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# **High-throughput prediction and analysis of drug-protein interactions in the druggable human proteome**

A dissertation submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy at the Virginia Commonwealth University.

by

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May 17, 2018

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May 2018

# Acknowledgment

First, I would like to express my deep gratitude to my supervisor Dr. Lukasz Kurgan for all his continuous motivation, guidance, support, encouragement, enthusiasm, knowledge, and time that have helped me over the last few years to become a better researcher. Dr. Kurgan is the best advisor for directing my development in work and also the best mentor for answering my concerns in life.

I am grateful to the members of my dissertation committee, Dr. Tomasz Arodz, Dr. Michal Brylinski, Dr. Krzysztof Cios, and Dr. Vladimir Uversky. Their constructive suggestions and inspiring comments helped me to clarify my understanding of the project and improve the quality of this work.

I would like to thank other members and visitors of the BioMine lab for their collaboration and support.

Thanks to my friends and all the people who helped me to complete my PhD journey.

Last, but not least, I would like to thank my family for their unconditional love and endless encouragement. Thanks to our parents for taking care of their kids and our kid. Thanks to my marvelous wife Xiao for everything. Also thanks to our son Jonathan for being cute and bringing happiness and surprise to our life.

## **Dedication**

This dissertation is dedicated to my wife, our parents, and our son.

## Preface

This dissertation is an original work conducted by Chen Wang. It includes materials and results from the following publications and submitted works.

- [1] Wang C, Hu G, Wang K, Brylinski M, Xie L, Kurgan LA. PDID: database of molecular-level putative protein-drug interactions in the structural human proteome. *Bioinformatics*, 32(4): 579-586, 2016
- [2] Wang C, Kurgan LA. Survey of similarity-based prediction of drug-protein interactions. Revision submitted to the *Current Medicinal Chemistry* journal on April 15, 2018.
- [3] Wang C, Kurgan LA. Review and comparative assessment of similarity-based methods for prediction of drug-protein interactions in the druggable human proteome. Submitted to the *Briefings in Bioinformatics* journal on May 1, 2018.

Chapter 3 of this dissertation is based on Ref [1]. Materials from Chapter 4 and 5 have been submitted for publication as Ref [2] and [3], respectively.

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# Abstract

HIGH-THROUGHPUT PREDICTION AND ANALYSIS OF DRUG-PROTEIN INTERACTIONS IN THE DRUGGABLE HUMAN PROTEOME

by Chen Wang, Ph.D.

A dissertation submitted in partial fulfillment of the requirements for the degree of Doctor of Philosophy at the Virginia Commonwealth University.

Virginia Commonwealth University, 2018

Supervisor: Lukasz Kurgan  
Ph.D., Qimonda Endowed Professor, Department of Computer Science

Drugs exert their (therapeutic) effects via molecular-level interactions with proteins and other biomolecules. Computational prediction of drug-protein interactions plays a significant role in the effort to improve our current and limited knowledge of these interactions. The use of the putative drug-protein interactions could facilitate the discovery of novel applications of drugs, assist in cataloging their targets, and help to explain the details of medicinal efficacy and side-effects of drugs. We investigate current studies related to the computational prediction of drug-protein interactions and categorize them into protein structure-based and similarity-based methods. We

evaluate three representative structure-based predictors and develop a Protein-Drug Interaction Database (PDID) that includes the putative drug targets generated by these three methods for the entire structural human proteome. To address the fact that only a limited set of proteins has known structures, we study the similarity-based methods that do not require this information. We review a comprehensive set of 35 high-impact similarity-based predictors and develop a novel, high-quality benchmark database. We group these predictors based on three types of similarities and their combinations that they use. We discuss and compare key architectural aspects of these methods including their source databases, internal databases and predictive models. Using our novel benchmark database, we perform comparative empirical analysis of predictive performance of seven types of representative predictors that utilize each type of similarity individually or in all possible combinations. We assess predictive quality at the database-wide drug-protein interaction level and we are the first to also include evaluation across individual drugs. Our comprehensive analysis shows that predictors that use more similarity types outperform methods that employ fewer similarities, and that the model combining all three types of similarities secures AUC of 0.93. We offer a first-of-its-kind analysis of sensitivity of predictive performance to intrinsic and extrinsic characteristics of the considered predictors. We find that predictive performance is sensitive to low levels of similarities between sequences of the drug targets and several extrinsic properties of the input drug structures, drug profiles and drug targets.

# Chapter 1 Introduction

Proteins are fundamental components of all organisms. They are essential to virtually all biological processes in cells. At the molecular level, proteins perform their functions by interacting with a wide range of molecules including other proteins, DNA, RNAs, and a variety of other smaller ligands.

Drug is a chemical substance that is used to prevent, treat, or cure a disease. Drugs work through molecular interactions with biological macromolecules, such as proteins and nucleic acids, which are typically referred to as drug targets. Approximately 90% of the existing drugs interact with human genome-encoded proteins [1], and this is why we focus on the druggable human proteome (collection of all the human proteins that are interacting with drugs). The molecular interactions between proteins and drugs typically inhibit or stimulate the cellular functions of proteins where such changes of functional states lead to the therapeutic effects or side effects [2]. Knowledge of the associations between drug compounds and their protein targets is essential for a wide range of pharmaceutical and bioinformatics studies. These studies include screening drug candidates that targets specific disease-associated genes/proteins [3-6], drug repurposing (searching for targets associated with diseases that are not yet known to benefit from the existing drugs) [7-11], discovery and characterization of side-effects that stem from the interactions with non-therapeutic off-targets [12-16], and elucidation of the druggable human proteome, which is

defined as the complement of human proteins that interact with drugs [1, 17-20]. Many databases house information on drug-protein interactions (DPIs) and capture knowledge on drugs and targets to facilitate these studies [21, 22]. However, these databases are relatively incomplete. They cover a small portion (~15%) of human proteins that are already known to be drug targets and for which the three-dimensional (3D) structures are known [23]. The databases are complemented by computational methods that generate putative drug-protein pairs on a large, up to the whole proteome scale. These predictions can be used to facilitate discovery of new DPIs by constraining the scope of expensive and time consuming in vitro and in vivo experiments that are employed to discover and validate the putative DPIs [24-26]. They are also utilized to develop databases of pre-computed putative DPIs [27-29] and were used to facilitate discovery of the therapeutic mechanisms and side-effects of drugs [16, 30, 31].

Computational prediction of DPIs typically incorporates information about drugs and structures or sequences of target proteins. Inspired by recent surveys [32-34], we define two categories of computational methods for DPI predictions: 1) Protein structure-based methods and 2) similarity-based methods that do not use 3D structures of the target proteins. The first group search for binding sites (the locations on the protein surface where binding occurs) from protein 3D structures. This group could be divided into two subgroups: molecular docking and structural alignment. The molecular docking models the physical interactions, including geometric complementarity, between a given drug and protein surface to detect potential binding sites. The structural alignment finds binding sites that are similar to known binding sites based on protein structure alignment. The second group of methods explores similarities between structures and profiles of drugs and non-structural information about their target proteins with known DPIs to predict novel DPIs. The protein structure-based methods use more information, and therefore the



predictive quality of their results is typically higher than the predictive quality of the second group of methods. However, the protein structure-based methods are limited to the proteins that have known 3D structures or for which structures can be accurately predicted. The similarity-based methods rely on protein sequences, drug structures and profiles that are more widely accessible than protein structures. For instance, in March 2017, 5870 protein structures are available in the RCSB Protein Data Bank (PDB [35], a comprehensive repository for three-dimensional structures of proteins and nucleic acids) for 19,077 human protein-coding genes [36], while there are 70,946 gene products (that include isoforms of proteins) in the Universal Protein Resource (UniProt [37]), a comprehensive repository for protein sequences and annotations [38]. In contrast to the protein structure-based methods, the similarity-based methods can be applied to predict potential protein targets. Additionally, in general, the protein structure-based methods, in particular the molecular docking approaches, are computationally more costly than the similarity-based methods. Altogether, the similarity-based methods cover a larger population of target proteins and are less computationally intensive compared to the structure-based methods.

## **1.1 Goals of the dissertation**

The objectives of this dissertation are to review and characterize a comprehensive collection of methods for the prediction of DPIs, assess their predictive performance, and provide access to their predictions. These objectives are addressed with the following three goals:

- 1) **Evaluation of protein structure-based predictions of DPIs and development and deployment of DPI database.** We empirically assess predictive performance of several protein structure-based DPI predictors for selected representative drugs over the entire

structural human proteome. We develop and deploy a large-scale database of putative and native DPIs for the entire structural human proteome.

- 2) **Review of the similarity-based DPI predictors.** We provide a comprehensive and in-depth review of a comprehensive collection of high-impact similarity-based methods for DPI predictions. This review substantially improves and expands over the existing reviews on this topic.
- 3) **Empirical assessment and comparative analysis of similarity-based DPI predictors and their consensuses.** We implement, empirically evaluate, and compare representative similarity-based DPI predictors on a novel and high-quality benchmark database. We include new ways to assess predictive performance, including analysis of the relation between the predictive quality and characteristics of the predictors. We also deploy implementations of the representative methods as a webservice.

In this dissertation, we first introduce background knowledge concerning the biological foundations of drug-protein interactions and basic information about computational predictions in Chapter 2. Then we report empirical findings and provide detailed discussions for each of the three goals stated above in Chapters 3, 4, and 5, respectively. Finally, Chapter 6 presents summary, conclusions, and possible directions for future works.

## **Chapter 2 Background on drug-protein interactions**

In this Chapter we introduce the essential knowledge concerning protein sequences and structures and their importance to characterize the molecular details of the DPIs. We discuss significance of computational prediction of DPIs and briefly review the current structure-based and similarity-based methods for the prediction of DPIs.

### **2.1 Protein sequence and structure**

Proteins are involved in virtually all cellular processes and functions. Examples of these functions include transcription, translation, gene regulation, cell metabolism, and molecular transport. Proteins are built from a sequence of 20 different amino acids that are linearly ordered in a polypeptide chain and connected by peptide bonds. These peptide bonds and  $\alpha$ -carbon atoms in the concatenated amino acids constitute of the protein backbone. The sequence of amino acids determines the shape of the corresponding protein and is typically referred to as protein primary structure.

The shape of a protein is formed to a large extent by interactions between amino acids. Protein structure consists of a collection of the local structures (segments in the primary structure). These segments of the local structures are called the protein secondary structures. Typical secondary structures include  $\alpha$  helices,  $\beta$  sheets,  $\beta$  strands, turns, coils, loops, etc. Formation of these

structures is mostly determined by hydrogen bonds that connect the sequence of amino acids in the protein backbone.

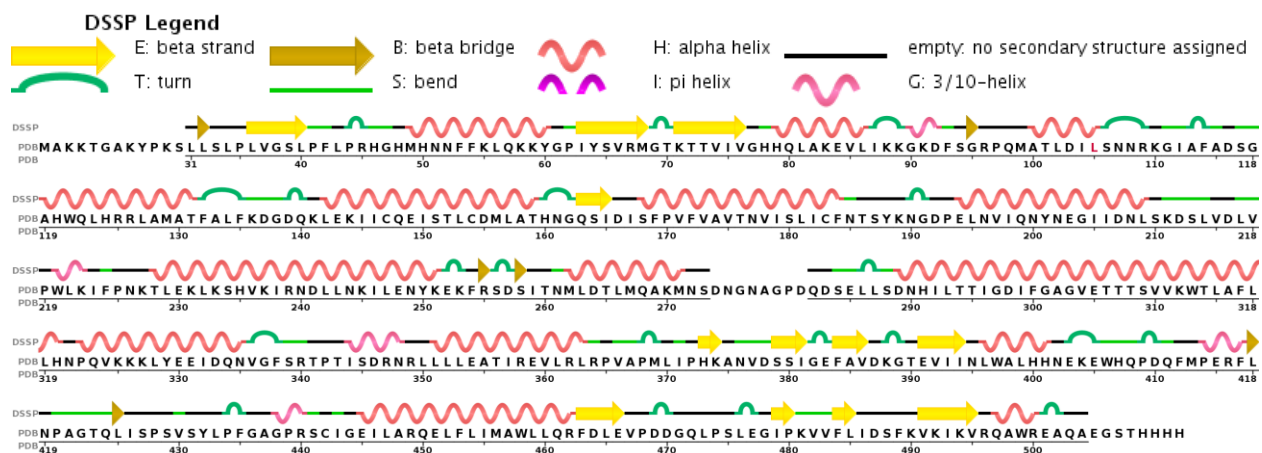
The set of secondary structures folds into a specific spatial arrangement, typically forming a compact globular molecule. This arrangement defines the protein tertiary structure. The process of folding the sequence into this three-dimensional molecule relies on hydrophobic interactions with solvent and tertiary interactions between amino acids. An illustration of hierarchical protein structures for an example protein (PDB ID: 4NKX [39]) is shown in Figure 1. The sequence (Figure 1a) is collected from PDB [35]. The secondary structure (Figure 1b) is annotated by Dictionary of Protein Secondary Structure (DSSP) [40, 41]. DSSP is a program that computes secondary structure assignments for PDB entries, which are graphically illustrated in PDB [35]. We use Protein Workshop [42] to visualize the tertiary structure using a ribbon style format (Figure 1c) and with rendering of its molecular surface (Figure 1d).

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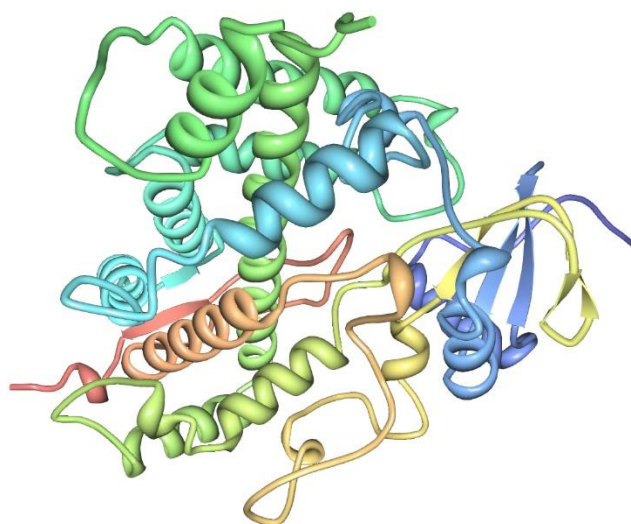
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PDB:
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PDB:
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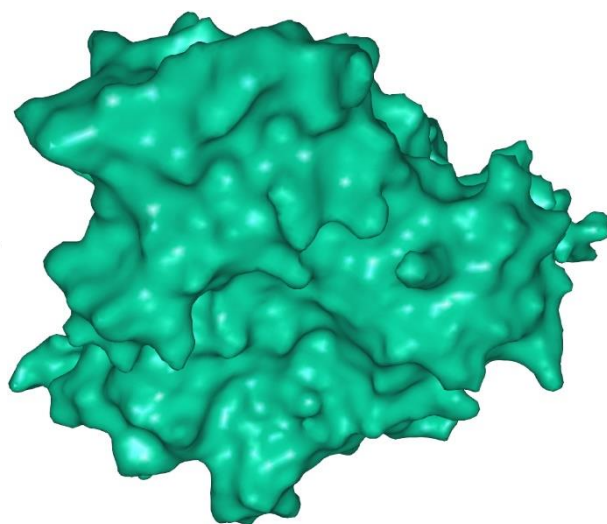
(a)



(b)



(c)



(d)

Figure 1. Protein sequence and structures of an example protein. This protein is collected from PDB ID: 4NKX [39]. (a) Sequence (primary structure) that is represented by single-letter codes for amino acids. (b) Secondary structure that is generated by DSSP [40, 41] and visualized in PDB [35]. (c) Tertiary structure that is visualized by Protein Workshop [42] and represented using ribbons-style format. (d) Molecular surface of the tertiary structure that is rendered with Protein Workshop [42].

## 2.2 Drug and drug-protein interaction

Drugs are chemical substances that are used to prevent, treat, or cure diseases in human and other living organisms. Drugs exert their therapeutic effects (desired) or side-effects (undesired) through interactions with biological targets including proteins, DNA, RNA, and membrane components such as lipid and carbohydrates [43]. There are significant challenges to accurately and comprehensively define targets, consistently map these targets to specific proteins and genes, and comprehensively compile and update repositories of targets [44]. We are very far from having all-inclusive and consistent repositories that include all existing drug targets and that specify a precise number for different categories of targets, especially for the nucleic acids and other non-protein partners. However, ongoing attempts have provided a consensus on the overall landscape of drug targets. An early and influential study in 2002 conceptualized the druggable genome for the first time and showed that the majority of marketed drug targets are proteins, with DNAs and other miscellaneous biomolecules accounting for only 3% of targets [18]. Recently, researchers estimated that 44% of unique human targets associated with approved drugs were G-protein-coupled receptors, nuclear receptors, protein kinases and ion channels, while 29% were enzymes and 15% were transporter proteins [45]; all of these are proteins. Furthermore, as reflected in their review [45] and a more recent update [1], these protein families make up between 93% and 95% of drug-target interactions. Additionally, a recent comprehensive analysis provided a similar perspective on the characteristics of current drug targets: 96% of 893 mechanistic drug targets were mapped to proteins while the remaining 4% of targets are nucleic acids and other biomolecules. Moreover, the protein targets are responsible for the clinical efficacy of 89% of 1578 FDA-approved drugs and involved in 93% of all identified drug-target interactions [44]. Considering that such predominant fraction of targets are proteins, we focus on the DPIs in this dissertation.

Drug discovery and development requires a large amount of money and time to address identification of the potential targets, to search for drug leads, to analyze massive quantities of data to select promising leads, to validate leads in a wet-lab, and to perform clinical trials [46]. High-quality identification and validation of DPIs is a vital prerequisite to investigate new drugs and determine their targets. This is important since drugs may interact with undesired targets (off-targets) that result in adverse events or side-effects, precluding further drug development and use. The chemical screening with cell assays is used to measure drug-protein binding affinity (how tightly a drug lead compound binds to a selected protein target). However, such experiments are limited in scope as they screen against a relatively small panel of protein targets [47, 48]. For instance, SafetyScreen44 panel screens against 44 targets recommended by four major pharmaceutical companies including AstraZeneca, GlaxoSmithKline, Novartis, and Pfizer [49]. Moreover, Novartis screens against interactions with a panel of 24 targets associated with severe side-effects and high hit rates [50], Pfizer screens against between 15 and 30 targets [51], and Roche uses a panel of 48 targets [52]. Therefore, there is a need to develop high-throughput computational methods for the prediction of DPIs. In particular, to develop methods that can screen a given drug against a comprehensive set of thousands of protein targets that make up the human proteome. The computational methods that identify putative DPIs by exploiting information about both drugs and proteins can be used for that purpose. Depending on whether the three-dimensional structure of a protein is used (known) or not, the prediction methods could be categorized into two groups: protein structure-based methods and similarity-based methods that do not rely on protein structures. Next, we define and discuss these two groups of methods.

