	111	TIRBANIBULIN	2
ZANAMIVIR	1	ERLOTINIB	109	VENETOCLAX	2
OSELTAMIVIR	1	LAPATINIB	16	SAQUINAVIR	11
FOMEPIZOLE	2	VANDETANIB	114	RITONAVIR	8
SITAGLIPTIN	13	AFATINIB	41	INDINAVIR	7
SAXAGLIPTIN	20	OSIMERTINIB	8	NELFINAVIR	8
LINAGLIPTIN	1	NERATINIB	4	LOPINAVIR	2
ALOGLIPTIN	1	SORAFENIB	140	ATAZANAVIR	1
ELTROMBOPAG	1	PAZOPANIB	107	MARAVIROC	3
ARGATROBAN	1	AXITINIB	102	ELTROMBOPAG	1
DABIGATRAN	2	REGORAFENIB	20	PALBOCICLIB	38
MIRABEGRON	2	LENVATINIB	10	RIBOCICLIB	14
DASATINIB	158	IMATINIB	78	ABEMACICLIB	17
NILOTINIB	63	CERITINIB	9	TALAZOPARIB	3
PONATINIB	13	OLAPARIB	4	CABOZANTINIB	5
BOSUTINIB	74	RUCAPARIB	17	ACALABRUTINIB	3
CRIZOTINIB	148	NIRAPARIB	2	VEMURAFENIB	18
TOFACITINIB	34	IBRUTINIB	40	SUNITINIB	270

^aDetails are available in Supporting Information 3. (The reason why the counts in Table 2 are different from the number of mechanisms listed for each drug in Supporting Information 3 is that the counts in Table 2 reflect the deduplicated counts of the mechanisms which also have been highlighted in Supporting Information 3).

mj/dd_pd for Embase. The retrieved citations were deduplicated using Systematic Review Assistant-Deduplication Module (SRA-DM)²⁷⁷ (the retrieved citations from each database and their deduplicated sum are available for each drug in Supporting Information 2). I manually (not by automated methods such as natural language processing) reviewed²⁷⁶ the citations and extracted mechanisms that were experimentally shown or suggested to mediate the effects related to the therapeutic effect for which the drug was initially approved but were not mediated by the “target(s)” the drug was discovered based on. To rule out the downstream effects of the binding of drugs to their “targets,” I excluded from the extracted “off-target” mechanisms, those that were mediated by the first shell or the second shell interacting proteins. I retrieved these interactors from STRING v11²⁷⁸ with these settings: “experiments” or “databases” for active interaction sources; highest confidence (0.900) for the minimum required interaction score; 500 for the maximum number of interactors in the first and the second shells. Those “off-target” mechanisms that were based on the direct binding of the drugs to the “off-target” proteins were exempt from this exclusion criterion. Because in many cases, several different studies had referred to the same mechanism for the therapeutic effect of one drug, I documented and cited all of these different studies but highlighted only one of such duplicates. The reason why the counts in Table 2 are different from the number of mechanisms listed for each drug in Supporting Information 3 is that the counts in Table 2 reflect the deduplicated counts of the mechanisms which are also mentioned in front of each drug in the tables of Supporting Information 3. To summarize, the extracted mechanisms needed to have these criteria:

- (1) Based on the reviewed experimental pharmacological studies, they were proposed to mediate, to any extent, the therapeutic effects the drug was approved for.
- (2) They depended neither on the “target(s)” the drug was discovered based on nor the first or second shell

interacting proteins of these “target(s)”, except where the mechanisms were based on direct binding of the drugs to these first or second shell interacting proteins.

2.2.3. Results and Discussion. The systematic review (which included a manual²⁷⁶ review of 31027 unique articles) confirmed the hypothesis. Many “target-based” drugs have numerous “off-target” therapeutic mechanisms (Table 2 and Supporting Information 3). For example, donepezil, which was discovered and developed as an acetylcholinesterase inhibitor, was found to have 40 therapeutic mechanisms independent of acetylcholinesterase, including anti-inflammatory and immunomodulatory effects;^{279–286} vasoprotective,^{287–293} neuroprotective,^{294–302} and antioxidant properties;^{285,288,303,304} inhibiting neuronal apoptosis,^{305–307} increasing neurogenesis via several pathways³⁰⁸ like brain derived neurotrophic factor,³⁰⁹ insulin-like growth factor 1,^{310–312} and SRC;^{313,314} stimulating oligodendrocyte differentiation and myelin-related gene expression;³¹⁵ direct effects on microtubule affinity regulating kinase 4,³¹⁶ nicotinic acetylcholine receptors,^{317,318} sigma nonopioid intracellular receptor 1,^{319–324} and calcium, potassium, and sodium channels,^{298,299,307,325} downregulating miRNA-206;³²⁶ preventing glutamate neurotoxicity;^{327–331} protecting against oxygen–glucose deprivation-induced injury;^{307,332–335} regulating serum adipokine levels;³³⁶ increasing the expression of autoantibodies against amyloid beta;³³⁷ increasing the activity of α -secretase and decreasing the activity of β -secretase;^{338,339} reducing the production^{339,340} and increasing the clearance of amyloid beta;^{341,342} reducing the phosphorylation of tau;^{340,343} and increasing the trafficking and activity of ADAM10 and ADAM17.³⁴⁴

Another example is crizotinib. Independent of inhibiting MET and ALK, it binds to 146 other kinases with considerable affinities,^{345,346} induces oxidative DNA damage and apoptosis,^{347–350} and has immunomodulatory effects through inhibit-

ing the macrophage stimulating 1 receptor and upregulating the major histocompatibility complex molecules.^{348,351–353}

This implies that the contribution of target-based drug discovery to approved drugs is even far less than 9.4%. If it was solely up to the scheme of reductionist target-based drug discovery, none of these “off-target” therapeutic mechanisms would have existed. They have been unconsciously and blindly selected because of the terminal assessments of therapeutic effects and do not necessarily accompany all molecules selected based on their binding to single “targets.” Notably, these counts are inevitably restricted to mechanisms that have been unraveled thus far; it is reasonable to expect that the actual “numbers” would be much higher.³⁵⁴

2.3. Is Binding the “Target” with High Affinity Even Relevant? **2.3.1. Rationale.** Now that we have observed that most drugs have been discovered by phenotypic observations and even the “target-based” drugs are not as “target-based” as claimed, how much is binding “targets” with high affinity, the holy grail of target-based drug discovery, relevant at all for the therapeutic effects of drugs? By selecting and filtering for molecules with higher binding affinities for a “target,” target-based drug discovery is based on this presumption that drugs with therapeutic effects are enriched among molecules with higher binding affinities for the “target.” A rough implication of this presumption is that the drugs which have already been approved probably have relatively higher binding affinities for the “target” that mediates their therapeutic effects, at least when their mechanisms of action are based on competitive antagonism and inhibition.

2.3.2. Methods. To test this presumption of target-based drug discovery that drugs with therapeutic effects are enriched among molecules with higher binding affinities for their “target,” I investigated the percentile rank of each approved drug’s affinity for each of its therapeutic “targets” among all ChEMBL³⁵⁵ ligands of that “target.” I retrieved the targets of approved drugs from “a comprehensive map of molecular drug targets” (Supporting Information S2 of ref 356, archived) which has compiled the “therapeutic targets” of approved drugs which are defined as “those proteins or other biomolecules (such as DNA, RNA, heparin, and peptides) to which the drug directly binds, and which are responsible for the therapeutic efficacy of the drug.”³⁵⁶ I excluded drug-target pairs with these mechanisms of action: agonists, activators, biopharmaceuticals, channel-openers, modulators, activators, allosteric antagonists, partial agonists, inverse agonists, DNA and RNA inhibitors, “cell membrane inhibitors,” releasing agents, and chelating agents. Then I retrieved the available binding measurements for the remaining “targets” from ChEMBL27³⁵⁵ with these curations: measurements lacking a pChEMBL value or with pChEMBL values expressed in any relation other than “equal to” like “smaller than” or “bigger than” were excluded; measurements expressed in other than IC_{50} or K_i values were excluded; based on a previous study on the comparability of measures of inhibitory activity,³⁵⁷ 0.30 was added to pChEMBL values of measurements expressed in IC_{50} values to make the measurements more comparable; pChEMBLs of molecules with more than one remaining measurement were averaged, and one final pChEMBL was recorded for each ligand. After excluding “targets” with less than 100 remaining ligands, I calculated the percentile rank (inclusive) of the affinity of the approved drugs among the remaining ligands for each target. Percentile ranks of all salt and protonation alternative forms of each drug (available

in ChEMBL) were averaged, weighted based on the count of measurements for each form.