## 2.3 Protein structure-based methods

A binding site is a location on the surface of a protein where the intermolecular interaction occurs. The structure of binding site typically looks like an open pocket or cavity that provides geometrical fit for the structure of the drug. The surface of the pocket not only offers geometric complementarity between protein and drug structures but also has to provide favorable physical characteristics like charge and hydrophobicity. Progesterone is an FDA-approved drug to support and regulate embryo implantation, pregnancy maintenance, and the development of mammary tissue for milk production [53]. Human cytochrome P450 17A1 and progesterone receptor are two representative targets of progesterone that have structures in complex with this molecule. Figure 2a shows the 3D structure of the cytochrome P450 17A1 (PDB ID: 4NKX [39]) and Figure 2c shows a binding site where this protein interacts with progesterone compound. The binding site is a pocket with a specific shape and size that fit the progesterone molecule which is displayed with red balls and sticks. Similar protein structures may have similar cavities/pockets that could interact with the same drug. Figure 2b is the structure of human progesterone receptor (PDB ID: 1A28 [54]) and Figure 2d is its binding site for progesterone. These two protein structures are globally dissimilar with noticeable differences (Root-mean-square deviation of atomic positions = 5.49 Å), which can be observed when comparing Figure 2a and Figure 2b. However, the binding sites, i.e., the pockets in Figure 2c and Figure 2d, are composed of similar spatial arrangement of secondary structures that include three long helices. Significant structural similarity between these two binding sites have been identified in Ref. [55].



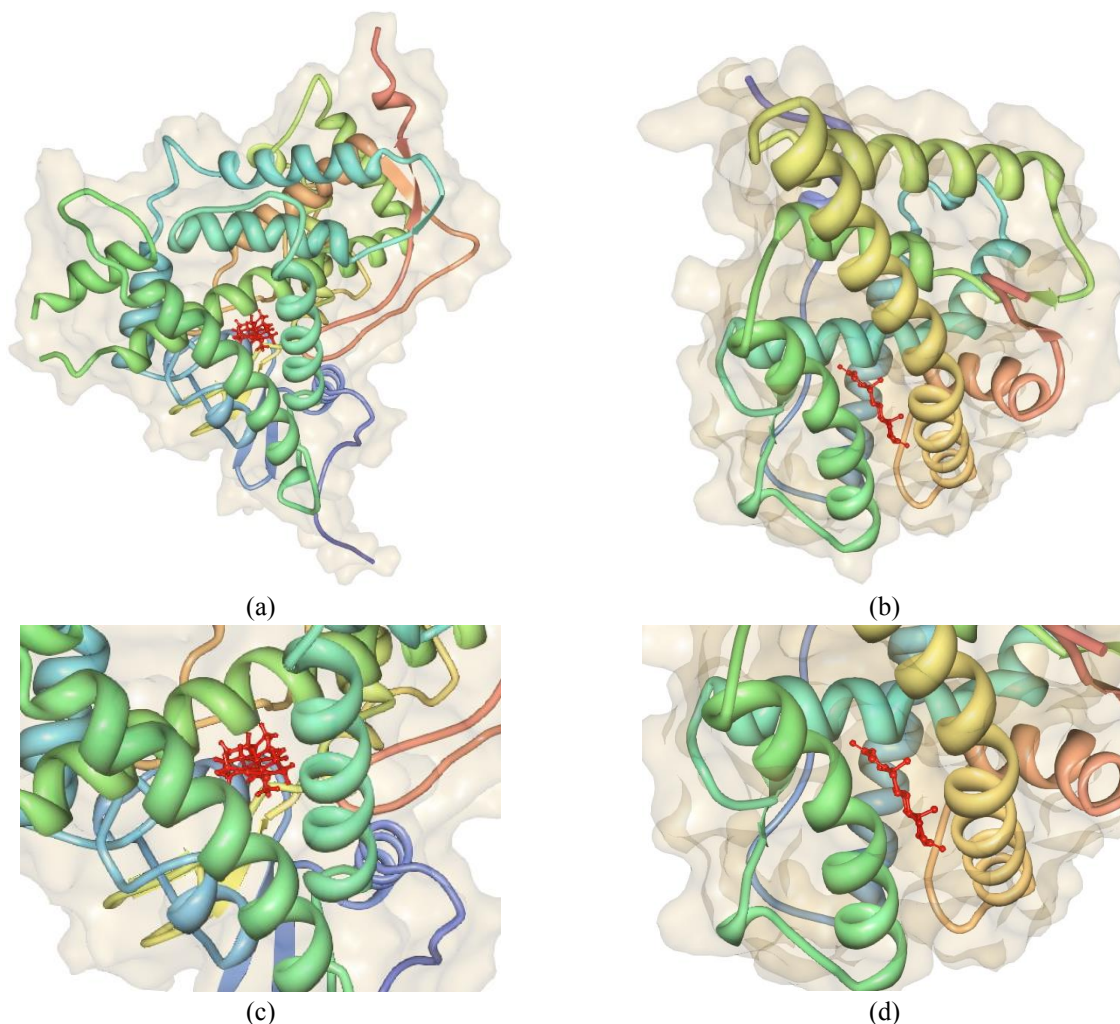


Figure 2. Two structurally dissimilar protein structures and their similar binding sites for progesterone. (a) The structure of human epidermal growth factor receptor inactive tyrosine kinase domain complexed with progesterone (PDB ID: 4NKX [39]). (b) The structure of human epidermal growth factor receptor tyrosine kinase domain complexed with progesterone (PDB ID: 1A28 [54]). (c) Progesterone and its binding site on 4NKX. (d) Progesterone and its binding site on 1A28. Protein molecules are represented by green surfaces. Progesterone molecule is represented by red balls and sticks. We use Protein Workshop [42] to visualize these structures.

The assertion that the same drug may bind to structurally similar proteins with similar binding sites provides an opportunity for prediction of DPIs using proteins structures. Thus, the protein structure-based prediction of DPIs for a given drug could be done by searching for sites that are similar to the known binding sites of this drug.

There are three classes of structure-based prediction methods that implement different trade-offs between accuracy and computational cost. These methods are based on searching for the

similar sites using a reduced representation of protein structure or complete all-atom structure of protein, and by docking the all-atom structure of ligand into the all-atom structure of the target proteins.

The fastest class of methods utilizes the reduced representation, usually in the form of a numeric vector that summarizes geometry and physicochemical properties of binding sites. Representative examples of such methods that find similar binding sites are PatchSurfer [56, 57] and method by Tomii's group [58]. The latter algorithm was recently used to create the PoSSuM database [59, 60] that includes 49 million pairs of similar binding sites computed from the known binding sites of 194 drug-like molecules over all protein structures from PDB. Given the large number of these putative binding sites it is likely that many of them are false positives and would have to be further screened via a more advanced method.

The second class of methods that is characterized by a lower throughput performs docking of a given compound into protein structures to find which proteins harbor binding sites that are complementary to the given ligand. Molecular docking predicts an optimized position and orientation of a drug molecule relative to a target protein molecule so that the drug fits the binding site and forms a stable interaction. Docking method relies on two steps. The first step is searching all possible rotational and translational orientations of the poses of a drug-protein pair. The second step is scoring and ranking the poses by a particular measurement that indicates the strength of binding affinity for each possible pose. An example platform that utilizes such type of docking to find targets of a given ligand, specifically focusing on screening a given drug against a large collection of targets, is INVDOCK [61]. Given the relatively high computational cost of docking, we highlight the availability of the BioDrugScreen database [28]. This database stores results of docking with AutoDock and scores these putative interactions based on several scoring functions,

such as AutoDock, GoldScore, X-Score, ChemScore, PMF, and DFIRE. This docking-based database covers about 1600 drug-like molecules and 2000 cavities on the surfaces of close to 1600 human proteins. However, these results are limited to interactions that are localized in cavities on the protein surface rather than exploring the whole surface. This limitation is motivated by a prohibitively high computational costs of searching the entire surface. BioDrugScreen uses Relibase+ algorithm [62] to identify pockets of interest, while INVDOCK uses an older algorithm by Kuntz and colleagues [63].

The third class of methods is complementary to docking. These methods are not constrained to surface pockets and produce accurate predictions of the drug-protein binding at the molecular level. They implement inverse ligand binding where structure(s) of the known drug-protein complex(es), called template(s), is used to predict other protein targets together with the corresponding binding sites for the same drug. There are two ways to find potential binding sites based on similarity to known binding sites, one based on the similarity of the corresponding protein fold and another based on similarity of binding pockets. The first approach is implemented by the FINDSITE [64, 65] and eFindSite [66, 67] methods and the other approach by the SMAP [68-70] and IsoMIF [71, 72] algorithms. The eFindSite predictor is an improved version of the FINDSITE method that uses meta-threading with the eThread [73, 74] and an advanced clustering algorithm [75] to optimize the selection of the ligand-bound templates for a given query structure. The eFindSite method was empirically shown to outperform FINDSITE and several geometrical methods for detection of pockets [66]. SMAP is designed based on a sequence order-independent profile-profile alignment (SOIPPA) which finds evolutionary and functional relationships across the space of protein structures [68-70]. SMAP utilizes a shape descriptor to characterize the structure of the protein template and the SOIPPA algorithm to detect and align similar pockets

between the query and template proteins. A recent study shows that eFindSite/FINDSITE and SMAP accurately predict targets even when the corresponding structure of the query protein and the template(s) are substantially different, i.e., they are from different SCOP folds [76]. IsoMIF applies GetCleft [77] algorithm to identify pockets on the surfaces of proteins, uses six chemical probes to represent atoms of pockets, and employs subgraph-matching algorithm to compute similarities of binding pockets so that putative binding sites could be predicted by comparison with known binding pockets [71]. A recent large-scale analysis utilizes IsoMIF to identify opportunities to repurpose drugs and to explain side-effects for ~400 drugs and ~8000 proteins and to validate quality of these putative interactions by comparing them with docking simulations [78]. We discuss details of the FINDSITE, eFindSite and SMAP methods in Chapter 3.

## **2.4 Similarity-based methods**

The protein structure-based methods utilize the 3D structure of the target protein(s). However, recent works estimate that only about 20% to 30% of the human proteins have 3D structures [79-81], which means that the protein structure-based methods are limited to a relatively small fraction of the human proteome. Moreover, they cannot be used for proteins with a substantial amount of intrinsically disordered regions [20] while recent works show that as many as 44% of human proteins contain at least one long (30 or more consecutive residues) disordered region [82-84]. Finally, the computational cost of the structure-based predictions for even this small set of proteins is typically high, particularly for the docking [32]. At the same time, the entire human proteome that has a full complement of ~70,000 sequences when including isoforms (source: UniProt reference proteome ID UP000005640) that can be covered by the similarity-based predictions of DPIs. The similarity-based methods are built based on two assertions: 1) similar drugs likely target

the same proteins; and 2) that similar targets tend to interact with the same drugs [32, 85-87]. This is motivated in part by a quote from James W. Black, winner of the 1988 Nobel Prize in Medicine: “the most fruitful basis for the discovery of a new drug is to start with an old drug” [88].

The similarity-based methods for the prediction of DPIs rely on two components: an internal database of known DPIs and a predictive model. They work in three steps. First, a user provides inputs in the form of drug structure, drug profile and/or its target sequence(s), whatever is available. In the second step, similarities between the input drug structure and/or profile and the structures and/or profiles of the drugs in the internal database are computed. If the target(s) of the query drug are known as input or can be retrieved from the internal database (the query drug is already included in the database), then the similarities between the query target and all targets in the database are also computed. In the third step, the predictive model combines the similarities to produce a propensity score that quantifies a likelihood that the query drug interacts with relevant protein targets that are included in the internal database, i.e., the propensity of putative DPI. Novel putative interactions generated by these methods could suggest potential ways to repurpose the existing drugs and also could explain molecular levels details behind side-effects.

Table 1. List of surveys concerning similarity-based DPI predictors. These surveys were published in the past five years. The bottom row corresponds to our review that is described in Chapter 4.

Survey	Year	Number of predictors reviewed	Number of recent predictors reviewed (published since 2013)
Ding et al. [32]	2013	10	2
Pahikkala et al. [89]	2014	2	1
Mousavian et al. [90]	2014	27	16
Chen et al. [21]	2015	17	10
Cichonska et al. [91]	2015	17	9
Lavecchia et al. [92]	2016	11	9
Hart et al. [93]	2016	8	6
Shahreza et al. [94]	2017	17	8
Fang et al. [95]	2017	10	5
Ezzat et al. [96]	2018	28	17
Hao et al. [97]	2018	12	9
Our review	2018	35	22

The similarity-based methods utilize different approaches to express and quantify the similarities. The predictive quality of the similarity-based methods is critically dependent on how the similarities are quantified and whether and how they are combined. Eleven survey articles that were published in the last five years have summarized the development and frontiers of the prediction of DPIs for the similarity-based methods [21, 32, 89-97]. Table 1 chronologically lists these surveys and summarizes the number of prediction methods that are analyzed including the number of recent methods which were published in the past five years. In this dissertation, we present our own review (bottom row in Table 1) of 35 selected similarity-based methods including 22 recent studies that appeared in the past five years. Compared to the existing surveys, our analysis is broader than most of the existing reviews (35 vs between 2 and 28 approaches in total) and more current (22 vs between 1 and 17 recent approaches). Criteria of selection of these approaches are described in Chapter 4. Besides the predictive models, some of these reviews also summarize the databases of DPIs [21, 22, 32, 91, 92, 94, 95] and the assessment of predictive results [32, 89, 96, 97] that are employed in prediction approaches. We present our review and compare it at a greater depth with the other surveys in Chapter 4.

# **Chapter 3 Evaluation of protein structure-based predictions of drug-protein interactions and development and deployment of protein-drug interaction database**

In this chapter we assess the predictive quality of three representative protein structure-based methods for the predictions of DPIs. Using results produced by these methods, we develop and deploy a DPI database that covers interactions between 51 popular, FDA-approved drugs and the proteins from the structural human proteome. This repository provides a query interface to search a comprehensive set of putative DPIs that are generated by the predictors, as well as annotations of native DPIs collected from relevant databases.

## **3.1 Motivation to develop a novel database**

The significant majority of the molecular targets of drugs are proteins and there are several databases of the already characterized DPIs. DrugBank [98-102] provides access to biochemical and pharmacological information about a large set of 7759 drugs, including 1600 FDA-approved compounds, and their known 4104 protein targets. Therapeutic Target Database [43, 103-107] offers a comprehensive coverage of over 20,000 drugs, including close to 15,000 experimental drugs, and their interactions with 2360 protein targets. This database also links targets and drugs

to about 900 diseases. Other databases expand beyond the drug molecules to cover small drug-like ligands. BindingDB [108-112] gives experimentally measured binding affinities between about 7000 known protein targets and a large set of almost half a million of small ligands. ChEMBL [113-116] contains structures, physicochemical properties and bioactivity (e.g. binding constants, pharmacology data) of drug-like small molecules. The current release of ChEMBL incorporates 1.7 million distinct compounds and 13.5 million bioactivity data points which are mapped to over 10 thousand protein targets, where the corresponding binding sites are defined at varying levels of granularity (protein, protein domain, or residue-level). SuperTarget [117, 118] includes about 6200 protein targets from several dozens of species and close to 200,000 drug-like compounds. It integrates drug-related information from BindingDB, DrugBank, and the SuperCyp database of cytochrome-drug interactions [119], adverse drug effects from SIDER [120, 121], drug metabolism, and pathways and Gene Ontology (GO) terms for the target proteins. The PROMISCUOUS database [122] integrates data from DrugBank, SuperTarget, and SuperCyp and covers about 6500 protein targets and over 25 thousands drug-like compounds that are annotated with side-effects. This database also provides facilities that can be used to predict novel targets based on the structural similarity between drugs and between side-effect profiles of drugs. STITCH [123-127] combines information from many sources of experimentally and manually curated interactions between small ligands and proteins including ChEMBL, PDB, DrugBank, Therapeutic Target Database, text mining of articles from MEDLINE and PubMed, and several other resources. It currently houses data on 390,000 chemicals and 3.6 million proteins. The recently released IntSide database [128] links about 1000 drugs with their human protein targets collected from DrugBank and STITCH, and with close to 1200 side-effects and other annotations of associated diseases, pathways, and cellular functions. While most of these resources summarize the



interactions at the protein or residue level, scPDB [129, 130] includes molecular-level (all-atom) information for native binding sites in proteins structures collected from PDB [35] that are suitable for docking of drug-like ligands. It includes molecular-level details of about 9200 binding sites (all-atom annotation of binding sites and list of ligand-binding residues grouped by various types of bonds) and binding modes (all-atom position of ligand inside the site) for 3600 proteins, and a summary of physicochemical properties of approximately 5600 drug-like ligands.

However, many of the established drugs interact not only with the intended therapeutic target protein(s) but also with other protein targets (off-targets). Individual compounds were shown to on average target 6.3 proteins [10, 131]. Given a high degree of incompleteness of this information [131, 132], the number of off-targets is likely substantially higher. To compare, DrugBank includes 15199 DPIs for 7759 drugs with the average number of targets per drug at 1.96, which further substantiates the claim of the incompleteness of the currently available data. This polypharmacology can be both beneficial, when a given drug can be repurposed for a different disease, and harmful, leading to the side-effects [132]. A couple of high-profile examples include imatinib that was repurposed for treatment of gastrointestinal stromal tumors [133] and sorafenib for the kidney and liver cancers [134]. The incompleteness of the data combined with the importance of polypharmacology motivates research towards the elucidation of novel and more comprehensive set of DPIs.

Conventional (non-computational) methods for the identification of novel off-targets rely on an in vitro counter-screen of a given drug against a small set of a few dozens of enzymes and receptors [49-52, 135]. Compared to the experimental screens, computational methods that find novel drug targets are more cost- and time-effective, allow screening of a larger number of targets and provide insights into the molecular-level mechanisms of DPIs [136]. These *in-silico* methods

are successful in the context of drug repositioning and identification of off-targets [137]. A couple of databases that focus on the putative protein-drug and druggable protein-protein interactions were recently released. BioDrugScreen [28] stores results of docking of about 1600 small drug-like molecules against 1589 known proteins targets in human, which were annotated based on DrugBank and HCPIN [138] databases. Docking was run for close to 2000 cavities on the surfaces of these proteins, for the total of about 3 million receptor-ligand complexes. Druggable Protein-protein Interaction Assessment System (Dr. PIAS) [139, 140] is a database of druggable protein-protein interactions (PPIs) predicted by a machine learning method. This database lists druggable interactions predicted from over 83 thousand PPIs in human, mouse, and rat, but they are not associated with specific compounds.

We developed Protein-Drug Interaction Database (PDID) that complements existing repositories and addresses the lack of access to a comprehensive set of putative DPIs [29]. This database relies on predictions generated by three representative protein structure-based methods, eFindSite [66, 67], SMAP [68-70], and ILbind [76]. These methods are complementary and independent of docking that was used in the BioDrugScreen database. They were also shown empirically to provide high-quality predictions of drug targets [76], and their results were already successfully used to predict novel off-targets. Examples include applications to find new off-targets of estrogen receptor modulators [141], cholesteryl ester transfer protein inhibitors [30], comtan [142], inhibitors of *Trypanosoma brucei* RNA editing ligase 1 [143], nelfinavir [31], raloxifene [144], and cyclosporine A [16]. We describe in detail and re-assess the selected three representative methods to provide a more recent estimate and comparative analysis of their predictive performance before we describe the PDID database.

## 3.2 Considered protein structure-based predictors

The fundamental principle of protein structure-based predictors is to transfer the binding sites from known drug-protein complexes to a protein that is structurally similar to these known drug-complexed proteins. There are two ways to measure the similarity between the input protein structure and the known drug-protein complexes: one applies the similarity of the corresponding protein fold, such as FINDSITE [64, 65] and eFindSite [66, 67] algorithms, and the other that exploits the similarity of binding sites, such as SMAP [68-70] and IsoMIF [71, 72] methods.