2.3.3. Results and Discussion. While affinities of a notable number of approved drugs for their therapeutic “targets” are relatively low, most of them incline toward the highest percentile ranks (Figure 5). (The detailed data for all of the drug-target

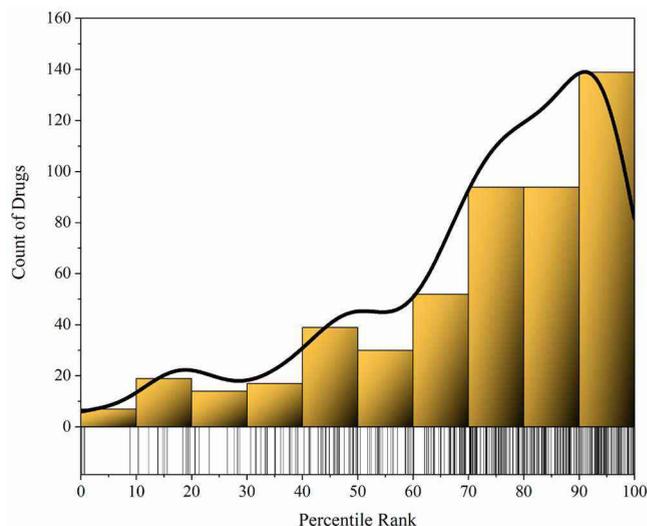


Figure 5. Percentile ranks of the affinity of approved drugs among all ChEMBL ligands of their therapeutic “targets.”

pairs are available in Supporting Information 4, and the summary data are available at Supporting Information 5.) This suggests that binding to “targets” with high affinity is relevant for therapeutic effects. Considering this alongside the minor contribution of target-based drug discovery to approved drugs and the numerous “off-target” therapeutic mechanisms of “target-based” drugs, it can be stated that binding to single “therapeutic targets” with high affinity is only a single aspect of a drug’s therapeutic effect on phenotypes.

2.4. Problems with the Theoretical Foundation of Target-Based Drug Discovery. We can reach a more definitive conclusion regarding the efficiency and rationality of target-based drug discovery by assessing the soundness of its theoretical basis.

2.4.1. Where Does the Reductionism of Target-Based Drug Discovery Come from? In an introductory speech on drug discovery and design I heard a few years ago, the human body was likened to a clock, a disorder was likened to a defect in a cogwheel of this clock, and the purpose of drug discovery was presented as designing a molecule which could bind this defective cogwheel. This simile showcases a deep-seated fallacy of target-based drug discovery: The functioning of the human body is presumed to be comparable to that of a machine. The machine mindset toward biological systems is a reductionist fallacy that has been pervasive for a few centuries.^{358–363} It stems from our humane approach to designing and building systems. When we aim to design and build a specific system, while designing it, we design each part with specific functions in mind for that part in the eventual function of the whole system. Because of this, each function or dysfunction of a car or a spaceship can be traced back to specific parts by a *chain of tasks*. The fallacy of the machine mindset is its presupposition that this delineated chain of tasks between parts and functions is universal among all systems. Biological systems are not the result of the

same approach to designing systems. They are highly complex and the result of evolution by means of selection. Selection does not assign specific roles to parts. It only selects among the diverse ultimate outputs and phenotypes of systems created by random variations.

All organisms, similar to cities, the Internet, and the stock market, are *self-organizing*^{364–366} complex systems. Their parts are not *chained* to their behaviors. Even though some elements may have accentuated roles in some functions or dysfunctions, there is usually no clear-cut and separable delineation.^{363,367} This leads to several general distinctive features in complex systems compared to chained systems: extensive multifunctionality of different parts;³⁶⁸ continuous and spectral, rather than clear-cut and binary-like causal relationships between the states of parts and systems' ultimate behaviors;³⁶⁹ capability of “self-control” by frequent and extensive feedback between the individual parts and the whole system;^{362,370,371} extensive redundancy;^{372–374} vestigiality;³⁷⁵ and degeneracy or multiple realizability, in which several nonidentical sets of processes yield identical ultimate outputs.^{125,376–378}

Thus, a central problem with the theoretical framework of target-based drug discovery is that following the fallacy of the machine mindset and neglecting the differences between complex and chained systems, it has a too simplistic attitude toward the organization and function of biological processes. See ref 147 for a mathematical discussion of the implications of the complexities of biological systems and “the impossibility for a stimulus imposed on a single node of a network to generate a substantial modification of the general system behavior when in the presence of non-strictly linear causal chains.”

2.4.2. Where Does the Efficiency of Higher-Level Observations Come from? We have presented a significant amount of evidence to support the contention that phenotypic drug discovery is more efficient than reductionist target-based drug discovery. But why is that? Is it only because of the fact that many disorders are not reducible to a single protein? If so, can drug discovery based on multiple targets, as in polypharmacological approaches,¹⁴³ be similarly efficient?

Fortunately, integrated information theory (IIT) provides a mathematical and formal framework³⁷⁹ to investigate this.³⁸⁰ Although this formalized theory, whose predictions are corroborated by empirical and mathematical evidence,^{381–386} is under investigation and has received some criticism for its validity in explaining consciousness,^{387,388} its applicability for investigating causal structures of diverse systems from the “intrinsic perspective” of systems themselves is well-documented.^{382,383,389–393} Succinctly, IIT investigates “how the parts of the system, by being in a specific state, constrain the potential past and future states of the system itself”.³⁹⁰

Based on IIT, it has been shown that describing the states of systems at spatiotemporally coarse-grained higher levels can increase information and intrinsic cause-effect power (Φ) (Figure 6).^{378,389–391,394–397} This increase is mainly because of the increased captured specificity of a system's mechanisms at higher levels as noisy (indeterministic) and degenerate micro elements get grouped into more deterministic and less degenerate higher-level descriptions. Later, along with confirmation in a biological model, it was demonstrated that spatiotemporal higher-level descriptions can provide even more intrinsic cause-effect power through *black-boxing* compared to average-based coarse-graining, especially in systems with heterogeneous, integrated specialized parts, epitomized by organisms.^{391,394} Black-boxing was first proposed in cybernetics

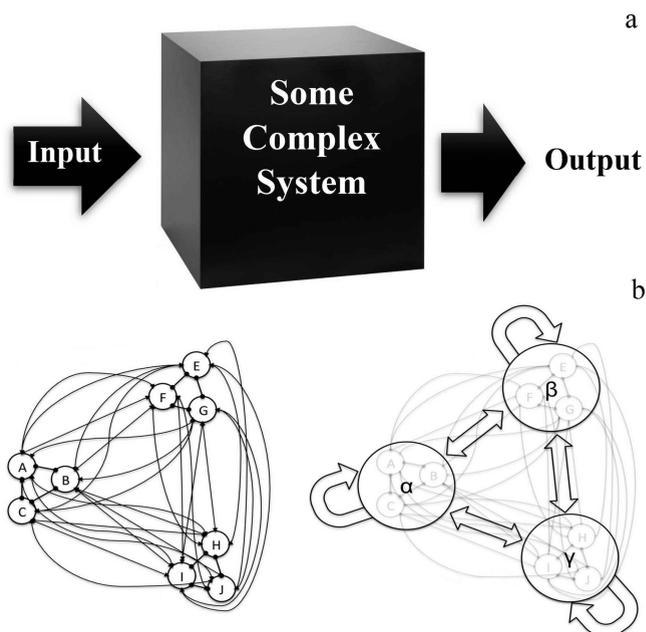


Figure 6. Two methods of going from lower to higher levels. (a) Black-boxing; (b) average-based coarse-graining; from ref 389. Copyright 2013 by National Academy of Sciences.

to enable the modeling of highly complicated and complex systems by hiding their inner workings and only taking into account their inputs and outputs.^{398–400} It should be noted that, as one of the fathers of cybernetics, Ross Ashby, articulated, “Black Box theory is, however, even wider in application than these professional studies. The child who tries to open a door has to manipulate the handle (the input) so as to produce the desired movement at the latch (the output); and he has to learn how to control the one by the other without being able to see the internal mechanism that links them. In our daily lives we are confronted at every turn with systems whose internal mechanisms are not fully open to inspection, and which must be treated by the methods appropriate to the Black Box.”⁴⁰⁰ It can be said that coarse-graining and black-boxing increase cause-effect power and informativeness by capturing simpler higher-level attractor states of highly complex lower levels^{147,401} and parameter space compression.⁴⁰² References 403–416 present a few other examples of increased simplicity and informativeness at higher levels.