### 3.2.1 FINDSITE and eFindSite

FINDSITE predicts binding sites for an input protein using template protein(s) which have the structure(s) in complex with a given input drug [64, 65]. These template proteins come from a database of templates (a set of non-redundant high-quality structures of drug-protein complexes curated from the PDB database) that is part of the FINDSITE algorithm. FINDSITE accepts either an experimentally determined structure annotated in PDB or a putative structure modelled computationally with TASSER [145-147], MODELLER [148, 149] or PROSPECTOR\_3 [150], three accurate protein structure modelling algorithms. We use experimentally determined structures for the input proteins in our experiments. The protocol of FINDSITE is briefly described as the following four steps:

- 1) A threading algorithm, PROSPECTOR\_3 [150] is utilized to find template proteins for the input protein from the template database. PROSPECTOR\_3 threading recognizes template proteins which likely have similar structural folds when compared to the input protein based on sequence alignment and predicted secondary structure, given the sequence of the input

protein. The identified template proteins are supposed to be structurally similar to the input protein, no matter whether or not they have high sequence similarity to the input protein.

- 2) The template proteins that are known to be in complex with the input drug are selected from the template set which is obtained by the threading alignment. Then the template set is expanded by including homologous proteins of the current templates. Consequently, we get a set of template proteins that interact with the input drug, have known three-dimensional structures of drug-protein complex, are likely structurally similar to the input protein, and are possibly remotely homologous to the input protein.
- 3) A structural alignment algorithm, TM-align [151], is utilized to superimpose the structures of template proteins (including their drug-complexes) into the structure of the input protein. A set of superimposed atomic coordinates for each template protein is generated in this step.
- 4) The superimposed coordinates of the center of the input drug in each template structure are clustered based on spatial distance with a threshold distance equal to  $8\text{\AA}$ . The geometric center of each cluster is a predicted position of the input drug into the input protein structure, which represents a putative binding site for this input drug-protein pair. These predicted binding sites could be ranked by the number of templates from the corresponding cluster where each binding site (cluster center) comes from.

Besides a putative position of the center of the given drug, FINDSITE also outputs other information that allows ranking predictions across different input proteins: (i) TM-score, a structural alignment score generated by TM-align; (ii) root mean square deviation (RMSD) of the C $\alpha$  atoms in the aligned region between input protein and templates by TM-align; (iii) alignment length which is number of residues aligned with the template protein structure by TM-align; (iv) fraction of templates that share the predicted binding site (cluster center); (v) sequence identity

calculated over the residues aligned by the TM-align; (vi) number of predicted binding sites; and (vii) number of predicted binding residues.

As an improved version of FINDSITE, eFindSite combines multiple threading approaches by machine learning models to select template proteins and employs an advanced clustering algorithm to predict the putative binding sites [66, 67]. More specifically, eThread [73, 74], a meta-threading approach that applies Naïve Bayes classifier to build a consensus threading alignment from ten individual threading algorithms, is utilized to identify template proteins; this concerns the steps 1) and 2) of FINDSITE. Moreover, eFindSite also improves steps 3) and 4) of FINDSITE. This concerns an approach to superimpose template structures to the input protein and to cluster binding sites in the template structures. First, Affinity Propagation [75] is utilized to cluster the structures of template drug-protein complexes based on structural similarities between templates computed with fr-TM-align [152]. Second, the clustered template structures are superimposed into the structure of input protein. Finally, the resulting superimposed locations of drug from each clustered template constitute the predicted position of the input drug, which in turn can be used to annotate putative binding sites in the structures of the input proteins.

### **3.2.2 SMAP**

SMAP works by generating potential binding pockets in the input protein structure and next finding whether these pockets are similar to the known binding pockets in the drug-binding proteins [68-70]. It relies on a geometric representation of protein structure to characterize binding sites [68] and a sequence profile alignment to compare binding sites [69]. The protocol of SMAP algorithm is summarized in the following five steps:

- 1) SMAP reduces the representation of an input protein structure by using only the coordinates of alpha carbon ( $C\alpha$ ) atoms which are the first carbon atoms attached to the carboxyl group

of an amino acid. These  $C\alpha$  atoms are represented as vertices in a graph. A convex hull algorithm, Delaunay tessellation, is applied to partition the  $C\alpha$  atoms into tetrahedra (triangular pyramids) that are defined by the graph edges [68].

- 2) The Delaunay tessellation is constrained by removing tetrahedra that include edges (atomic distances) longer than  $30\text{\AA}$  because such distance implies a open binding pocket on the molecular surface, not an enclosed sphere. The outside layer of the remained convex hull defines a environmental boundary which surrounds the input protein and its binding pockets. Next, the tetrahedra larger than  $7.5\text{\AA}$  are removed. This cut-off length is related to the average radius between two amino acids that are in contact with each other. The remaining tetrahedra on the outside of the structure form a protein boundary. The removed tetrahedra which are the tetrahedra located between the protein boundary and the environmental boundary, make up the possible positions where drugs could be located.
- 3) The distance and orientation of each  $C\alpha$  atom to the protein boundary and environmental boundary is computed. Based on these values, a geometric potential is computed using specific formulas listed in Ref. [68] for each  $C\alpha$  atom. The geometric potential quantifies the positions of a  $C\alpha$  atom and its neighbor atoms relative to the environmental boundary, and the relative positions between this  $C\alpha$  atom and its neighbor  $C\alpha$  atoms.
- 4) The possible positions of drugs obtained in step 2) are clustered based on their overlap in circumscribed spheres of the corresponding tetrahedron. The cluster centers represent the predicted potential positions of the drugs that could bind to the given protein. If a  $C\alpha$  atom is located within  $10\text{\AA}$  from the predicted potential positions and the edge between these two atoms are not cut by other circumscribed spheres, this  $C\alpha$  atom (that represents a drug-binding

amino acid) is predicted as a part of a binding site. This way the amino acids that make up specific binding pockets are defined.

- 5) The predicted potential positions of drugs generated in step 4) represent a candidate drug-binding position but without specifying for which specific drug. SMAP uses a sequence order independent profile-profile alignment (SOIPPA) method to align the candidate drug-binding sites (the corresponding amino acids) in the input protein to the known binding sites in the template proteins which are found in complex with the input drug in PDB [69]. Next, a candidate binding site is mapped to a known binding site of the specific input drug if the SOIPPA alignment shows that these two sites are similar enough. SOIPPA algorithm is designed to compare and align two subgraphs that are extracted from the geometric representations of the input protein and the template protein. The computation of the alignment uses the geometric potential scores computed in step 3). The binding sites from the template protein are aligned and superimposed as the candidate sites in the input protein. A alignment score is computed based on the position specific score matrix [153] to measure the similarity of these binding sites.

SMAP outputs seven measurements that can be used to rank binding site similarity between the input protein and the template protein: (i) local alignment (pairs of aligned residues) between drug-binding sites in the input and template proteins; (ii) alignment score generated by SOIPPA; (iii)  $p$ -value that estimates the statistical significance of the alignment score by considering a random set of PDB chains; (iv) volume of overlapping binding pockets between the input protein and the template protein computed in the structure of input protein; (v) the same volume computed in the structure of template protein; (vi) Tanimoto coefficient between the two proteins; (vii) root mean square deviation (RMSD) between the binding sites in the input and template proteins.

### 3.2.3 ILbind

The inverse ligand binding (ILbind) predictor is an ensemble machine learning predictor of drug-binding sites for a specific input drug. ILbind uses selected outputs (the outputs were chosen based on an empirical feature selection process) generated by FINDSITE and SMAP [76] as its inputs. This meta-approach exploits the fact that FINDSITE and SMAP use complementary approaches for the prediction. FINDSITE's prediction is based on similarity of protein structures while SMAP's prediction is based on similarity of binding pockets. ILbind was designed to provide predictions for a wide range of drugs and nutraceuticals. First, a dataset of ~150 drugs was clustered into three structurally similar clusters. These clusters were represented by three drugs that correspondingly have diverse structures: N-Acetyl-D-glucosamine (NAG), Adenosine-5'-Diphosphate (ADP), and Palmitic Acid (PLM) [76]. Structures of five randomly chosen complexes of proteins with each of these three drugs were used to design ILbind, resulting in total of 15 configurations. Correspondingly, 15 Support Vector Machine (SVM) models were designed using a training dataset. A total of 14 outputs (features) from FINDSITE and SMAP were ranked by their average AUC values on the training set. Next, a wrapper-based best-first search to select features was applied using cross-validation on the training dataset. The search started from including only the top ranked feature, and added next feature from the ranked set of features to the feature set if the inclusion of this feature increased AUC value when compared with the feature set before including this feature. Between the 15 SVM models, the selected feature sets typically contain two or more features which correspond to the outputs from both FINDSITE and SMAP.

Given an input drug and the structure of an input protein, ILbind works in two steps:

- 1) Compute predictions with the 15 SVM models using the selected outputs of FINDSITE and SMAP as the inputs.



- 2) Use the consensus (average) of the 15 SVM predictions as the predicted propensity for binding to the input drug.

Since ILbind does not predict the putative position of the center of the input drug, these positions are borrowed from the outputs of FINDSITE and SMAP.

### **3.3 Assessment of predictive quality**

We assessed predictive performance of eFindSite, SMAP, and ILbind to demonstrate that predictions from these methods have practical value. This assessment was performed on a set of 25 representative drugs that are currently included in PDID. These compounds were selected from 25 clusters of chemically similar drug structures (one compound from each cluster) that were generated from the 355 drugs that could be found in complex with proteins in PDB at the time of the experiment. The evaluation follows the protocol from [16]. Briefly, native targets of the 25 drugs were collected from PDB, BindingDB, and DrugBank and we compare predictions from the three methods on the structural human proteome against these native drug targets. We clustered proteins in the structural human proteome at 90% sequence identity using BLASTCLUST [153, 154] and evaluated the results on the corresponding clusters, i.e., a given cluster is considered to be a native target of given drug (predicted to bind the drug) if at least one protein in this cluster shares at least 90% identity with a native target of that drug (at least one protein in this cluster is predicted to bind that drug). The clustering assures that the evaluation is not biased towards targets that are overrepresented with many structures of similar folds.

Empirical results demonstrate that the three methods are characterized by practical levels of predictive quality. The average AUCs over the 25 drugs of eFindSite, SMAP and ILbind equal 0.63, 0.74 and 0.76, respectively (Figure 3a). Although ILbind outperforms the other two methods,

which is expected given that it combines results of these methods and which is consistent with the results in [76], different methods perform better for different drugs. More specifically, eFindSite provides the highest AUC for 5 drugs, SMAP for 6 drugs, and ILbind for the remaining 14 drugs. Figure 3b gives average true positive rates (fractions of correctly predicted native targets) in the function of the fraction of predicted protein targets sorted in the descending order by the propensities for the interaction generated by each of the three predictors. This figure shows that 40% of the native targets (true positive rate = 0.4) are found among the top 4% of predictions from ILbind and SMAP and among the top 14% of predictions from eFindSite.

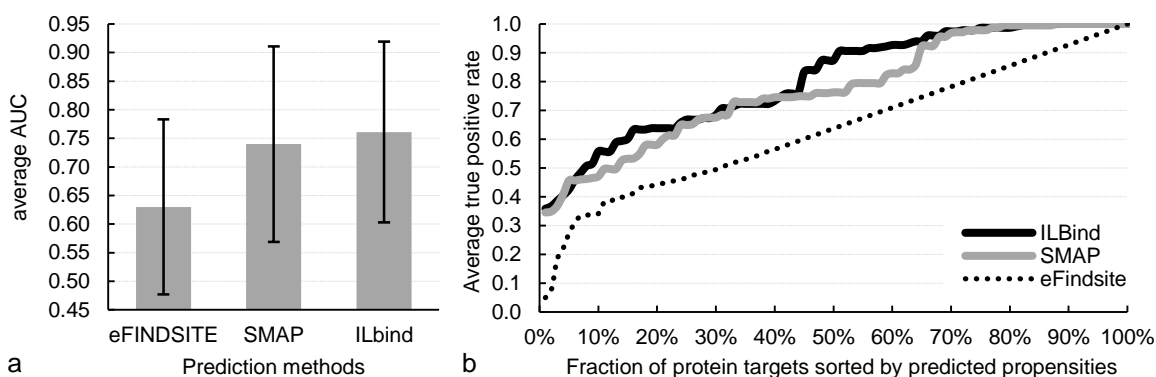


Figure 3. Predictive quality of eFindSite, SMAP, and ILbind for the 25 representative drugs. Panel a shows the average AUC computed over the 25 drugs; error bars give the corresponding standard deviations. Panel b shows average true positive rate (fraction of correctly predicted native targets) computed over the 25 drugs in the function of the ranking of predictions; the  $x$ -axis shows fraction of predicted protein targets sorted in the descending order by the predicted propensities for the interaction.

We observe that predictive performance of these three methods varies between compounds and depends on their size. Higher AUCs are characteristic for medium sized drugs (with a molecular weight between 200 and 400 g/mol) and lower AUCs for either small (below 200 g/mol) or large (over 400 g/mol) drugs. To compare, the average AUCs for the small/medium/large drugs for eFindSite, SMAP and ILbind are 0.56/0.68/0.58, 0.7/0.83/0.58, and 0.7/0.86/0.59, respectively. Example small and large compounds for which predictive quality is relatively low are salicylic acid (138.1 g/mol; average AUC over the three methods of 0.50), isoflurane (184.5 g/mol; 0.60),

suramin (1297.3 g/mol; 0.55), and cyanocobalamin (1355.4 g/mol; 0.57). Example drugs for which prediction are more accurate are naproxen (230.3 g/mol; 0.88), furosemide (330.7 g/mol; 0.94), and prednisone (358.4 g/mol; 0.87).

## **3.4 Protein-drug interaction database**

### **3.4.1 Contents and availability**

We collected the structural human proteome from PDB by removing low-resolution structures ( $> 3\text{\AA}$ ) and following [16, 141] we kept proteins for which sequences were mapped to human proteins in Ensembl [155]. More specifically, structures of chains with at least 90% sequence identity quantified using BLAST [154, 156] with default parameters to any human protein from 68th release of Ensembl were selected. As a result, we include a total of 9652 human and human-like high-resolution structures that correspond to 3746 unique human proteins. Protein chains that correspond to these PDB structures were mapped to UniProt [157] to facilitate mapping of proteins between PDID, PDB, DrugBank and BindingDB.

The PDID database includes drugs which were solved structurally in complex with at least one protein; this is necessary to predict targets. There are 355 such drugs in PDB which we extracted with PDBsum [158]. The current release 1.1 of PDID includes 51 drugs compared to the release 1.0 that had 26 drugs, all of which were selected from the 355 drugs. We clustered structures of the 355 drugs using their structural fingerprint expressed with Tanimoto coefficient and sampled at least one drug from each of the resulting 25 clusters to select the 51 drugs. Thus, the selected drugs comprehensively sample the structural drug space. These drugs are listed in Table 2 and include popular antibiotics, anti-inflammatory, anti-viral and anti-cancers agents,

immunosuppressants, and drugs for the treatment of osteoporosis, diabetes, heart attack, hypertension, edema, angina, glaucoma and other diseases.

Table 2. Drugs included in the current release 1.1 of PDID.

Drug name	Formula	PDB ID	# complexes	Primary use
acetazolamide	C <sub>4</sub> H <sub>6</sub> N <sub>4</sub> O <sub>3</sub> S <sub>2</sub>	AZM	22	treatment of glaucoma, edema and epilepsy
acyclovir	C <sub>8</sub> H <sub>11</sub> N <sub>5</sub> O <sub>3</sub>	AC2	5	anti-viral for herpes, chickenpox, and shingles
adenosine	C <sub>10</sub> H <sub>13</sub> N <sub>5</sub> O <sub>4</sub>	ADN	107	treatment of cardiac arrhythmia
alendronate	C <sub>4</sub> H <sub>9</sub> NO <sub>7</sub> P <sub>2</sub>	AHD	3	treatment of osteoporosis
ampicillin	C <sub>16</sub> H <sub>19</sub> N <sub>3</sub> O <sub>4</sub> S	AIC	8	antibiotic
bepidil	C <sub>24</sub> H <sub>34</sub> N <sub>2</sub> O	BEP	2	treatment of angina
caffeine	C <sub>8</sub> H <sub>10</sub> N <sub>4</sub> O <sub>2</sub>	CFF	10	stimulant
captopril	C <sub>9</sub> H <sub>15</sub> NO <sub>3</sub> S	MCO	5	treatment of hypertension
cerulenin	C <sub>12</sub> H <sub>19</sub> NO <sub>3</sub>	CER	8	antibiotic
chloramphenicol	C <sub>11</sub> H <sub>12</sub> CL <sub>2</sub> N <sub>2</sub> O <sub>5</sub>	CLM	16	antibiotic
chloroquine	C <sub>18</sub> H <sub>26</sub> CLN <sub>3</sub>	OTX	1	treatment of malaria
clavulanate	C <sub>8</sub> H <sub>9</sub> NO <sub>5</sub>	J01	4	antibiotic
cyanocobalamin	C <sub>63</sub> H <sub>88</sub> CON <sub>14</sub> O <sub>14</sub> P <sub>1</sub>	CNC	10	vitamin B12 activity
cyclosporin A	C <sub>62</sub> H <sub>111</sub> N <sub>11</sub> O <sub>12</sub>	CSA	30	Immunosuppressant
didanosine	C <sub>10</sub> H <sub>12</sub> N <sub>4</sub> O <sub>3</sub>	2DI	1	anti-viral for HIV
dopamine	C <sub>8</sub> H <sub>11</sub> NO <sub>2</sub>	LDP	9	treatment of hypotension and cardiac arrest
efavirenz	C <sub>14</sub> H <sub>9</sub> CLF <sub>3</sub> NO <sub>2</sub>	EFZ	6	anti-viral for HIV
erlotinib	C <sub>22</sub> H <sub>23</sub> N <sub>3</sub> O <sub>4</sub>	AQ4	3	anti-cancer
ertapenem	C <sub>22</sub> H <sub>27</sub> N <sub>3</sub> O <sub>7</sub> S	1RG	3	antibiotic
erythromycin	C <sub>37</sub> H <sub>67</sub> NO <sub>13</sub>	ERY	9	antibiotic
estradiol	C <sub>18</sub> H <sub>24</sub> O <sub>2</sub>	EST	28	hormonal contraception
exemestane	C <sub>20</sub> H <sub>24</sub> O <sub>2</sub>	EXM	1	anti-cancer
furosemide	C <sub>12</sub> H <sub>11</sub> CLN <sub>2</sub> O <sub>5</sub> S	FUN	3	treatment of hypertension and edema
gemcitabine	C <sub>9</sub> H <sub>11</sub> F <sub>2</sub> N <sub>3</sub> O <sub>4</sub>	GEO	3	anti-cancer
ibuprofen	C <sub>13</sub> H <sub>18</sub> O <sub>2</sub>	IBP	9	anti-inflammatory
imipenem	C <sub>12</sub> H <sub>19</sub> N <sub>3</sub> O <sub>4</sub> S	IM2	12	antibiotic
indomethacin	C <sub>19</sub> H <sub>16</sub> CLNO <sub>4</sub>	IMN	24	anti-inflammatory
isoflurane	C <sub>3</sub> H <sub>2</sub> CLF <sub>5</sub> O	ICF	2	anesthetic
kanamycin	C <sub>18</sub> H <sub>36</sub> N <sub>4</sub> O <sub>11</sub>	KAN	21	antibiotic
l-carnitine	C <sub>7</sub> H <sub>16</sub> NO <sub>3</sub>	152	8	treatment of heart attack and heart failure
mercaptopurine	C <sub>5</sub> H <sub>4</sub> N <sub>4</sub> S	PM6	2	immunosuppressant
naproxen	C <sub>14</sub> H <sub>14</sub> O <sub>3</sub>	NPS	4	anti-inflammatory
niflumic acid	C <sub>13</sub> H <sub>9</sub> F <sub>3</sub> N <sub>2</sub> O <sub>2</sub>	NFL	2	anti-inflammatory
nitroxoline	C <sub>9</sub> H <sub>6</sub> N <sub>2</sub> O <sub>3</sub>	HNQ	1	antibiotic
pentamidine	C <sub>19</sub> H <sub>24</sub> N <sub>4</sub> O <sub>2</sub>	PNT	7	anti-microbial
pioglitazone	C <sub>19</sub> H <sub>20</sub> N <sub>2</sub> O <sub>3</sub> S	P1B	2	treatment of diabetes
ponatinib	C <sub>29</sub> H <sub>27</sub> F <sub>3</sub> N <sub>6</sub> O	OLI	3	anti-cancer
prednisone	C <sub>21</sub> H <sub>26</sub> O <sub>5</sub>	PDN	8	immunosuppressant
progesterone	C <sub>21</sub> H <sub>30</sub> O <sub>2</sub>	STR	15	hormone replacement therapy
rifampin	C <sub>43</sub> H <sub>58</sub> N <sub>4</sub> O <sub>12</sub>	RFP	7	antibiotic
ritonavir	C <sub>37</sub> H <sub>48</sub> N <sub>6</sub> O <sub>5</sub> S <sub>2</sub>	RIT	12	anti-viral for HIV
salicylic acid	C <sub>7</sub> H <sub>6</sub> O <sub>3</sub>	SAL	36	treatment of acne
saxagliptin	C <sub>18</sub> H <sub>25</sub> N <sub>3</sub> O <sub>2</sub>	BJM	1	treatment of diabetes
streptomycin	C <sub>21</sub> H <sub>39</sub> N <sub>7</sub> O <sub>12</sub>	SRY	14	antibiotic
sulindac	C <sub>20</sub> H <sub>17</sub> FO <sub>3</sub> S	SUZ	7	anti-inflammatory
suramin	C <sub>51</sub> H <sub>40</sub> N <sub>6</sub> O <sub>23</sub> S <sub>6</sub>	SVR	12	anti-microbial
tobramycin	C <sub>18</sub> H <sub>37</sub> N <sub>5</sub> O <sub>9</sub>	TOY	6	antibiotic
tretinoin	C <sub>20</sub> H <sub>28</sub> O <sub>2</sub>	REA	30	treatment of acne
vidarabine	C <sub>10</sub> H <sub>13</sub> N <sub>5</sub> O <sub>4</sub>	RAB	2	antibiotic
zidovudine	C <sub>10</sub> H <sub>13</sub> N <sub>5</sub> O <sub>4</sub>	AZZ	4	anti-viral for HIV
zoledronate	C <sub>5</sub> H <sub>10</sub> N <sub>2</sub> O <sub>7</sub> P <sub>2</sub>	ZOL	12	treatment of osteoporosis