All of these imply that even if target-based drug discovery recorded the effects of molecules on all proteins and every other single component of the human body,^{143,147} as in a hypothetical and impractically ideal polypharmacological target-based scheme, it would still have inferior efficiency compared to phenotypic drug discovery. Because it investigates the effects of molecules on the human body at higher levels (*black-boxing*), phenotypic drug discovery is endowed with superior cause-effect power and informativeness. This is notably crucial in the context of what question is the best to ask and what variable is the best to target in generative and predictive machine learning models used in drug discovery.^{58,59}

3. TARGET-BASED DRUG DISCOVERY IS VALUABLE

Throughout the history of drug discovery, various technologies, including computational chemistry, high-throughput screening, and combinatorial chemistry, have emerged that, at first, garnered significant attention and optimism but, over time,

their limitations also came into focus. These tools have now become essential components integrated into many drug discovery campaigns, albeit with realistic expectations. The data analyzed in this study suggest that a similar awareness of the limitations of target-based drug discovery is needed in the field. However, it should be acknowledged that the numerous target-based tools which have been developed during the previous decades can be of immense assistance in the path forward.

First, some disorders, such as monogenetic Mendelian disorders, which can be reduced to single or a few proteins are, to varying extents, amenable to be approached by target-based drug discovery. The feasibility of reducing some disorders to a few proteins is also illustrated by the success of some monoclonal antibodies. Second, target-based drug discovery is an important asset in the context of analog-based drug discovery for modifying and refining structures. Analog-based drug discovery is itself a valuable tool for obtaining incremental, yet still important, improvements in medications.¹⁵³ Additionally, gathering sufficient and suitable higher-level data might be too inefficient and burdensome for some disorders. Among such burdens, the possible need to sacrifice a considerable number of animals is noteworthy, even though technologies like organoids, organs-on-chips, and *in silico* testing can mitigate this need. Target-based tools can greatly contribute in these cases. Another important role of target-based tools is analyzing the lower-level basis of therapeutic effects. The lower-level data obtained from target-based approaches can be employed in approaches like systems biology, systems pharmacology,^{139–143,147} and multi-scale modeling⁴¹⁷ in order to help study how therapeutic effects emerge from lower-level phenomena. Such analyses can be of great value when they are appropriately integrated into drug discovery frameworks that try to derive benefit from both lower-level and higher-level data, like the framework suggested below.

4. CONCLUDING REMARKS

Based on the large amount of data that we have analyzed, the currently dominant reductionist approaches in drug discovery seem to be inefficient. Instead, prioritizing higher-level observations in selecting and optimizing molecules seems to be an evidence-based approach to increase efficiency. We have seen that rational drug discovery emerged from the attempts to guide and focus the empirical screening of random substances based on available scientific evidence. It can be said that reductionist target-based drug discovery is irrational in this sense as the available scientific evidence seems to contradict its methodology. The key problem and deviation in the transition from rational drug discovery to reductionist target-based drug discovery has been the extent of the employed reductionism. There is a large difference between rational drug discovery using the knowledge of the mechanism-of-action of drugs and, on the other side, the attempt of reductionist target-based drug discovery to reduce the therapeutic effects of drugs to single “target” proteins. For example, the five great pioneers of rational drug discovery mentioned earlier, Ehrlich, Hitchings, Elion, Black, and Janssen, four of whom have received Nobel Prizes in physiology or medicine, discovered all of those numerous approved drugs based on phenotypic observations,^{89–95,97} despite all of the underlying hypotheses that they had developed and used to direct these observations^{88,96,98–103} (see [Supporting Information 1](#)).

The important point is that, generally, therapeutic effects cannot be reduced to a molecule binding to a few proteins. This irreducibility was illustrated in [section 1.6.2](#) and in [Supporting](#)

[Information 3](#) where we found out that many of the approved drugs with target-based origins benefit from numerous off-target mechanisms for their therapeutic effects. By solely focusing on a single component of therapeutic effects, reductionist target-based drug discovery severely limits its efficiency. In contrast, phenotypic observations have a more direct and closer connection to the ultimate sought-after therapeutic effects. By black-boxing^{398–400} the immense complexity of the body and its disorders, phenotypic drug discovery can circumvent all of the complexities inside the body and directly aim for the ultimate goal, which is a therapeutic effect rather than a hypothetical, lower-level component of that goal. This more direct and closer connection can provide higher predictivity, which itself has a substantial effect on the approval rate.^{49,58,59}

It might be argued against my criticisms that target-based drug discovery exploits the benefit of phenotypic observations in animals and humans, to varying extents (see [ref 418](#) for an example). Indeed, this is true and was the basis of our investigations in [section 1.6.2](#). However, as pointed out earlier, the problem is that phenotypic observations within target-based drug discovery do not primarily inform the design of structures since they are only used as terminal filters in a one-way serial funneling manner^{46,56,57} (see [Figure 6](#) of [ref 62](#) for an illustration of this point). The structures of molecules are designed in the first place based on their binding affinity to the target and only filtered in the last steps based on their therapeutic effects. In contrast, in phenotypic drug discovery, molecules are selected based on directly observing the phenotypic effects of all molecules. As demonstrated in [section 1.6.2](#) and [Supporting Information 3](#), the binding of a molecule to single proteins is but one component of therapeutic effects, and there may be too weak a correlation between binding to a single target with high affinity and eliciting a therapeutic effect. Therefore, many drugs that are filtered out in the initial steps due to their low binding affinity may actually possess far more potent therapeutic effects than those that get selected based on their high binding affinity and are even subsequently selected in animal studies. In other words, the low predictivity of discovering drugs based on their binding affinity to a few proteins significantly limits and lowers the predictivity of the whole pipeline of a drug discovery framework whose cornerstone is the binding affinity of a molecule to a single protein instead of the therapeutic effects themselves.⁴⁹ This implicates any such approach, albeit some have tried to balance the reductionism of target-based drug discovery by considering factors other than binding a single target, like tissue exposure and the differences that any individual patient may have.^{419,420}

The increased predictivity that higher-level observations can provide has important implications for the application of artificial intelligence and machine learning in drug discovery. The presented data suggest that, generally, these powerful technologies are not currently being used to answer the right question.^{58,59} The ultimate goal is to design and select molecules with desired therapeutic effects on phenotypes, and the question needs to be posed commensurate with this objective.^{49,50} Nevertheless, based on target-based drug discovery, this goal is segmented and reduced to ancillary⁵⁸ goals like designing molecules with higher affinities for a single “target”;⁴²¹ ancillary goals which, based on the evidence presented here, may have little to do with that ultimate objective. Drawing upon our discussion in [section 1.6.4](#), selecting and optimizing molecules based on therapeutic effects themselves, rather than a single component of these effects, can provide far more cause-effect