The PDID database provides access to pre-computed results of computationally expensive all-atom predictions by eFindSite and SMAP. Their average runtime for a single protein structure and a given drug is about 30 minutes on a single CPU; the runtime of ILbind is negligible since it is based a consensus of results generated by the two predictors. This high computational cost makes *ad hoc* predictions for a given user query (a given drug or a given protein) computationally impractical.

The current version of PDID includes results of about 1.1 million predictions of targets over the 10 thousand structures and 51 drugs, with the corresponding 5172, 7184, and 4444 putative targets of these drugs generated by ILbind, SMAP, and eFindSite. It also includes 730 known targets of the 51 drugs mapped from and linked to the corresponding records in DrugBank, BindingDB, and PDB. Figure 4 shows the number of native and putative targets for each drug. The median number of putative DPIs equals 23, 30, and 31 for SMAP, eFindSite, and ILbind, respectively, compared to the median of 8 based on the known interactions collected from DrugBank, BindingDB and PDB.

PDID is freely available at <http://biomine.cs.vcu.edu/servers/PDID/>. The backend of this database is implemented with the MySQL relational database and query pages using PHP script. Protein targets are linked to PDB, UniProt, BindingDB and DrugBank. Drugs are linked to the corresponding records in PDB, BindingDB, and DrugBank. Protein and drugs are linked with each other through their known and putative interactions. The interactions are defined at the molecular level, i.e., coordinates of the location of the drug in the protein structure file are included. Besides displaying this information in the browser window, PDID provides access to the source files with the sequence and structure of the target proteins. We also offer download of the parsable raw source datasets in text format under the “Datasets” section on the main page. They include the

current version of the structural human proteome (IDs of all considered protein structures), a list of drugs, and predicted targets for each drug together with scores from each of the three prediction methods and the corresponding coordinates of the putative positions of the center of the drug.

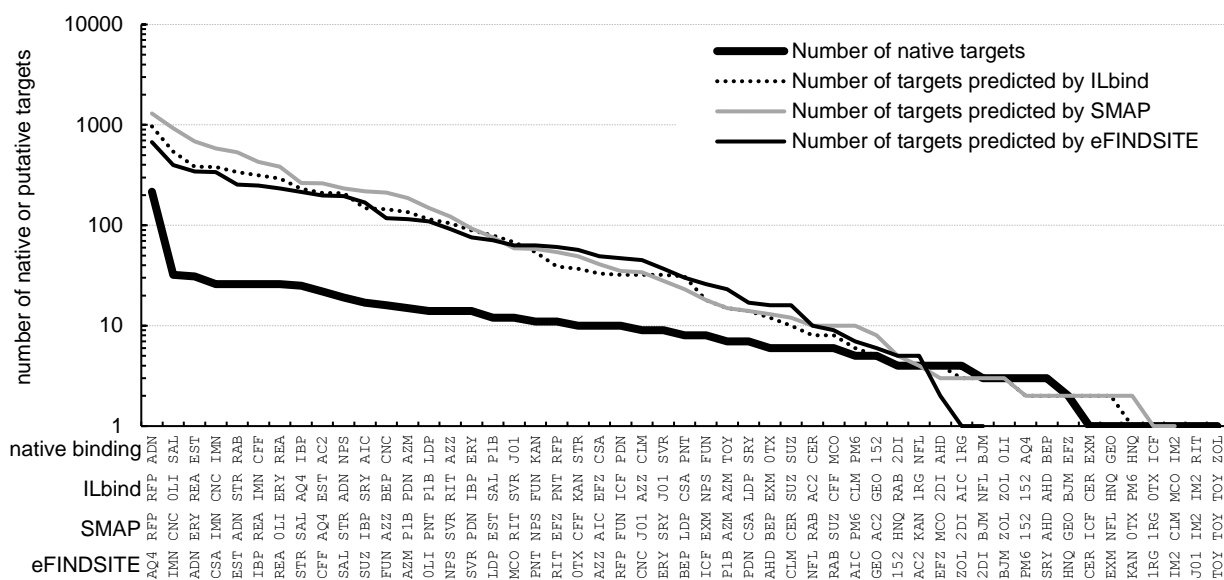


Figure 4. Number of native and putative targets for the considered 51 drugs. The native targets are based on the combined annotations from PDB, DrugBank, and BindingDB. The predictions were generated by ILbind, SMAP and eFindSite. The drugs, which are shown on the x-axis, are sorted by their corresponding number of targets in the descending order and separately for each of the four annotations.

### 3.4.2 User interface

The main page of PDID includes an overview of the contents of the database, provides access to three available search types (by drug name, by ID of the protein target, and by a sequence of the protein target), lists links to the source datasets and related resources, and gives the release date. It also includes link to the “About” page that explains contents of the database and introduces related methods, and to the “Help & Tutorial” page that explains the interface of the main page and the three types of output pages that correspond to the three search types (Figure 5).

**Statistics** [?](#)

	Number of drugs	51
Statistics	Number of proteins	3746
overall	Number of protein structures	9652
	Number of predictions of interactions	1088789
	Number of known targets	730
	Number of putative targets predicted by ILbind	5172
	Number of putative targets predicted by SMAP	7184
Statistics	Number of putative targets predicted by eFindSite	4444
per	Median number of known targets per drug	8
protein	Median number of putative targets predicted by ILbind per drug	31
	Median number of putative targets predicted by SMAP per drug	23
	Median number of putative targets predicted by eFindSite per drug	30

**Search Drug/Protein/Sequence from Database** [?](#)

Search by Drug Name:

Search by PDB ID of Protein Target:

*Protein ID and chain ID are both required, and formatted as protein\_chain. Example:12CA\_A*

Search by Protein Sequence

Enter Protein Sequence in FASTA FORMAT:

Minimal E-value:

**HINT:** The [?](#) symbols indicate availability of (additional) explanations. Clicking [?](#) opens a new window with help and hints related to the selected section/task.

**Materials**

- [STRUCTURAL HUMAN PROTEOME](#)
- [LIST OF DRUGS](#)
- [ENTIRE DATABASE](#) - The users could download the database file and make local query using **MySQL**
- [PUTATIVE TARGETS WITH COORDINATES OF THE PREDICTED CENTERS OF LIGANDS](#)

Figure 5. Main page of the PDID database. The main page includes statistics of drugs, proteins and interactions, three types of queries in the database, download links of partial or entire database, and pointers to help and tutorial pages that can be accessed by clicking on the “?” icon.

The search by drug name returns a table with details of known and putative targets including links to the corresponding records in PDB, DrugBank and BindingDB, links to files with structure and sequence of each target, and propensities for binding output by ILbind, SMAP, and eFindSite (Figure 6a). Targets are sorted by the number of methods that predict them as binding (propensities

shown in green font indicate that binding is predicted) and by the scores generated by the most accurate ILbind when the number is the same. A more detailed description of the formatting and contents of this output page can be found at [http://biomine.cs.vcu.edu/servers/PDID/help.html#drug\\_page](http://biomine.cs.vcu.edu/servers/PDID/help.html#drug_page). Each target protein is available as a link that leads to a web page with the summary of results for this protein.

The search by protein ID returns a web page that maps this ID into corresponding UniProt protein (quality of mapping is annotated using sequence similarity), gives links to the sequence and structure files, and provides customizable visualization of the structure together with the localization of the putative (red dots) and known (blue sticks) ligands. The page also includes a table that summarizes information about drugs that are known and predicted to bind this protein (Figure 6b). This information includes color-coded scores generated by each method that produced the predictions and the corresponding predicted location of the drug in the protein structure. We use JSmol [159] to visualize structures and BLAST to compute sequence similarity. A more detailed description of this web page is available at [http://biomine.cs.vcu.edu/servers/PDID/help.html#prot\\_page](http://biomine.cs.vcu.edu/servers/PDID/help.html#prot_page).

The search based on protein sequence invokes BLAST that compares the input chain with the target sequences included in the databases. The most similar target is selected given that its similarity quantified with the *e*-value is better than a user-defined cutoff; default *e*-value cutoff equals 0.001. The resulting web page displays the alignment of the query and target proteins and the summary of results for the aligned target protein; the format of the summary is the same as for the query based on the protein ID.



### PROTEIN TARGETS FOR MERCAPTOPYRINE(PMG) ?

More information about Mercaptopurine(PMG) could be found at  
 PDB: <http://www.rcsb.org/pdb/ligand/ligandsupply.do?hetID=PMG>  
 DrugBank: <http://www.drugbank.ca/drugs/DB01033>

The table lists all proteins from the structural human-like proteome that are sorted by the IBind binding propensity. For each protein target, the table includes annotations of known binding events from BindingDB, DrugBank, and PDB, and binding predicted by IBind, SMAP, and eFindSite. Click protein name to obtain results per selected protein target.

PDB ID	Protein Name (Synonym)	Organism	Sequence File	Structure File	Type of Annotation	Source Database	Sequence Similarity to Known Target [%]	Binding Prediction Score to bind		
								ILbind binding propensity	SMAP raw score	eFindSite confidence score
2E1Q_A	XANTHINE DEHYDROGENASE/OXIDASE (XANTHINE DEHYDROGENASE; XD; XANTHINE OXIDASE; XO; XANTHINE OXIDOREDUCTASE)	HOMO SAPIENS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Known to Bind	DrugBank	99.9	0.91	123.33	0.28
1WYG_A	XANTHINE DEHYDROGENASE/OXIDASE	RATTUS NORVEGICUS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Known to Bind	DrugBank	90.3	0.91	122.16	0.28
2E3T_A	XANTHINE DEHYDROGENASE/OXIDASE	RATTUS NORVEGICUS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Known to Bind	DrugBank	90.5	0.91	122.34	0.29
3AN1_A	XANTHINE DEHYDROGENASE/OXIDASE (XANTHINE DEHYDROGENASE; XD; XANTHINE OXIDASE; XO; XANTHINE OXIDOREDUCTASE)	RATTUS NORVEGICUS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Known to Bind	DrugBank	90.5	0.91	115.70	0.28
2BZG_A	THIOPURINE S-METHYLTRANSFERASE (THIOPURINE METHYLTRANSFERASE)	HOMO SAPIENS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Known to Bind	DrugBank	100	0.87	135.84	0.41
3TMI_A	ATP-DEPENDENT RNA HELICASE DOX58 (RIG-1; DEAD BOX PROTEIN 58; RETINOIC ACID-INDUCIBLE GENE 1 PROTEIN)	HOMO SAPIENS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Predicted to Bind			0.77	47.56	
3HHM_A	PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KINASE CATALYTIC SUBUNIT ALPHA ISOFORM (PI3-KINASE P110 SUBUNIT ALPHA; PTDINS-3-KINASE P110; PI3K)	HOMO SAPIENS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Predicted to Bind			0.76	45.65	
3HNC_A	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE SUBUNIT (RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SUBUNIT R1; RIBONUCLEOTIDE REDUCTASE LARGE SUBUNIT)	HOMO SAPIENS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Predicted to Bind			0.75	42.31	
3TLM_A	SARCOPLASMIC/ENDOPLASMIC RETICULUM CALCIUM ATPASE 1 (SERCAL1; SR CA(2+)-ATPASE 1; CALCIUM PUMP 1; CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE; FAST TWTCH SKELETAL MUSCLE ISOFORM; ENDOPLASMIC RETICULUM CLASS 1/2 CA(2+)-ATPASE)	BOS TAURUS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	Predicted to Bind			0.75	41.52	
1HK3_A	SERUM ALBUMIN	HOMO SAPIENS	<a href="#">CLICK TO OPEN</a>	<a href="#">CLICK TO OPEN</a>	No Interaction			0.75	45.26	

(a)

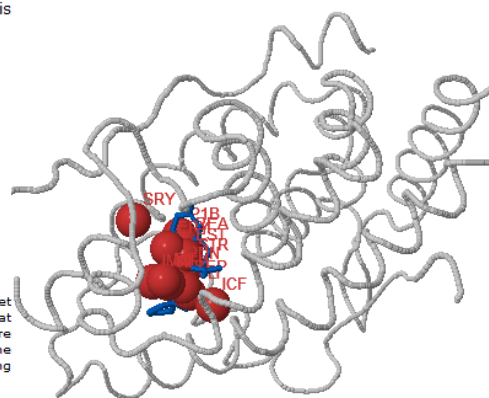
### RESULTS FOR MINERALOCORTICOID RECEPTOR {MR} ?

The structure of MINERALOCORTICOID RECEPTOR {MR} is identified as **2OAX** (chain A) in PDB.

**2OAX** shares 99.6% similarity with **B0ZBF6** in UniProt.

The protein sequence file could be downloaded [HERE](#).

The protein structure file could be downloaded [HERE](#).



The panel on the right shows structure of the protein target (using gray trace of the backbone), position of ligands that are in complex with this protein (using blue sticks; they are included in the structure file), and the predicted center of the drug molecule (using red balls) as summarized in the 'Binding to drugs' table.

The structure is editable, it can be rotated and zoomed with a mouse.

JSmol

#### Binding to drugs ?

Drug ID	Drug Name	Annotated as Known Target		Predicted as Target			Predicted Coordinates of the Center of the Drug Molecule [X;Y;Z]	Binding Summary	
		Type of interaction	Source database	ILbind binding propensity	SMAP raw score	eFindSite confidence score		Known target?	# methods predicting the protein as target
PDN	PREDNISONE	In Complex	PDB	0.87	295.63	0.49	-20.745;59.983;4.164	Yes	2
STR	PROGESTERONE	In Complex	PDB	0.87	297.88	0.4	-19.437;59.756;3.684	Yes	2
EST	ESTRADIOL	Known to Bind	BINDINGDB	0.86	132.57	0.47	-18.900;59.988;5.307	Yes	2
RIT	RITONAVIR	Known to Bind	BINDINGDB	0.7	62.28		-22.241;59.420;8.579	Yes	1
IMN	INDOMETHACIN			0.82	78.04	0.81	-19.86;67.169;10.877	No	3
RFP	RIFAMPIN			0.81	92.85	0.92	-21.901;59.351;6.597	No	3
REA	TRETINOIN			0.82	77.53	0.43	-17.837;61.083;3.900	No	2

(b)

Figure 6. Results of queries against the PDID database. Panel a shows results for a query for mercaptopurine. Detailed description of this webpage is given at [http://biomine.cs.vcu.edu/servers/PDID/help.html#drug\\_page](http://biomine.cs.vcu.edu/servers/PDID/help.html#drug_page). Panel b gives results form a query for mineralocorticoid receptor protein. Detailed explanations of this page are available at [http://biomine.cs.vcu.edu/servers/PDID/help.html#prot\\_page](http://biomine.cs.vcu.edu/servers/PDID/help.html#prot_page). The “?” icon opens the corresponding help page.

### 3.5 Conclusions

PDID provides access to all putative targets (between 4444 and 7184, depending on the prediction method used) of several dozens of popular drugs. These data are based on close to 1.1 million of all-atom predictions over the entire structural human proteome (10 thousand structures for over 3700 proteins). Our database offers four unique features:

- 1) It incorporates accurate predictions generated by three representative protein structure-based methods.
- 2) It provides predictions for a comprehensively defined structural human proteome. We borrow structures of similar proteins from other organisms and cluster similar proteins to reduce redundancy.
- 3) It includes molecular level information on localization of the putative position of the center of drugs in the structures of the corresponding protein targets.
- 4) It includes comprehensive annotations of known drug targets that are linked to their sources: DrugBank, BindingDB, and PDB.

Numerous drugs are highly promiscuous and we do not know many of their targets. PDID addresses this issue by providing access to a complete set of putative DPIs and a set of known DPIs in the structural human proteome. Our database includes data that otherwise would be accessible only to individuals and research groups with significant computational expertise and resources. The putative interactions were generated by three accurate predictors that were shown to produce results that have previously led to finding new drug targets [16, 30, 31, 141-144]. PDID complements the existing BioDrugScreen database that relies on docking. The database integrates annotations of known protein targets collected across DrugBank, BindingDB, and PDB. It also

links proteins to the corresponding records in UniProt and provides coordinates of the location of binding sites in the structures of the putative drug targets.