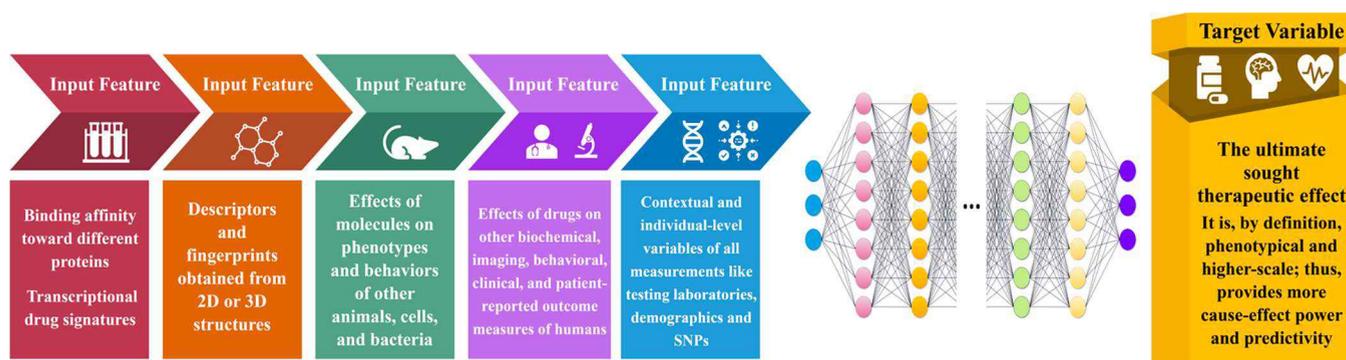


Figure 7. A preliminary proposal for a drug discovery approach which respects the primacy of therapeutic effects and gets benefit from both the tools which have been used in target-based drug discovery and the immense potential of artificial intelligence. Patterns can be recognized by various machine learning methods (e.g., deep neural networks as in this figure) between the structures of molecules and their aimed therapeutic effects. The data of the effects of drugs on lower levels and mesoscales and contextual and individual-level variables of the measurements can also be added to the input data to increase the accuracy of the recognized patterns and the trained model.

power. Apart from the rate of successfully demonstrating therapeutic efficacy in clinical studies and securing marketing approval,^{49,58,59} this can greatly influence the magnitude of the effect size, the clinical significance, and the real-world value of approved drugs;^{422,423} important aspects of approved drugs that, as we discussed early in the article, have been the subject of criticism by experts and available evidence.

As a very preliminary proposal, it is conceivable to develop machine learning models whose target variables would be measures of the therapeutic effect of molecules in humans or some highly predictive model. The input features of these models could be the diverse variables of the effects of drugs on lower levels; e.g., the binding affinity of drugs to various proteins, as in proteome-wide affinity fingerprints, transcriptional drug signatures, and descriptors and fingerprints obtained from the 2D or 3D structures of the molecules themselves (Figure 7). A potential starting point for building such models could be mining the animal and human data available in the published literature (and also unpublished data like electronic health data,^{424–426} patient-reported outcomes,⁴²⁷ and proprietary data). This immense trove of data that has been obtained at the expense of millions of lives, billions of dollars, and decades of research can be mined and capitalized through approaches like systematic review. Contextual and other individual-level variables can also be added to the input features to enhance accuracy. Of course, this framework is very preliminary, and the gathering of sufficient data with acceptable quality, both at lower and higher levels, might be impractical in many cases to build decent machine learning models. Nonetheless, such an approach, which may be termed *systematic review with cheminformatics meta-analysis*, can provide valuable initial qualitative insights even in these cases.⁴²⁸

We may hope that after becoming aware of the limitations of target-based drug discovery, having been armed with its capabilities and advanced technologies like machine learning and deep learning, high-content imaging, high-throughput phenotypic assays,^{429,430} wearable biosensors,⁴³¹ Internet-of-things, organoids,^{432,433} and electronic health data,^{424–426} while also paying more attention to conceptual progress,⁴³⁴ we will not only be able to surpass the current low productivity but even to supplant current gold-standard drugs with safer and far more effective alternatives.

5. LIMITATIONS

Emerging target-based approaches like protein-degrading technologies have the potential to alleviate the overall inefficiency of target-based drug discovery in the future; however, because of their recent emergence, they were not represented in this analysis.

Concerning section 1.6.1, it must be noted that there are no established criteria and definitions to determine which drugs should be classified as target-based or phenotype-based. Consequently, the definitions provided here might be contested. For instance, one could argue that any drug discovered with a specific “target” in mind should be considered target-based. It should be remembered that terms like target-based, phenotype-based, discovery origin, and drug-class are all abstract and arbitrary concepts and constructs, and any attempt to find concrete definitions in the outside world may be futile. Given the lack of pre-established definitions, the definitions used in this analysis are inevitably subjective. Nevertheless, I have tried my best to provide simple definitions that would be pragmatic and maximally useful for our purpose and also would provide the most objectivity in the categorizations.⁴³⁵ These criteria also align with those employed in the seminal study of Swinney and Anthony.⁵⁴ Furthermore, since the process of drug discovery is highly complex and unique for each approved drug, attempting to fit it into discrete and concise categories can introduce subjectivity in both defining and assigning the categories,^{436,437} I have tried to mitigate this binary bias by trying to fully document the path I went through to identify and assign each discovery origin. I also highlighted (in yellow) the parts which better display the rationale behind the assigned labels. These facilitate remaining conscious of the whole process of the discovery of each drug beyond the discrete labels and their statistics.

I was not able to find the discovery origins of several drugs. In some cases, the discovery origin was not unambiguously identifiable, and it was not recorded what observation first identified a relationship between a therapeutic class and its therapeutic effect. The discovery origins of those drugs whose accurate discovery accounts were not found but were undoubtedly discovered based on phenotypical observations, according to their discovery year and the trends of the discovery year, were categorized as nonhuman or *ex vivo* phenotype. There were instances where I found a discovery-related paper, for example in PubMed, but could not find its full-text webpage. Since feature trees are biology-agnostic, establishing a static

cutoff limit for defining analogs was not feasible. For example, although mechlorthamine and chlorambucil have near-identical pharmacophores, their distinct auxophores result in low global similarity. Consistent with the seminal study of Swinney and Anthony, biologics were excluded from the comparison of drug discovery approaches. I have attributed the discovery origins of all me-too drugs to the discovery origins of their leading first-in-class drugs. Confirmation bias may have influenced my search for discovery origins. I have included drugs that have received accelerated conditional approval.

Concerning section 1.6.2, the mechanisms of organisms' behaviors are hardly localizable.^{363,367,438} Even state-of-the-art methods like using si-RNA to illuminate the mechanism-of-action of drugs have many flaws,^{439–441} as do animal studies using pharmacological tool compounds to investigate the mechanisms of drugs. Many studies that I used in investigating the “off-target” therapeutic mechanisms of “target-based” drugs were of this kind. The relevance of some of the “off-target” mechanisms I have counted to the therapeutic effects of the drugs is based on general association rather than explicit evidence, particularly those derived from kinome inhibition assays. Furthermore, despite my best efforts, it is possible that some mechanisms that have been counted as independent therapeutic mechanisms may still be traced back to the same underlying mechanism.

As for section 1.6.3, while ChEMBL compiles ligands for each protein without imposing restrictions based on low or high affinity, it is plausible to hypothesize that the ligands retrieved from ChEMBL for each protein are enriched with molecules exhibiting higher affinities compared to randomly selected ligands whose affinities to that protein have not been measured. As a result, it is reasonable to hypothesize that the percentile ranks of the affinity of the approved drugs among random molecules would be higher than among the ChEMBL ligands for each protein.

■ ASSOCIATED CONTENT

Data Availability Statement

All relevant data are available in the Supporting Information section of the article. In Supporting Information 1, the titles of the drugs are hyperlinked to their web pages on Inxight Drugs¹⁵¹ or DrugBank.⁴⁴² These links have been archived, mostly between the 16th and 18th of June 2021, and can be accessed via Wayback Machine (web.archive.org). Below most target-tables in Supporting Information 2, there is a permalink to the STRING protein–protein interaction network for that target, as well as other relevant files. Code Availability: The analysis workflow used in section 2.3 is available at <https://kni.me/s/qI6JhDcsvL4JPmfB>.

SI Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acs.jmedchem.2c01737>.

Supporting Information 1: detailed discovery origins of all approved drugs (PDF)

Supporting Information 2: retrieved citations for the systematic review of “off-target” therapeutic mechanisms of target-based drugs (ZIP)

Supporting Information 3: “off-target” therapeutic mechanisms of “target-based” drugs (PDF)

Supporting Information 4: detailed data of the analysis of the percentile ranks of the affinity of approved drugs

among all ChEMBL ligands of their therapeutic targets (ZIP)

Supporting Information 5: summary data of the analysis of the percentile ranks of the affinity of approved drugs among all ChEMBL ligands of their therapeutic targets (XLSX)

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Notes

The author declares the following competing financial interest(s): I declare that I have two patent applications relevant to this manuscript.

Biography

Arash Sadri has recently completed his Doctor of Pharmacy (PharmD) program at Tehran University of Medical Sciences (2014–2022). Following his dream of discovering drugs, Arash has developed a keen interest in cheminformatics, computer-aided drug design, computational biology, and systems pharmacology. He has invented a new binding affinity prediction approach called Consensually Docked 5D-QSAR and serves as a research consultant at Aras Pharmaceutical. Additionally, Arash has founded Lyceum Scientific Charity to uphold two core principles of science: the pursuit of truth above all else and serving the public good.

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