PDID can be used to systematically catalog DPIs and to facilitate various studies related to polypharmacology of drugs [160], such as explaining side-effects caused by interactions with off-targets and for the drug repurposing. Relevant recent examples include the use of predictions with ILbind to find three novel off-targets of cyclosporine A that explain nephrotoxicity associated with the use of this immunosuppressant [16]. Another example involves repurposing of raloxifene, which is used for prevention and treatment of osteoporosis, as a potential compound to treat *Pseudomonas aeruginosa* infections based on predictions with the SMAP method [144].

However, as discussed in section 2.4, the protein structure-based approaches cover only a relatively small part the entire human proteome. This is due to the fact that most proteins do not have structures. A perhaps extreme example of that are GPCRs, a big family of drug targets composed of mostly membrane proteins, which almost entirely lack structures [161, 162]. This motivates us to investigate the other category of methods for the prediction of DPIs – the similarity-based predictions which do not rely on the knowledge of protein structures.

# **Chapter 4 Review of the similarity-based predictions of drug-protein interactions**

In this chapter, we investigate the current similarity-based methods for the prediction of DPIs. Starting from several recent reviews and a series of selected predictors, we distill the main types of similarities that are used to predict DPIs and categorize the available predictors according to the type(s) of similarities they use and whether they combine these similarities together. We qualitatively compare these approaches in the context of their methodological underpinnings, data that they cover, and how they were assessed. We also analyze their advantages and drawbacks and make a note of missing aspects related to how they were evaluated in the past.

## **4.1 Overview of recent surveys**

A total of 11 surveys that were written in the last five years have focused on the similarity-based methods [21, 32, 89-97]. We also note two other articles that focus on related topics including biological profiles [163] and machine learning tools [164] that are employed in DPI predictions. The 11 surveys summarize relevant databases, review representative methods, and discuss common criteria that are used to evaluate predictive performance. Table 3 assesses scope of these articles with the number of methods they reviewed, coverage of recent predictors,

inclusion of summary of databases used by the considered predictors, and presence of empirical assessment and analysis of sensitivity of predictive quality. The two most comprehensive surveys cover 28 [96] and 27 predictors [90] while the remaining nine articles discuss fewer than 20 methods. In most cases, over half of the methods that were reviewed was published in the past five years. This reflects growing interest in the similarity-based predictors. However, at least eight methods that were published in 2016 and 2017 [165-172] were not included in any of these articles. While most of the surveys provide a brief discussion of the available DPI databases, these are not necessarily the databases that are used by specific predictors to compute the similarity values. In fact, only one article provides a more complete discussion that introduces specific databases which are utilized by a small set of ten predictors that this survey covers [32]. A complete summary of the DPI databases that covers modern methods is still missing, which is why we discuss this topic. We survey 35 predictors and investigate two types of relevant databases: internal databases which are intrinsic to the predictors and source databases that are used to derive the internal databases. Moreover, only four surveys provide empirical assessment of predictive performance of similarity-based DPI predictors [32, 89, 96, 97]. While they provide quantitative and comparative analysis, they focus on a limited set of approaches. In particular, they only consider certain types and combinations of similarities. They also do not perform sensitivity analysis, i.e., they do not analyze whether and how predictive performance changes with intrinsic and extrinsic characteristics of the considered predictors. To summarize, while the previous surveys offer useful insights they also have several drawbacks. In particular, they miss several recent similarity-based DPI predictors, provide shallow treatment of databases used by these predictors, offer incomplete empirical analysis, and do not include sensitivity analysis.

Table 3. Overview of surveys of the similarity-based methods for the DPI prediction. The surveys are sorted chronologically according to their publication year. The check symbol indicates that a given measure (column) is included in a given survey (row) while a blank cell means absence of a given measure. The last row corresponds to this review.

Survey	Year	Number of predictors reviewed	Number of recent predictors reviewed (published since 2013)	Summary of source and internal databases that each predictor uses	Empirical assessment of predictive performance	Comparative analysis of predictors that use different numbers and types of similarities	Sensitivity analysis
Ding et al. [32]	2013	10	2	√	√		
Pahikkala et al. [89]	2014	2	1		√		
Mousavian et al. [90]	2014	27	16				
Chen et al. [21]	2015	17	10				
Cichonska et al. [91]	2015	17	9				
Lavecchia et al. [92]	2016	11	9				
Hart et al. [93]	2016	8	6				
Shahreza et al. [94]	2017	17	8				
Fang et al. [95]	2017	10	5				
Ezzat et al. [96]	2018	28	17		√		
Hao et al. [97]	2018	12	9		√		
This dissertation	2018	35	22	√	√	√	√

In this dissertation, we focus on a comprehensive set of 35 similarity-based DPI predictors that were published in the last decade, including the largest set of recent predictors when compared to previous surveys. The considered predictors comprise of 22 recent tools that were published in the last five years and eight latest methods that were published since 2016. This way our review includes the latest advances in the DPI predictions. We define the three main types of similarities that these 35 methods use to predict compound-protein interactions, describe key architectural details of these tools and comment on their impact. We also offer in-depth summary of the internal and source databases that these predictors use and discuss how these databases are linked. Moreover, under the third goal we also combine multiple sources databases to build a novel benchmark dataset that we use to perform comprehensive empirical evaluation. The empirical evaluation that we perform as part of the third goal (details are given in Chapter 5) encompasses representative approaches that rely on each of three main types of drug and protein similarities and ensemble predictors that combine two and three types of similarities. Besides providing the overall

predictive performance of the considered predictors, we are the first to consider predictive quality across individual drugs. Finally, our first-of-its-kind sensitivity analysis investigates whether and how the predictive performance depends on several intrinsic and extrinsic factors, e.g., the number of targets that are a priori known for a given drug.

The chapter starts with the selection of representative similarity-based predictors. We provide discussion of their source databases to build up the background to survey the selected predictors. These databases include native DPIs that are used to implement predictions by the similarity-based predictors. We summarize their timeline, impact, data contents, and overlap. Next, we investigate the timeline, impact, and availability of the 35 selected predictors. Moreover, we compare the contents of their internal databases and review the types of similarities that they utilize. After that, we provide a timeline that links the chronological record of source databases with the emergence of the 35 predictors. We also analyze how different types of similarities were used and combined over time to develop these methods.

## **4.2 Selection and overview of similarity-based DPI predictors**

To cover a complete landscape of top-tier similarity-based predictors of DPIs, we collected corresponding articles that were published in high-impact venues. We searched the PubMed repository [173] in April 2018 for relevant articles using the following query: (predict\* [Title/Abstract] AND (“drug target interaction” [Title/Abstract] OR “drug protein interaction” [Title/Abstract])). The query generated 170 possibly germane articles. We manually processed these results to select articles that describe similarity-based predictors that were published in reputable journals, i.e., journals with impact factor > 3.5. We collected the impact factors from the latest Journal Citation Reports that was released by Clarivate Analytics (formerly Thomson

Reuters) on June 14, 2017 [174]. This version of JCR is based on the citation data in 2016 and reveals the scientific impact of a JCR-indexed journal by quantifying the ratio between the number of 2016 citations to the articles published in this journal in 2014-2015 and the number of articles published in this journal in 2014-2015. The resulting 35 similarity-based DPI predictors are included in this review [165-172, 175-201]. This list is longer than the lists covered in the prior surveys which also include methods published in conference proceedings, lower impact factor journals as well as methods that target ligand/chemical-protein interactions besides DPIs.

The similarity-based predictors of DPIs are implemented based on the assertions that similar drugs may share the same protein targets and that similar proteins may interact with the same drugs. To identify putative interaction between a given drug and protein, a predictive model typically searches its internal database for drugs that are similar to the given drug and their known targets that are similar to the given target protein. Therefore, the core aspect that defines these predictions is how to measure the drug-drug and protein-protein similarities. Analysis of the 35 similarity-based DPI predictors reveals that the similarities are typically quantified using information about the chemical structures of drugs, side-effect profiles of drugs, and sequences of their protein targets. In other words, the predictors rely on three main types of similarities: chemical similarity of drugs (DCS), drug profile similarity (DPS), and protein sequence similarity (PSS). Some predictors employ one type of similarity to infer putative DPIs. Other methods combine multiple types of similarities motivated by an assumption that this may improve predictive quality when compared to using just a single type of similarity.

The similarity-based predictive methods are composed of two components: an internal database of known DPIs and a predictive model. Prediction of DPIs is performed in three steps. First, a user provides inputs in the form of drug structure, drug profile, and/or protein sequence(s)



of known target(s) for an input drug, whatever is necessary for the selected similarity-based approach. In the second step, similarities between the input drug structure (profile) and the structures (profiles) of the drugs in the internal database are computed. If target(s) of the query drug are known or can be collected from the internal database (the query drug is already included in the database), then similarity between the known target of the query drug and all proteins targets in the database is also quantified. In the third step, the predictive model combines the similarities to produce a propensity which quantifies likelihood that the query drug interacts with relevant protein targets which are included in the internal database.

The architectures of these predictive models are designed and tuned for their corresponding internal databases. Thus, data quality of the internal database largely determines the predictive performance of similarity-based DPI predictors. The internal databases typically consist of a set of native DPIs that are aggregated and collated from multiple source databases which store curated annotations of DPIs. Next, we review the source databases that are used to derive the internal databases of the 35 selected methods.

### **4.3 Source databases**

We investigate the 35 predictors to come up with a list of all source databases that they use to derive the corresponding internal databases. In total, we found 12 publicly accessible source databases that these methods utilize. They include, in chronological order of publication: PDSP Ki [202], BRENDA [203-211], BindingDB [108-112], TTD [43, 103-107], KEGG BRITE [212-218], DrugBank [98-102], GLIDA [219, 220], KEGG DRUG [212-218], SuperTarget [117, 118], Matador [117], STITCH [123-127], and ChEMBL [113-116]. One of the selected predictors, SEA (Similarity Ensemble Approach) [175, 221], utilizes a collection of drugs and associated targets

from a commercial MDL Drug Data Report (MDDR) [222, 223]. This database is not available publicly and thus it is excluded from our analysis. Next, we summarize the contents, timeline, impact, and relationships between these 12 publicly available source databases.

#### **4.3.1 Timeline and impact**

Besides storing the data and providing facilities to conveniently query and access the data, databases must be maintained and regularly updated. They also should be periodically disseminated to inform the users about their contents and the available features. One way to measure the impact of these databases is to tally the citation counts for the scientific articles that introduce these databases and their updated versions.

Table 4. Timeline and impact of the source databases of drug-protein interactions. The source databases were used to derive the internal databases of the 35 selected similarity-based predictors. The timeline is a chronological summary of publications and releases for these source databases. The impact measures citation counts for the publications of databases. This table is sorted chronologically according to the date of the first publication. The data of this table was collected on April 1, 2018.

Source database	Date of the first publication <sup>1</sup>	Date of the first release <sup>2</sup>	Date of the latest publication <sup>3</sup>	Date of the latest release <sup>4</sup>	Date of the first predictor <sup>5</sup>	All citations <sup>6</sup>	Annual citations <sup>7</sup>
PDSP Ki [202]	8/1/2000	11/1/1999	N/A	4/1/2018	7/11/2008	231	13
BRENDA [203-211]	10/1/2000	10/1/2000	10/19/2016	1/1/2018	7/1/2008	2557	146
BindingDB [108-112]	12/1/2001	11/1/2000	10/19/2015	4/1/2018	3/4/2016	1398	86
TTD [43, 103-107]	1/1/2002	1/1/2002	11/13/2017	10/4/2017	3/25/2013	961	59
KEGG BRITE [212-218]	1/1/2006	4/1/2005	11/29/2016	4/1/2018	7/1/2008	*13974	*1140
DrugBank [98-102]	1/1/2006	1/1/2006	11/8/2017	4/2/2018	7/1/2008	5822	475
GLIDA [219, 220]	1/1/2006	1/1/2006	11/5/2007	10/10/2010	3/1/2011	194	16
KEGG DRUG [212-218]	1/1/2006	7/1/2005	11/29/2016	3/29/2018	9/3/2012	*13974	*1140
SuperTarget [117, 118]	10/16/2007	10/16/2007	11/8/2011	11/8/2011	7/1/2008	410	39
Matador [117]	10/16/2007	10/16/2007	N/A	10/16/2007	7/11/2008	316	30
STITCH [123-127]	12/15/2007	8/9/2007	11/20/2015	6/30/2016	6/10/2015	1068	104
ChEMBL [113-116]	9/23/2011	10/27/2009	11/28/2016	5/1/2017	7/8/2013	2434	373

<sup>1</sup> The date when a given source database was originally published in a scientific article. It corresponds to the publication date of early access, if available. Otherwise, the date of the journal issue where the first publication appeared is used.

<sup>2</sup> The date when a given database was first made available, which typically is before the database was originally published. We collect these dates from the release notes or time stamps recorded on the database websites, if available, and we use the date of the first publication, otherwise.

<sup>3</sup> The date of the most recent republished article that introduced an updated version of a given database after the database was originally published.

<sup>4</sup> The date of the most recent release of a given database, which typically is after the latest republishing.

<sup>5</sup> The date when a given source database was first to be utilized to derive the internal database of a predictor.

<sup>6</sup> The “All citations” column is the total number of citations that include citations to the first publication and all republished articles for a given source database. The citation counts were collected from Google Scholar.

<sup>7</sup> The “Annual citations” column is the average citation counts per one calendar year (365 days) over the period from the first publication date until April 1, 2018, rounded to the nearest integer.

\* KEGG BRITE and KEGG DRUG are a part of the Kyoto Encyclopedia of Genes and Genomes (KEGG) project. They were published together with the KEGG database and all of its affiliated databases. The citation data for these two databases include the citations to the entire KEGG database, and they cannot be distributed to each affiliated database of KEGG. These counts are relatively high because they reflect the citations to all 23 databases affiliated with KEGG by now.

Table 4 provides a summary of the 12 source databases. It includes information about publications that introduce the original and the updated versions of these databases as well as the corresponding citation data. The source databases are sorted chronologically according to the date of their first publication. Specifically, we use the date of the early access online publication when it was available. Otherwise, we use the date of the journal issue in which the first publication has appeared. Apart from the date of the first publication, we also list the date when the database was first made available, which typically is before the database was published. We collect these first release dates from the release notes or time stamps recorded on the database websites, if available,

and we use the first publication date otherwise. In this chronological order, the four earliest source databases debuted between August 2000 and January 2002. The next seven databases were published several years later, between 2006 and 2007. The last source database was published in 2011. Eleven out of the twelve sources were published within about one year after their first public release. The one exception, the ChEMBL database was first published two years after its initial release. ChEMBL was originally a commercial database called StARLite that was launched before 2005, acquired by EMBL-EBI in 2008, released to the public in 2009, and finally published in 2011 [224-226]. Given that all these databases were originally released by 2007 or built based on an earlier database, the data stored in these 12 source databases are being accumulated for at least ten years.

Most of the source databases have been regularly updated and republished. Besides just the addition of new data, these updates typically include new features and improved user interface. We list the publication date of the latest republished article and the most recent release date for each source database as of April 1, 2018. These two dates together with the first release and the first publication dates provide interesting insights into the progress of the database development. Considering the latest republishing and release dates, GLIDA, SuperTarget, and Matador have not been republished or updated in the last six years. This suggests that they are no longer actively maintained. The PDSP Ki database is actively and frequently updated, but it has never been republished since it was originally published 17 years ago. Meanwhile, the other eight source databases are being updated and republished regularly. Frequent dissemination informs the users about new contents and features and also may help to attract additional users. In general, these frequently updated sources are relatively more mature since they gradually accumulate DPIs, include more recent data, and typically offer a more refined interface and a longer list of features.

Another relevant aspect is to mark when the source databases were de facto used to build the similarity-based predictors of DPIs. Thus, Table 4 shows the date when the earliest predictor has utilized a given source database to derive its internal database of known DPIs. The list of the source databases that were first used to develop the predictors includes PDSP Ki, BRENDA, KEGG BRITE, DrugBank, SuperTarget, and Matador. The earlier adoption of these source databases reflects to a certain degree their popularity and impact. Moreover, these source databases were also used for other purposes including protein structure-based prediction of DPIs [78, 227, 228] and development of various cheminformatics and bioinformatics methods and datasets [229-233].

Table 4 summarizes citations for the 12 source databases. The citations are one way to quantify the impact of these resources. The citation counts were collected from Google Scholar (<http://scholar.google.com/>) on April 1, 2018. We list the total number of citations that include citations to the first publication and all subsequent publications of a given database. Every source database has received at least about two hundred citations. BRENDA, BindingDB, DrugBank, ChEMBL, KEGG BRITE, KEGG DRUG, and STITCH have accumulated over one thousand citations. A notable exception is the KEGG BRITE and KEGG DRUG databases, which are part of the Kyoto Encyclopedia of Genes and Genomes (KEGG) project since 2005. They were published together with the KEGG database and all of its other affiliated databases in 2006 [212]. Currently, KEGG includes 23 individual databases including, for example, KEGG PATHWAY that provides pathway maps of molecular interaction, reaction and relation networks. The citation data for KEGG BRITE and KEGG DRUG includes the citations to the entire KEGG database; these citations cannot be attributed to individual KEGG resources. The citation counts to KEGG BRITE and KEGG DRUG are so high because they reflect the citations to all 23 databases affiliated with KEGG.

An arguably more robust measure to quantify impact are the annual citation counts. The annual counts are defined as the average citation frequency per one calendar year (365 days) computed over the period from the date of the first publication until the date when we acquired the citation data (April 1, 2018). These counts accommodate for the differences in the age of the source databases. PDSP Ki, GLIDA, SuperTarget, and Matador received moderate (<50) numbers of annual citations. These relatively low citation counts could be a result of a lack of effort to update GLIDA, SuperTarget, and Matador which were last updated in 2011 or earlier. PDSP Ki is frequently updated but it was last published in 2000. On the other hand, BRENDA, BindingDB, TTD, and STITCH have received relatively high (50-150) annual citations. This is likely because these are mature resources that have ten years of history of regular republishing and updates. Noticeably, DrugBank and ChEMBL attract over 300 citations per year. They were also regularly updated and republished. Their success can be attributed to the high-quality of their data contents, a broad range of functional features, and a user-friendly web interface. Next, we review the data contents for the 12 source databases.

#### **4.3.2 Data contents**

Typically, multiple source databases are used to derive an internal database of a given predictor. They are used as a source for information about drugs, their protein targets, and native DPis. Table 5 summarizes information about the number of relevant drugs or drug-like compounds that are known to interact with protein targets, the number of these targets, and the number of annotated drug- and compound-protein interactions for the 12 source databases. These data were collected from the latest release of each database on April 1, 2018. We captured the numbers from the release notes or statistics page if they were available. Otherwise, we tallied the numbers from

the data dumps. BRENDA, a database dedicated to enzyme functions, does not provide specific statistics and data downloads. Thus, we could not calculate the quantities for this database.

Table 5. Data contents of the source databases of drug-protein interactions. These source databases were used to derive the internal databases of the 35 selected similarity-based predictors. The data of this table correspond to the latest release of each database as of April 2018. The numerical data were captured from the release notes or statistics page if they were available. Otherwise, we counted the numbers from the data dumps of each database.

Type	Database	Abbr. <sup>1</sup>	Drugs <sup>2</sup>	Proteins <sup>3</sup>	DPIs <sup>4</sup>	DPIs/drug <sup>5</sup>	URL
Drug	Matador	MA	801	2,901	15,843	19.8	<a href="http://matador.embl.de">http://matador.embl.de</a>
	KEGG BRITE	KB	5,045	1,061	14,222	2.8	<a href="http://www.genome.jp/kegg/brite.html">http://www.genome.jp/kegg/brite.html</a>
	KEGG DRUG	KD	5,045	1,061	14,222	2.8	<a href="http://www.genome.jp/kegg/drug/">http://www.genome.jp/kegg/drug/</a>
	DrugBank	DR	10,562	5,020	23,380	2.2	<a href="http://www.drugbank.ca">http://www.drugbank.ca</a>
	PDSP Ki	PK	11,569	1,673	63,619	5.5	<a href="http://kidbdev.med.unc.edu/databases/kidb.php">http://kidbdev.med.unc.edu/databases/kidb.php</a>
	TTD	TT	23,486	3,036	33,467	1.4	<a href="http://bidd.nus.edu.sg/BIDD-Databases/TTD/TTD.asp">http://bidd.nus.edu.sg/BIDD-Databases/TTD/TTD.asp</a>
Bioactive compound	GLIDA	GL	23,214	410	30,410	1.3	<a href="http://pharminfo.pharm.kyoto-u.ac.jp/services/glida/">http://pharminfo.pharm.kyoto-u.ac.jp/services/glida/</a>
	STITCH	ST	*156,686	*3,908,233	*148,826,348	*949.8	<a href="http://stitch.embl.de">http://stitch.embl.de</a>
	SuperTarget	SU	195,770	6,219	332,828	1.7	<a href="http://bioinformatics.charite.de/supertarget/">http://bioinformatics.charite.de/supertarget/</a>
	BindingDB	BI	644,978	7,042	1,439,799	2.2	<a href="http://www.bindingdb.org/bind/index.jsp">http://www.bindingdb.org/bind/index.jsp</a>
	ChEMBL	CH	2,101,843	11,538	14,675,320	7.0	<a href="http://www.ebi.ac.uk/chembl/">http://www.ebi.ac.uk/chembl/</a>
	BRENDA	BR	Unavailable	Unavailable	Unavailable	Unavailable	<a href="http://www.brenda-enzymes.org/index.php">http://www.brenda-enzymes.org/index.php</a>

<sup>1</sup> Abbreviated name of a given source database. The abbreviations are used to denote the source databases of predictors in Table 8.

<sup>2</sup> The number of drugs and drug-like compounds that are known to interact with protein targets in a given source database.

<sup>3</sup> The number of proteins that are targeted by drugs and drug-like compounds in a given source database.

<sup>4</sup> The “DPIs” column is the number of known DPIs that are stored in a given database.

<sup>5</sup> The “DPIs/drug” column is the average number of DPIs per drug, which is calculated by dividing the “DPIs” column to the “Drugs” column for a given database. Unavailable means that these numbers are missing because BRENDA does not provide specific statistics and downloads for the entire collection of DPIs that it store.

\* The numerical data for the STITCH database includes both direct and indirect DPIs, while data for other databases include only the direct interactions. The indirect interactions are based on effects of signaling pathways where effects of drugs are propagated onto proteins that interact with other proteins that directly interact with these drugs. The indirect interactions in this database cannot be separated from the direct interactions, and thus the corresponding numbers are higher than expected.

Table 5 categorizes the source databases into two types depending on if they are dedicated to drugs or a more generic set of bioactive compounds. The first type of six databases including PDSP Ki, TTD, DrugBank, Matador, KEGG BRITE, and KEGG DRUG focus on approved, under a clinical trial, and experimental drugs. The other six source databases include both drugs and other bioactive compounds that typically are small molecules with drug-like properties. Consequently, the first type of databases has fewer compounds, between 8 hundred and 23 thousand, compared to the second group that includes between 23 thousand and over 2 million compounds. Table 5 is sorted by the number of compounds within each of the two categories. Except for BRENDA for which data are not available and GLIDA that is dedicated solely to the G protein-coupled receptors

(GPCR), the bioactive compound-centric databases have more DPIs and protein targets than the drug-centric databases. Specifically, the six smaller databases include between 15 and 60 thousand interactions, compared to the group of larger sources that features up to 148 million interactions. The largest compound repository, ChEMBL, stores a comprehensive set of two million bioactive compounds. This number is 90 times higher than the total number of the drugs in the largest repository that focuses exclusively on drugs, TTD. Unsurprisingly, the number of compound-protein interactions in ChEMBL is 440 times larger than the number of DPIs in TTD.

The main focus of these databases is typically on the human protein targets. The druggable human proteome, which is defined as all human proteins that interact with current drugs, is estimated to comprise of between 1000 and 3000 proteins [1, 18-20]. The numbers of protein targets in the source databases typically vary between about 1000 and 12,000, with a median value of 3036. Half of these databases are larger than the druggable proteome because they cover proteins from other organisms. For example, BindingDB contains targets from over 400 organisms. There are two exceptions that include GLIDA and STITCH. The GLIDA database focuses on the GPCRs, and thus, it is limited to the corresponding 410 GPCR proteins. STITCH covers over nine million proteins from 2031 organisms, which include a substantial number of putative and low-quality annotations of targets. We excluded these predicted and low-confidence interactions (using their confidence score  $< 0.7$ ) when calculating the numbers for Table 5. This resulted in a set of about 4 million targets and 149 million interactions. The reason why this database is so large is that STITCH includes both direct and indirect DPIs, while data in the other databases include only the direct interactions. The indirect interactions are derived based on signaling pathways where effects of drugs are propagated onto downstream proteins.



In each of the 12 source databases, the number of DPIs is greater than the number of drugs. This is a result of promiscuity of drugs that typically interact with multiple targets. The field of polypharmacology [234-236] and efforts in drug repurposing [7, 8, 10] depend on this promiscuity. However, drug promiscuity may also lead to undesired side-effects and unintended toxicities [12, 15, 16]. We measure the drug promiscuity in these source databases by calculating the average number of DPIs per drug (see DPIs/drug in Table 5). The median degrees of drug promiscuity for the 12 source databases is 2.8, which is close to the promiscuity measured using assays that ranges between 2.6 and 3.4 [237]. Ten databases have between 1.3 and 19.8 DPIs per drug. The STITCH database is again an exception. It includes a relatively dense mapping between proteins and drugs due to the inclusion of a considerable number of indirect interactions. The drug promiscuity has inspired the development of the similarity-based predictive models, where the similarity between targets is used to predict DPIs. It also provides an opportunity to use the currently known targets of a given drug to build models that predict other targets of the same drug.

Besides the interactions, these source databases also encompass rich annotations of the structures, functions, and properties of the drugs and targets, together with the corresponding references. For example, DrugBank provides over 200 such annotations. The native DPIs and the additional knowledge are accessible through the web interfaces of these sources. The corresponding URLs for the 12 source databases are listed in Table 5.

### **4.3.3 Relationships between source databases**

Each of the 12 source databases includes a different collection of DPIs. However, these source databases also overlap with each other. This is because different source databases collect the interactions from some of the same sources, and because some of them also directly import annotations from the other source database. Table 6 summarizes inputs that are used to derive data

stored in a given source database. The inputs include data coming from the 12 source databases, directly from literature, and from other resources. The first 12 inputs in the table indicate whether a given source database directly imports DPIs from another source databases. Seven source databases draw DPIs from between one and nine (for STITCH) other source databases. Moreover, some of the inputs are more popular than the others. Six of the nine input databases provide data for at least three source databases. For example, TTD is used as an input to four source databases including DrugBank, SuperTarget, Matador, and STITCH, compared to BRENDA, SuperTarget, and STITCH that are never used as inputs. The direct inclusion of source databases as inputs results in a substantial overlap between databases. For example, Matador shares a substantial overlap with SuperTarget since they both draw data from the same four source databases while SuperTarget also imports data from one more source. Interestingly, ChEMBL and BindingDB exchange data reciprocally. BindingDB obtains data on compound-protein binding affinities from ChEMBL and exports binding data that were extracted from patents to ChEMBL. Noticeably, STITCH includes the interactions taken from nine other source databases, which explains why Table 5 shows that it hosts the largest collection of interactions. Only the BRENDA database neither imports interactions directly from other source databases nor is used as an input.

Table 6. Relationships between source databases. Each row lists a source database, and each column specifies an input where the data of a given source database come from. The inputs include data coming from other source databases, literature, and other types of inputs. The “Literature” column denotes that the data are manually curated from scientific articles, patents, and annual reports of pharmaceutical companies. The “Other inputs” column includes predictions, experimental data, and other databases that are not named in the table. “x” indicates that a given source database draws data from a given input.

Source database	Inputs													
	PDSP Ki	BRENDA	BindingDB	TTD	KEGG BRITE	DrugBank	GLIDA	KEGG DRUG	SuperTarget	Matador	STITCH	ChEMBL	Literature	Other inputs
PDSP Ki													x	x
BRENDA													x	x
BindingDB	x											x	x	x
TTD													x	x
KEGG BRITE													x	x
DrugBank				x									x	x
GLIDA	x					x							x	x
KEGG DRUG													x	x
SuperTarget			x	x	x	x		x					x	x
Matador				x	x	x		x					x	x
STITCH	x		x	x	x	x	x	x		x		x	x	x
ChEMBL			x										x	x

Moreover, we list two additional types of inputs: literature and other inputs. The literature includes scientific articles, patents, and annual reports of pharmaceutical companies. The other inputs incorporate predictions, experimental data, and other input databases that exclude the 12 source databases. Table 6 shows that all 12 source databases include data coming directly from the literature. This is yet another factor that contributes to the overlap in the contents of the 12 source databases. The data coming from the literature typically includes information about experiments and assays that were used to validate bioactivity and measure affinities of interactions. This information provides context for the interactions. Every source database also acquires data from other inputs that include predictions, other databases such as the Comparative Toxicogenomics Database [238] and PubChem BioAssay [239], and experimental data that were not stored in a dedicated database, such as the data from Refs. [240, 241].

Our analysis reveals that each of the 12 source databases overlaps with at least one other source database. Table 6 qualitatively summarizes this overlap. A quantitative estimate would be extremely challenging. This is because these databases lack a uniform definition of drugs and targets and a consistent way to name and identify compounds and biomolecules. Even if the same literature is used to extract DPIs the resulting data could be different. For example, when the interaction is annotated at the gene level, the same gene could be mapped to different proteins and different types of protein identifiers, depending on which software and databases were used to perform the mapping. The assignments of information from literature to a precisely and uniquely defined set of drugs and protein targets is still an open challenge [44]. The bottom line is that different databases adopt different nomenclatures and identifiers to represent the drugs and proteins, which makes it virtually impossible to quantify the degree of overlap between the 12 databases. A few works have analyzed the overlap of drugs and targets for a small subset of these source databases [23, 177]. A study over a set of 502 approved drugs shows that 49% and 20% of the DPIs in DrugBank were included in Matador and PDSP Ki, respectively [177]. The data that are unique to DrugBank account for only 46% of its DPIs. Moreover, PDSP Ki shares 42% of its known interactions with Matador. As concluded by another investigation, DrugBank had 52% and 21% of drugs in common with ChEMBL and TTD, respectively [23]. The 74% and 55% of the protein targets stored in DrugBank were also included in ChEMBL and TTD, respectively. Moreover, ChEMBL covered 91% and 55% of the drugs and targets that were housed in TTD, respectively. These numeric analyses support our observation about the relatively large extent of overlap and also reflect the fact that source databases have their unique data.

We show that the 12 source databases were developed using some of the same data sources and some of them even swap the data with each other. These relationships lead to a certain amount

of overlap of information that they store. However, each source database also houses its own unique data, and therefore, they should be combined together to collect the most complete set of known DPIs. This is in fact the case for 22 out of the 35 methods that we survey. They use at least two source databases to develop their internal databases. Moreover, 17 methods, including KRM [176], BLM [179], Yamanishi et al. [180], GIP [182], NBI [183], KBMF2K [184], Cao et al. [186], BLM-NII [187], DT-Hybrid [189], DINIES [191], Shi et al. [192], RLS-KF [196], NRLMF [197], DASPfind [199], PUDTI [168], DVM [169], and iDTI-ESBoost [172] have utilized at least four source databases to create their internal DPI databases.

#### **4.3.4 Other drug-target interaction databases**

Besides the 12 source databases, we discuss another 19 databases that have not been adopted to develop the selected similarity-based predictors. These databases house the drug-target interactions accompanied by other information, such as details of mechanisms of DPIs [242], unstudied/dark targets [243], interactions at the gene level [244-250], structures of protein targets [29, 35, 251, 252], information about protein-protein and drug-drug interactions [253-261], side-effects of drugs [128], and information focused on specific diseases, such as cancer [262-266]. Some databases are constrained to a particular group of drugs [267] or a specific family of proteins [268]. Next, we discuss these 19 databases in greater depth.

DrugCentral (<http://drugcentral.org>) is a comprehensive knowledgebase that integrates information about drug actions and pharmacological indications, which can be used to elucidate therapeutic mechanisms mediated through DPIs [242]. The Pharos database (<http://pharos.nih.gov>) incorporates drug action data taken from DrugCentral to define druggable levels of protein targets and define unstudied/dark protein targets. These dark targets are not yet known to be involved in small molecule activities, but they are potentially druggable [243].

Some resources aggregate biological annotations and disease-related knowledge for the druggable genome, which is defined as a collection of genes that encode druggable proteins. These resources include the PharmGKB database (<http://www.pharmgkb.org>) [244], DGIdb (<http://dgidb.genome.wustl.edu>) [245, 246], the Drug2Gene database (<http://www.drug2gene.com>) [247], IUPHAR/BPS GtPdb (<http://www.guidetopharmacology.org>) [248, 249], and Open Targets (<http://www.targetvalidation.org>) [250].

The next three databases rely on the 3D structures of protein targets. The PDB database (<http://www.rcsb.org>) provides access to an extensive collection of 3D structures of drug-protein complexes [35, 251]. The BioLip database (<http://zhanglab.ccmb.med.umich.edu/BioLiP>) provides access to residue-level annotations of ligand-binding sites, binding affinity data, and biological functions for a comprehensive collection of proteins that have 3D structures [252]. The PDID (<http://biomine.cs.vcu.edu/servers/PDID>) is a structural human genome-wide repository of putative and native DPIs that are mapped into the 3D structures of protein targets [29]. It currently stores data about over one million interactions for 51 drugs.

A typical database focuses on DPIs. However, some drugs target protein-protein interactions and targets that are relevant to the same disease or condition can be modulated by multiple drugs. Several databases address these aspects. For example, three databases that focus on the druggability of protein-protein interactions include TIMBAL (<http://mordred.bioc.cam.ac.uk/timbal>) [253, 254], 2P2Idb (<http://2p2idb.cnrs-mrs.fr>) [255-257], and iPPI-DB (<http://www.ippidb.cdithem.fr>) [258, 259]. On the other hand, DCDB (<http://www.cls.zju.edu.cn/dcdb>) is a resource that centers on the therapeutic effects of multi drug combinations [260, 261].

The IntSide database (<http://inside.irbbarcelona.org>) focuses on drug side-effects. This database includes data about both therapeutic and off-targets, relevant pathways, biological functions, and chemical traits of drugs [128]. This information is particularly useful to explain and understand undesired responses to drug treatments.

The CancerResource (<http://data-analysis.charite.de/care>) [262, 263] and canSAR (<http://cansar.icr.ac.uk>) [264-266] databases aim to bridge cancer research with drug discovery. These two resources provide underlying information about drug-target interactions that are relevant to cancer treatment, such as data of gene expression, mutations in cancer-related genes, drug sensitivity in cancer cell lines, and pathways of drug targets.

Finally, some resources are dedicated to a particular collection of drugs or a specific family of protein targets. For example, the WITHDRAWN database (<http://cheminfo.charite.de/withdrawn>) includes data on targets and pathways of drugs that were recalled from the market due to toxicity or inefficacy [267]. The GLASS database (<http://zhanglab.ccmb.med.umich.edu/GLASS>) is exclusively focused on the ligand-protein interactions for the G protein-coupled receptors [268]. About 33% of currently used drugs target this family of proteins [44].

The additional information that can be extracted from these databases complements the information about drug-target interactions that can be obtained from the 12 source databases. We suppose that it would be beneficial for the future similarity-based predictors of DPIs to include these databases as sources.

## **4.4 Similarity-based predictors**

We review several key aspects of the 35 selected high-impact similarity-based DPI predictors. We classify these methods into different categories according to the types and numbers of similarities that they use. We summarize the timeline, impact, and availability of these predictors. We link their internal databases to the specific source databases that we discussed in section 4.3. We also discuss architectural details of these methods. Finally, we comment on the assessment of predictive performance that was adopted by the previous approaches.

### **4.4.1 Categorization of predictors**

The three types of similarities can be combined to formulate an ensemble predictor with the underlining goal to improve predictive quality when compared to using single similarity. Many of the predictors proposed in recent years rely on the ensembles that include two or three similarity types. Consequently, we categorize the 35 considered predictors into three groups: the methods that apply one type of similarity (1S), ensemble models that combine two types of similarities (2S), and ensembles of all three similarities (3S); see “Type of predictor” column in Table 8 and Table 9.

### **4.4.2 Timeline, impact, and availability**

The 35 similarity-based predictors were developed in the past decade. Table 7 lists these predictors in chronological order by their first publication dates. The first five predictors were published between 2007 and 2009. We note a steady pace of the development of methods between 2010 and 2015. Specifically, eight methods were released between 2010 and 2012, and another eight between 2013 and 2015. The pace has picked up recently and already 14 methods were



published between 2016 and the first quarter of 2018. These data reveal an increasing interest in the development of the similarity-based approaches.

Table 7. Timeline, impact, and availability of the 35 selected similarity-based DPI predictors. This table is sorted chronologically according to the date of publication. The data of this table was collected on April 1, 2018.

Predictor <sup>1</sup>	Date <sup>2</sup>	JIF <sup>3</sup>	Citations <sup>4</sup>	Annual citations <sup>5</sup>	Availability <sup>6</sup>	URL
SEA [175, 221]	2/7/2007	41.7	922	83	WS	<a href="http://sea.bkslab.org">http://sea.bkslab.org</a>
KRM [176]	7/1/2008	7.3	446	46	None	N/A
Campillos et al. [177]	7/11/2008	37.2	892	92	None	N/A
COPICAT [178, 269]	6/5/2009	4.5	41	5	WS	<a href="http://copicat.dna.bio.keio.ac.jp">http://copicat.dna.bio.keio.ac.jp</a>
BLM [179]	7/15/2009	7.3	265	30	SS	<a href="http://members.cbio.mines-paristech.fr/~yyamanishi/bipartitelocal/">http://members.cbio.mines-paristech.fr/~yyamanishi/bipartitelocal/</a>
Yamanishi et al. [180]	6/1/2010	7.3	249	32	None	N/A
Yabuuchi et al. [181]	3/1/2011	9.8	102	14	None	N/A
GIP [182]	9/4/2011	7.3	195	30	SS	<a href="http://cs.ru.nl/~tvanlaarhoven/drugtarget2011/">http://cs.ru.nl/~tvanlaarhoven/drugtarget2011/</a>
NBI [183]	5/10/2012	4.5	339	57	None	N/A
KBMF2K [184]	6/23/2012	7.3	125	22	SS	<a href="http://github.com/mehmetgonen/kbmf/">http://github.com/mehmetgonen/kbmf/</a>
PKR [185]	9/3/2012	7.3	71	13	None	N/A
Cao et al. [186]	9/24/2012	5.0	33	6	None	N/A
BLM-NII [187]	11/17/2012	7.3	109	20	None	N/A
Cheng et al. [188]	3/25/2013	3.8	49	10	None	N/A
DT-Hybrid [189]	5/29/2013	7.3	73	15	WS & SS	<a href="http://alpha.dmi.unict.it/dtweb/index.php">http://alpha.dmi.unict.it/dtweb/index.php</a>
PRW & NB [190]	7/8/2013	3.8	69	15	SS	<a href="http://pubs.acs.org/doi/suppl/10.1021/ci300435j">http://pubs.acs.org/doi/suppl/10.1021/ci300435j</a>
DINIES [191]	5/16/2014	10.2	44	11	WS	<a href="http://genome.jp/tools/dinies/">http://genome.jp/tools/dinies/</a>
Shi et al. [192]	5/6/2015	3.8	24	8	SS	<a href="http://web.hku.hk/~liym1018/projects/drug/drug.html">http://web.hku.hk/~liym1018/projects/drug/drug.html</a>
Liu et al. [193]	6/10/2015	7.3	24	9	None	N/A
RWR [194]	8/19/2015	4.2	11	4	None	N/A
SLP & RLS [195]	9/9/2015	4.3	6	2	SS	<a href="http://pan.baidu.com/s/1dDqDLuD">http://pan.baidu.com/s/1dDqDLuD</a>
RLS-KF [196]	1/14/2016	5.0	7	3	SS	<a href="http://github.com/minghao2016/RLS-KF/">http://github.com/minghao2016/RLS-KF/</a>
DrugMiner [165]	1/25/2016	6.4	14	6	WS	<a href="http://www.drugminer.org">http://www.drugminer.org</a>
NRLMF [197]	2/12/2016	4.5	34	16	SS	<a href="http://github.com/stephenliu0423/PyDTI/">http://github.com/stephenliu0423/PyDTI/</a>
SDTNBI [198]	3/4/2016	5.1	20	10	SS	<a href="http://lmmd.ecust.edu.cn/methods/sdtnbi/">http://lmmd.ecust.edu.cn/methods/sdtnbi/</a>
DASPFIND [199]	3/16/2016	4.2	14	7	WS	<a href="http://cbrc.kaust.edu.sa/daspfind/">http://cbrc.kaust.edu.sa/daspfind/</a>
DrugE-Rank [200]	6/11/2016	7.3	23	13	WS	<a href="http://datamining-iip.fudan.edu.cn/service/DrugE-Rank/">http://datamining-iip.fudan.edu.cn/service/DrugE-Rank/</a>
DBN [166]	3/6/2017	4.3	10	9	SS	<a href="http://github.com/Bjoux2/DeepDTIs_DBN/">http://github.com/Bjoux2/DeepDTIs_DBN/</a>
EnsemDT/KRR [201]	5/24/2017	3.8	4	5	None	N/A
Peón et al [167]	6/19/2017	4.3	3	4	None	N/A
PUDTI [168]	8/14/2017	4.3	0	0	None	N/A
DVM [169]	9/11/2017	4.3	1	2	None	N/A
DTINet [170]	9/18/2017	12.1	4	7	SS	<a href="http://github.com/luoyunan/DTINet/">http://github.com/luoyunan/DTINet/</a>
bSDTNBI [171, 270]	9/28/2017	3.8	2	4	SS	<a href="http://lmmd.ecust.edu.cn/methods/bsdtnbi/">http://lmmd.ecust.edu.cn/methods/bsdtnbi/</a>
iDTI-ESBoost [172]	12/18/2017	4.3	1	4	WS & SS	<a href="http://farshidrayhan.pythonanywhere.com/iDTI-ESBoost/">http://farshidrayhan.pythonanywhere.com/iDTI-ESBoost/</a>

<sup>1</sup> The name of each predictor is either provided in relevant publications or otherwise, named using the last name of its first author.

<sup>2</sup> The date of early access online publication or the date of journal issue where a given predictor was originally published.

<sup>3</sup> The “JIF” column is the journal impact factor of the journal where a given predictor appeared. The data were collected from the 2017 Journal Citation Reports that was released by Clarivate Analytics (formerly Thomson Reuters) on June 14, 2017.

<sup>4</sup> The “Citations” column is the number of citations to the article(s) of a predictor, which were collected from Google Scholar.

<sup>5</sup> The “Annual citations” column is the average citation counts per one calendar year (365 days) over the period from the publication date until April 1, 2018, rounded to the nearest integer.

<sup>6</sup> The type of publicly availability of implementations, where WS stands for webserver and SS for standalone software including either compiled or source code. None means the implementation is not offered and thus the corresponding URL is not applicable (N/A).

One way to measure the impact is to consider the impact factors of venues where these methods were published. The 35 predictors were published in high-impact venues with impact factors  $> 3.5$ . Table 7 lists the impact factors for these reputable journals, which are based on the 2017 Journal Citation Reports [174]. The impact factor values for a significant majority of these methods, 33 out of 35, range between 3.8 and 12.1. Two pioneering predictors were published in 2007 and 2008 in journals with the impact factors around 40 [175, 177]. Another way to measure the scientific impact of these methods is based on the citation counts for the articles that introduce these methods. Table 7 lists the corresponding total citation counts, which were collected from the Google Scholar on April 1, 2018. The median total of citations over the 35 methods equals 33. Noticeably, the three earliest predictors [175-177] have accumulated over 400 citations each over the last decade. Their combined number of citations (2260) is greater than the combined count of citations of the remaining 32 methods (1966). These three highly cited predictors have defined and used for the first time the three types of similarities. The SEA method is based on DCS [175]. The chronologically second method, KRM, was the first to use PSS, which was combined with DCS [176]. The third method by Campillos et al. has introduced DPS and used it together with DCS to make predictions [177]. There are also three other method that secured at least 200 citations. They include BLM [179], the predictor by Yamanishi et al. [180], and NBI [183]. The low citation counts for the recent methods that were published since 2016 should be dismissed because there was not enough time yet to accumulate citations. We also analyze a more robust number of annual citations. This number is defined as the total number of citations divided by the number of years (365-day periods), measured between the date of publication and April 1, 2018. The median annual citation number equals ten. The three highest cited predictors attract over 40 citations per year. Moreover, most of the 35 considered methods enjoy high levels of annual citations (median = 10),

in many cases exceeding the corresponding journal impact factors (median = 5). This result suggests that the similarity-based DPI predictors elicit strong interest of the scientific community.

Table 7 also summarizes availability of implementations for these predictors. The authors of eight methods [165, 172, 175, 178, 189, 191, 199, 200] have developed webservers that are geared towards less computer savvy users. The webservers are convenient to use because calculations are done on the server side and consequently the end users only need an internet connection and a web browser to process predictions. Fourteen predictors [166, 170-172, 179, 182, 184, 189, 190, 192, 195-198] are available as standalone software. In this case, the end users must install and use them on their own hardware. This requires more skill and effort but it also facilitates inclusion of these methods in other computational pipelines. Two methods [172, 189] are available as both standalone software and webserver. The URLs of these 20 publicly available approaches are listed in Table 7. The other 15 methods are not available publicly.

#### **4.4.3 Internal databases**

Every similarity-based predictor is implemented based on an internal database that includes known DPIs and relevant information about these drugs and proteins. The contents of internal databases are derived from the data that were collected from one or more of the 12 source databases that we reviewed in section 4.3. Table 8 lists the source databases that are used to generate the internal database of each predictor. Individual predictors utilize between one and six source databases, with a median of three. Specifically, 13 predictors collect data from a single source database, five from two or three sources, 16 from four sources, and one from six sources. The authors of KRM predictor [176] have released their internal database. This database combines DPIs collected from BRENDA (BR), KEGG BRITE (KB), DrugBank (DR), and SuperTarget (SU). This internal database was later reused by another 15 predictors that we review [168, 169, 172,

179, 180, 182-184, 186, 187, 189, 192, 196, 197, 199]. It was also used by a different set of 18 methods which we did not include in our analysis because of the relatively low impact factor of the venues where they were published [271-288]. The frequent reuse of this database explains to some extent why this predictor enjoys high citation counts in Table 7.

We observe that only up to 6 out of 12 source databases are used to develop an internal database. This is in spite of the fact that each of the 12 source databases includes data that are unique to that source, and that many other source databases are available, including the databases listed in section 4.3.4. We recommend that future predictors should rely on more comprehensive internal databases that integrate more source databases. However, this would require a significant effort to map and curate data across the sources that utilize different ways to define, name, and identify the drugs and protein targets.

Except for the 15 methods that reuse the internal database of KRM [176], the other predictors employ unique internal databases by combining data coming from different sets of source databases. Some predictors, such as NBI [183], SDTNBI [198], and DASPfind [199], use more than one internal database. In our analysis, we combine the contents of these internal databases for these three methods. Table 8 summarizes the main characteristics of the internal databases including the numbers of drugs, protein targets, DPIs, and average number of DPIs per drug. Table 8 shows that most of the internal databases cover between 276 and 7,739 drugs. Some of the internal databases also include other drug-like molecules, and correspondingly their sizes are larger and they span between 22,839 and 105,946 bioactive molecules. The number of protein targets in the internal databases ranges between 246 and 6,662. These are typically human proteins, except for nine methods that do not explicitly specify organism information of the proteins that they use (see “Focus on human proteins” column in Table 8). These numbers are comparable to an expected

scale of druggable human proteome, which is estimated to include between 1,000 and 3,000 proteins [1, 18-20]. Another important measure that quantifies coverage of the internal databases is the number of DPIs. This number varies between 1,731 and 155,208. While some databases include a large number of drugs or targets (e.g., databases for SEA, SDTNBI and EnsemDT/KRR predictors), they cover a relatively low number of DPIs per drug. The density of DPIs, which is calculated as the average number of DPIs per drug, varies widely between 1.1 and 11.5 (see “DPIs/drug” column in Table 8). Databases with low densities might be missing a substantial number of DPIs and consequently the corresponding predictors might provide inaccurate values of similarities. Moreover, higher density of interactions is likely associated with a more complete coverage of interactions for individual drugs. The corresponding internal databases can be used to provide a more reliable estimation of predictive quality at the drug level.

The medians of the main four characteristics of the internal databases over the 35 predictors are 932 drugs, 989 proteins, 5127 DPIs, and 5.1 DPIs per drug. The first three medians correspond to the frequently reused internal database of KRM predictor [176]. The corresponding medians for the latest releases of the 12 source databases in Table 5 are 23124 drugs, 3036 proteins, 33467 DPIs, and 2.8 DPIs per drug. Interestingly, the first three numbers are much higher while the last number is lower when compared to the sizes of the internal databases. This is in spite of the fact that individual predictors combine multiple source databases to derive their internal databases. One of the reasons why internal databases are relatively small is that they focus on particular collections of drugs and proteins. For example, the internal database of COPICAT [178, 269] includes only the 964 FDA-approved drugs, while its source database, DrugBank, also stores five thousand experimental drugs. The method developed by Liu et al. [193] focuses on *H. sapiens* and *C. elegans*, while its source databases also cover other organisms such as mouse and *E. coli*.

Another reason is that the internal databases are not being updated in contrast to the source databases that are frequently updated and grow in size [23]. In other words, some internal databases are based on outdated version(s) of the source database(s). For example, 16 predictors [168, 169, 172, 176, 179, 180, 182-184, 186, 187, 189, 192, 196, 197, 199], including some recent methods that were developed in 2017, utilize the same internal database [176] which has not been updated since it was published in 2008.

Although the internal databases include fewer drugs, proteins, and DPIs than the source databases, their median drug promiscuity at 5.1 DPIs per drug is 80% larger than the median promiscuity of the source databases, which equals 2.8. This increase is due to the aggregation of different DPIs for the same drugs that are coming from different source databases. The higher promiscuity suggests that the information about the interactions in the internal databases is more complete when compared to the individual source databases. This may benefit the similarity-based predictive models. For example, knowledge of a larger number of native targets would likely result in a larger set of candidate protein targets that could be explored to predict novel targets for a given drug. Also, a higher promiscuity increases the chances to identify proteins that are targeted by different drugs.

Table 8. Overview of the source and internal databases of the 35 similarity-based DPI predictors that were published in high impact venues. We group these methods into three categories: predictors using single type of similarity (1S), ensemble predictors employing two types of similarities (2S) and ensembles of three types of similarities (3S). We summarize the source databases that these predictors use to derive their internal databases. We provide information about the internal databases including number of drugs, proteins and DPIs, number of DPIs per drug, and number of data sources contained in the internal databases. We denote whether or not these methods focus on human proteins only. We also indicate whether a given predictor includes only interacting drug-protein pairs or both interacting and non-interacting pairs to evaluate predictive performance.

Type of predictor	Predictor	Year	Sources databases <sup>1</sup>	Number of sources	Drugs	Proteins	DPIs	DPIs/ drug	Focus on human proteins	Scope of evaluation
1S	SEA [175]	2007	MD	1	65,241	246	71,094	1.1		complete
	PRW & NB [190]	2013	CH	1	105,946	894	155,208	1.5	✓	interacting
	DrugMiner [165]	2016	DR	1	1,396	1,224	4,729	3.4	✓	complete
	SDTNBI [198]	2016	BI DR CH	3	22,839	1,541	57,726	2.5	✓	complete
	Peón et al. [167]	2017	CH	1	745	1,427	8,535	11.5		complete
	bSDTNBI [171]	2017	BI CH	2	276	453	1,796	6.5	✓	complete
2S	KRM [176]	2008	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	Campillos et al. [177]	2008	PK DR MA	3	502	N/A	4,857	9.7	✓	interacting
	COPICAT [178]	2009	DR	1	964	456	1,731	1.8		complete
	BLM [179]	2009	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	Yabuuchi et al. [181]	2011	GL	1	866	317	5,207	6.0		complete
	GIP [182]	2011	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	NBI [183]	2012	BR KB DR SU	4	5,330	4,785	17,610	3.3	✓	complete
	KBMF2K [184]	2012	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	Cao et al. [186]	2012	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	BLM-NII [187]	2012	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	Cheng et al. [188]	2013	TT DR	2	621	893	3,195	5.1		complete
	DT-Hybrid [189]	2013	BR KB DR SU	4	5,330	4,773	17,573	3.3	✓	complete
	RWR [194]	2015	DR	1	684	627	2,557	3.7		complete
	SLP & RLS [195]	2015	DR	1	786	809	3,681	4.7		complete
	RLS-KF [196]	2016	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	NRLMF [197]	2016	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	DASPfind [199]	2016	BR KB DR SU	4	3,897	6,662	12,919	3.3	✓	complete
	DrugE-Rank [200]	2016	DR	1	1,242	1,324	5,701	4.6	✓	complete
	DBN [166]	2017	DR	1	1,412	1,520	6,262	4.4		complete
	EnsemDT/KRR [201]	2017	DR	1	7,739	4,902	17,483	2.3		complete
PUDTI [168]	2017	BR KB DR SU	4	932	989	5,127	5.5	✓	complete	
DVM [169]	2017	BR KB DR SU	4	932	989	5,127	5.5	✓	complete	
iDTI-ESBoost [172]	2017	BR KB DR SU	4	932	989	5,127	5.5	✓	complete	
3S	Yamanishi et al. [180]	2010	BR KB DR SU	4	443	989	2,649	6.0	✓	complete
	PKR [185]	2012	KD	1	2,423	436	6,769	2.8	✓	complete
	DINIES [191]	2014	PK TT DR KD MA CH	6	678	277	1,804	2.7	✓	complete
	Shi et al. [192]	2015	BR KB DR SU	4	932	989	5,127	5.5	✓	complete
	Liu et al. [193]	2015	DR MA ST	3	2,486	3,356	7,369	3.0	✓	complete
	DTINet [170]	2017	DR	1	708	1,512	1,923	2.7	✓	complete
	This article	2018	PK TT DR CH + 15	19	449	1,469	34,456	76.7	✓	complete

<sup>1</sup>The source databases include MDDR (MD), PDSP Ki (PK), BRENDA (BR), BindingDB (BI), TTD (TT), KEGG BRITE (KB), DrugBank (DR), GLIDA (GL), KEGG DRUG (KD), SuperTarget (SU), Matador (MA), STITCH (ST), and ChEMBL (CH). This review relies primarily on the Drug2Gene resource where the data are derived from 19 source databases: PK TT DR CH + 15 other databases: CGDCP, ChEBI, CTD, HGNC, IUPHAR, Ligand Expo, MICAD, NCBI Gene, Pathway Commons DB, PDBsum, PharmGKB, PubChem Bioassay, PubChem Compound, PubChem Substance, and UniProt.

#### 4.4.4 Predictive models

The considered 35 predictors rely on three main types of similarities: chemical similarity (DCS), drug profile similarity (DPS), and protein sequence similarity (PSS). The three types of similarities can be combined to formulate an ensemble predictor with the underlining goal to improve predictive quality when compared to using a single similarity. Many of the predictors proposed in recent years rely on the ensembles that include two or three similarity types. Consequently, we categorize the 35 considered predictors into three groups: the methods that apply one type of similarity (1S), ensemble models that combine two types of similarities (2S), and ensembles of all three similarities (3S).

Table 9 includes six 1S predictors. Four methods [167, 171, 190, 198] measure DCS based on Tanimoto coefficient [289] that quantifies similarity between drug structures which are represented using molecular fingerprints [290, 291]. One predictor applies a statistical test over a set of DCSs based on Tanimoto coefficients between an input drug and a group of drugs in its internal database which are known to bind the input protein target [175]. The other method, DrugMiner, converts protein sequences into numeric feature vectors that represent physicochemical properties and amino acid compositions. Subsequently, it quantifies PSS for these feature vectors using machine learning algorithms and estimates druggability of a given protein based on its PSS to the known drug targets [165].

There are twenty three 2S models that utilize two types of similarities. Besides listing the similarity types we also define how they are combined together to generate predictions. Almost all of the 2S methods (21 out of 23) integrate DCS and PSS. Eleven predictors [176, 179, 182-184, 187, 189, 195-197, 199] quantify DCS using the SIMCOP algorithm [292, 293] while two other predictors [194, 200] utilize Tanimoto coefficient; these 13 methods rely on sequence alignment



algorithms such as BLAST [153] and Smith-Waterman [294] to measure PSS. A set of eight other methods represents drug structures and protein sequences using feature vectors that quantify DCS and PSS and they apply machine learning algorithms to generate predictions. These algorithms include kernel functions [168, 169, 178, 181, 186, 201], neural networks [166], and decision trees [172]. DPS is adopted rarely. Only two 2S predictors combine DPS with DCS [177, 188]. They define drug side-effect profile as a vector of binary values that indicate the presence or absence of specific side-effect terms. They quantify DPS based on weighted Tanimoto coefficients that measure similarities between side-effect profiles. The predictive models applied in these methods reveal that DPS could be used to infer DPIs in a similar way to DCS. This approach assumes that drugs that have similar side-effects are likely to target the same proteins. The drug profiles that were used in Ref. [177] have motivated the development of the SIDER database which stores drug side-effect information [120, 121]. This resource was later used in other works that we review including another 2S model [188] and three 3S methods [170, 185, 193]. However, SIDER focuses on marketed drugs and so the information about drug side-effects it provides is narrower when compared to drug structures that encompass a wider spectrum of drugs and protein sequences that span the entire human proteome. This is likely the reason why DPS is less frequently employed. Moreover, none of the 23 2S methods combines DPS with PSS. There are two ways in which the predictors combine two similarities. Five predictors apply a simple summation and weighted summation of two similarities [177, 187-189, 200]. The other predictors employ a more complex approach that typically involves operations such as maximum, multiplication, and geometric mean of multiple similarities.

There are six 3S methods that combine all three similarities. They utilize the same approaches to quantify DCS and PSS as the 1S and 2S models. Three of the six methods compute DPS based

on the cosine correlation coefficients between side-effect profiles [180, 185, 191] while two other models use Tanimoto coefficients [170, 193]. The sixth predictor [295] defines drug profiles using the ATC codes, which represent hierarchical classification of drugs and measure semantic similarity between ATC codes [192]. Like for the 2S methods, the 3S models utilize either a simple summation [191, 193] or a more complex approach to combine similarities [170, 180, 185, 192].

Table 9. Comparison of similarity-based DPI predictors. We review 35 methods that were published in high impact venues. We group these predictors into three categories (separated by horizontal line): predictors using one similarity (1S), predictors combining two types of similarities (2S), and predictors integrating three type of similarities (3S). Methods are sorted chronologically within each group. We summarize approaches that are used to quantify similarities and to compute ensembles of similarities for each predictor. We also summarize availability of empirical evaluation. This denotes inclusion of assessment of predictive quality, assessment of benefits of use of ensembles, assessment at per DPI and per drug levels, and analysis of sensitivity of predictive performance to intrinsic characteristics (similarity of inputs to the database) and extrinsic characteristics (information about the inputs) of predictors. The check symbol  $\checkmark$  means a given assessment is included in a given method (row) while a blank cell means it is not included. DCS: chemical similarity; DPS: drug profile similarity; PSS: protein sequence similarity; SE: SEA algorithm that measures DCS [175]; SI: SIMCOMP tool that quantifies DCS [292, 293]; TC: Tanimoto coefficient or other similarity score which measures similarity between binary or numeric vectors [289]; KF: kernel function that measures similarity between feature vectors used by machine learning algorithms; NN: neural networks; CO: correlation; SS: semantic similarity of drug profiles represented by the ATC codes [192]; AL: sequence alignment using PSI-BLAST [153] or Smith-Waterman algorithms [294]; and ML: machine learning tools that measure similarity between feature vectors.

Type of predictor	Predictor	Year	Similarities and their ensembles				Predictive quality		Benefit of ensemble		Sensitivity analysis	
			DCS	DPS	PSS	Ensemble	per DPI	per drug	per DPI	per drug	Intrinsic	Extrinsic
1S	SEA [175]	2007	SE			N/A	$\checkmark$		N/A	N/A		
	PRW & NB [190]	2013	TC			N/A	$\checkmark$		N/A	N/A		
	DrugMiner [165]	2016			ML	N/A	$\checkmark$		N/A	N/A		
	SDTNBI [198]	2016	TC			N/A	$\checkmark$		N/A	N/A		
	Peón et al. [167]	2017	TC			N/A	$\checkmark$		N/A	N/A		
	bSDTNBI [171]	2017	TC			N/A	$\checkmark$		N/A	N/A		
2S	KRM [176]	2008	SI		AL	C	$\checkmark$					
	Campillos et al. [177]	2008	TC	TC		S	$\checkmark$		$\checkmark$			
	COPICAT [178]	2009	KF		KF	C	$\checkmark$					
	BLM [179]	2009	SI		AL	C	$\checkmark$		$\checkmark$			
	Yabuuchi et al. [181]	2011	KF		KF	C	$\checkmark$		$\checkmark$			
	GIP [182]	2011	SI		AL	C	$\checkmark$					
	NBI [183]	2012	SI		AL	C	$\checkmark$		$\checkmark$			
	KBMF2K [184]	2012	SI		AL	C	$\checkmark$					
	Cao et al. [186]	2012	KF		KF	C	$\checkmark$					
	BLM-NII [187]	2012	SI		AL	S	$\checkmark$					
	Cheng et al. [188]	2013	TC	TC		S & C	$\checkmark$		$\checkmark$			
	DT-Hybrid [189]	2013	SI		AL	S	$\checkmark$					
	RWR [194]	2015	TC		AL	C	$\checkmark$					
	SLP & RLS [195]	2015	SI		AL	C	$\checkmark$					
	RLS-KF [196]	2016	SI		AL	C	$\checkmark$					
	NRLMF [197]	2016	SI		AL	C	$\checkmark$					
	DASPfind [199]	2016	SI		AL	C	$\checkmark$					
	DrugE-Rank [200]	2016	TC		AL	S	$\checkmark$		$\checkmark$			
	DBN [166]	2017	NN		NN	C	$\checkmark$					
	EnsemDT/KRR [201]	2017	KF		KF	C	$\checkmark$					
PUDTI [168]	2017	KF		KF	C	$\checkmark$						
DVM [169]	2017	KF		KF	C	$\checkmark$						
iDTI-ESBoost [172]	2017	ML		ML	C	$\checkmark$						
3S	Yamanishi et al. [180]	2010	SI	CO	AL	C	$\checkmark$		$\checkmark$			
	PKR [185]	2012	KF	CO	KF	C	$\checkmark$		$\checkmark$			
	DINIES [191]	2014	SI	CO	AL	S	$\checkmark$		$\checkmark$			
	Shi et al. [192]	2015	TC	SS	AL	C	$\checkmark$					
	Liu et al. [193]	2015	TC	TC	AL	S	$\checkmark$					
	DTINet [170]	2017	TC	TC	AL	C	$\checkmark$					
	This dissertation	N/A	TC	TC	AL	S	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$

#### 4.4.5 Timeline of the use of similarities and their ensembles

There are seven potential types of predictive models including three 1S, three 2S, and one 3S models. Figure 7 provides a timeline of the use of these seven types of predictive models for the 35 considered methods. In general, the ensemble-based models are much more widely utilized than the single similarity-based methods. The most frequently developed ensemble includes DCS and PSS. At least one of these methods was published every year except only for 2007, 2010, and 2014. The second most commonly used type of methods combines the three types of similarities. These methods were shown to outperform ensembles that are based on specific pairs of similarities, such as ensemble of DCS and PSS and ensemble of DPS and PSS [185]. However, a significant majority of current predictors combines only two similarities: DCS and PSS, without DPS. This is likely because the information on side-effects is not available in most of the source databases and this information used to be difficult to collect, especially before databases such as SIDER [120, 121] and MetaADEDDB [296] were developed. Also, the mapping of drugs from the side-effect databases into the drugs in the internal databases is non-trivial. Another reason why DPS is not an attractive option is the fact that the side-effect information is limited to the marketed drugs. Consequently, this limits the internal databases to this group of drugs. Unlike the two broadly adopted types of models mentioned above, the other types of models are published less frequently. These models rely on DCS, PSS, and the ensemble of DCS and DPS. Some designs, such as methods that use DPS and the ensemble of DPS and PSS, have not been employed among the 35 considered methods. In summary, the most popular configuration is the ensemble that combines DCS with another type(s) of similarity.

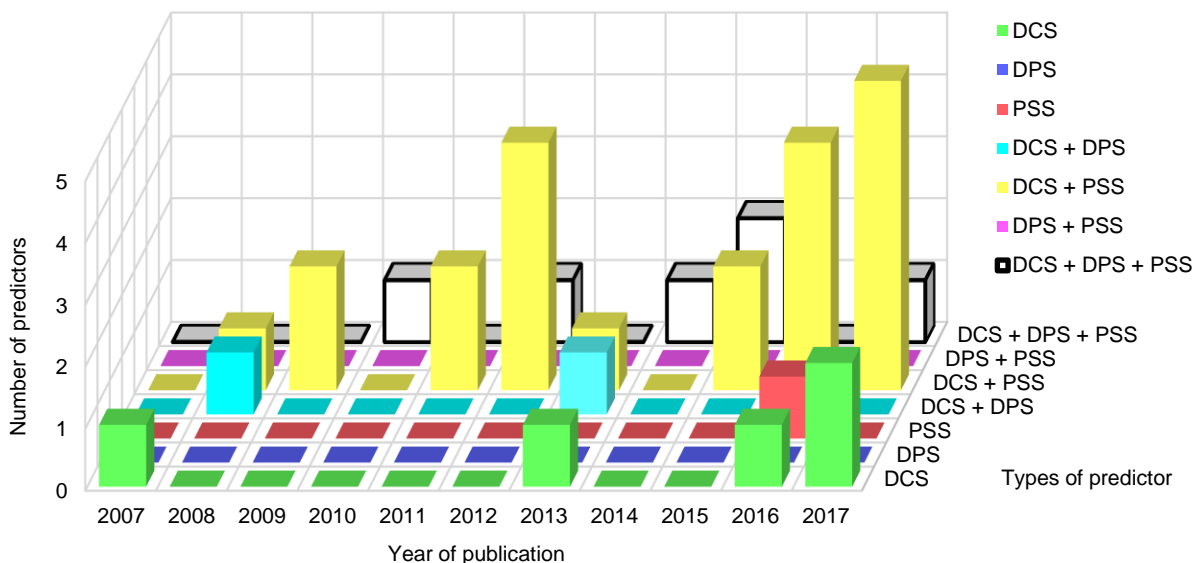


Figure 7. Timeline of similarity-based predictors of drug-protein interactions. The x-axis (width) denotes when the similarity-based predictors were published. The y-axis (depth) denotes the type of predictors. The z-axis (height) shows the number of a given predictors that were published in a given year. Green, blue, and red cubes represent drug chemical similarity (DCS), drug profile similarity (DPS), and protein sequence similarity-based predictors (PSS), respectively. The corresponding ensembles are color-coded according to the mixture of these three base colors shown in the figure legend.

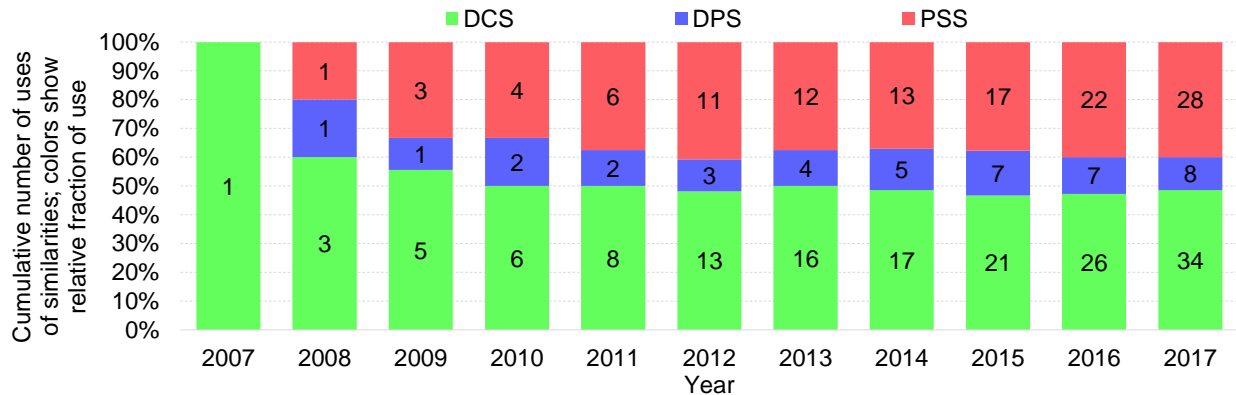


Figure 8. Use of individual similarities in predictors of drug-protein interactions. The x-axis denotes the year. The y-axis shows the fractions of cumulated numbers of uses of drug structure (green bars), drug profile (blue), and protein sequence (red) similarities up to a given year. Numbers inside the bars indicate the cumulative count of uses of each similarity. The similarity is counted when it is used individually by a single similarity-based predictor, and in tandem with other similarities by ensemble-based predictors.

Figure 8 shows how often an individual type of similarity was used over the last decade. We include their use individually and also as part of ensembles. Each bar in Figure 8 shows a cumulative number of times these similarities were used up to a given year. The colors inside the

bars reflect relative fraction of use of specific types of similarities. The first bar reveals that the first predictor that was published in 2007 was based on DCS [175]. The relative rate of use of DCS has gradually decreased between 2008 and 2010 when compared to the other two types of similarities. After 2010, the relative rate of use of the three types of similarities has stabilized; this is reflected by similar proportions of the three colors. The last bar reveals that in total the similarities were used 70 times by the considered set of 35 methods, which correspond to two similarities per method on average. DCS was used 49% of the time, while PSS and DPS were used 40% and 11% of the time, respectively. These fractions are consistent with the observation that the ensemble of DCS and PSS is the most frequently utilized type of predictive model. The relatively infrequent use of DPS is likely due to low drug coverage and difficulty to collect the information on drug side-effects. We believe that with the release and improvements to the databases that provide access to drug profiles, including SIDER and MetaADEDDB, this type of similarity will play a more prominent role in the development of future predictors.

#### **4.4.6 Critique of the current assessments of predictive performance**

Another important aspect of the considered DPI predictors is the assessment of their predictive performance. The predictions are provided at an interaction level, which means that the predictive models identify whether a given drug-protein pair interacts. Two early predictors were assessed solely using the interacting drug-protein pairs (see “Scope of evaluation” column in Table 8) [177, 190]. While such assessment evaluates true positive rate (TPR), which is defined as fraction of interactions that are correctly identified, it lacks the ability to assess specificity, which measures the fraction of correctly predicted non-interactions. The other 33 methods provide assessment for both interacting and non-interacting drug-protein pairs. This type of assessment is more complete as it measures not only TPR but also the capability to correctly identify the non-

interacting pairs that constitute majority of all possible drug-protein pairs. Moreover, the considered 35 predictors report their predictive performance over all drug-protein pairs that span multiple drugs. This means that they did not assess and compare predictive quality for individual drugs (see “Predictive quality” column in Table 9). However, drugs differ in their structures, profiles, and the number and type of protein partners that they bind to, and these factors likely impact the predictive performance.

Besides quantifying predictive performance, it is also essential to justify the use of ensembles. Since the ensembles require more computations and are more complex to implement than the 1S models, they must offer some benefits to balance these drawbacks. In particular, these benefits typically boil down to higher predictive performance when compared to the 1S methods. Only six out of 23 2S methods compare 2S model with 1S to quantify the corresponding improvement in the predictive quality evaluated per interaction (see “Benefit of ensemble” column in Table 9) [177, 179, 181, 183, 188, 200]. Additionally, three 3S methods provide empirical evidence that the ensemble of three similarities boosts the predictive quality at interaction level when compared to the 2S ensembles [180, 185, 191]. While this suggests that ensemble models may provide more accurate results than the 1S models, follow up studies are needed to explore the benefits of ensembles using both per interaction and per drug evaluation. Moreover, none of these methods has comprehensively compared all three 1S, three 2S, and one 3S models. Such analysis would provide important insights on the use of the similarity-based predictors.

Another interesting aspect is sensitivity of predictive performance to certain characteristics of predictors. For example, in a scenario where the query drug is dissimilar to the drugs in the internal database of a given predictor, DCS and DPS are likely to be ineffective. On the other hand, if the query drug has sufficient levels of similarity to some of the drugs in the internal database

then we can use these similar drugs to likely accurately predict the protein targets. Similarity between the user-provided inputs and the contents of the internal database of a given predictor relies on an intrinsic property of this predictor (i.e., its database). On the other hand, predictive performance could be also affected by extrinsic to the predictor and known a priori properties of the query drug and targets, such as the drug promiscuity. For instance, it might be easier to identify DPIs for a drug that target numerous proteins because this increases a chance to find many other similar targets in the internal database. Analysis of sensitivity of performance to these characteristics would help to calibrate the expectations of predictive quality and optimize the design of predictors for specific use cases. However, this type of sensitivity analysis was never addressed in the past studies (see “Sensitivity analysis” column in Table 9).

Besides quantifying predictive performance *in silico*, some of these predictive tools were also assessed experimentally. In that case, the correctness of the putative DPIs that they generate was additionally verified by *in vitro* binding assays and cell assays. This type of validation was done for the earliest predictor [175], the method that first defined DPS [177], and in one recent study [170].

## 4.5 Conclusions

We have discussed the timeline, impact, availability, contents, and architectures for the 35 high-impact similarity-based DPI predictors and the related 12 source databases.

The source databases store curated annotations of DPIs that are used to derive the internal databases of the predictors. Their contents were obtained from relevant literature, experiments, and other data repositories. Most of the 12 source databases also directly import the annotations of DPIs from the other source databases. Consequently, each source database stores its unique data



and also a certain amount of data that overlap with the other source databases. Moreover, some source databases focus on the interaction data for the approved and experimental drug compounds, while the others include the protein targets for a more generic collection of bioactive compounds that includes drugs and drug-like molecules. This contributes to the diversity of contents of the source databases, in terms of the number and type of compounds, protein targets, and DPIs. Drugs that are included in the source databases typically target multiple proteins. This drug promiscuity defines the field of polypharmacology and benefits the development of the similarity-based predictors. The source databases have accumulated data for over ten years and have been frequently used by the scientific community. This is reflected by the fact that they were cited at least 190 times each. Most of the databases are continually updated and periodical republished. Our analysis shows that the source databases that are more frequently updated and republished are also more often cited.

The similarity-based predictors have been developed at a steady pace over the past decade. These methods rely on the internal databases that typically include data derived from multiple source databases. We found that recent methods have used a larger number of source databases than the older methods, although this number is still relatively low compared to the number of available source databases. The internal databases generally include lower numbers of drugs, proteins, and interactions but higher degrees of drug promiscuity when contrasted with the corresponding source databases. A higher drug promiscuity allows the similarity-based predictors to screen a more complete set of candidate protein targets and increases likelihood of identifying targets shared by multiple drugs. Given these advantages, the future predictive models should exploit an even more comprehensive set of DPIs that would be collected from a larger number of source databases.

Most of the predictors have received a relatively high annual citation counts when compared to the corresponding impact factors of the journals where they were published. This points to the substantial impact of the similarity-based methods. These methods incorporate predictive models that quantify similarities between the input drugs and proteins and the drugs and their known targets in the internal databases. We show that they rely on a variety of approaches to quantify DCS, DPS, and PSS. Most of these predictors utilize ensembles that combine two or three types of similarities, were published in high impact venues and are highly cited. The three earliest predictors are the most cited. They were the first to use DCS and the ensemble of DCS and PSS/DPS. These pioneering works resulted in the DCS-centric trend for the development of the similarity-based models. The vast majority of the 35 methods applies DCS or ensemble models that combine DCS with DPS and/or PSS. The ensemble of DCS and PSS is the most commonly utilized type of predictive model. Our analysis of the frequencies of use of similarities has found that DCS and PSS have been utilized about 90% of the time, while DPS is relatively underutilized. The infrequent use of DPS likely results from the incompleteness and difficulty to use and collect the drug profiles. This motivates the need to further develop the drug side-effect profile databases, thereby facilitating a new generation of methods that would more heavily rely on DPS.

These studies assess predictive performance at the interaction level and some of them have demonstrated that the use of certain ensembles leads to improved predictive performance when compared to the use of a single similarity. However, a comprehensive empirical comparison of all types of similarities and their ensembles is missing. Although the current works perform empirical assessments over a large number of drug-protein pairs, primarily in the druggable human proteome, the density of DPIs in the databases that were utilized in these assessments is rather low. Moreover, per drug assessment of the predictive quality was not yet performed. Similarly, sensitivity of

predictive performance to characteristics of predictors was not yet studied. To this end, we provide comprehensive and in-depth empirical comparative analysis for a representative set of similarity-based predictors. First, we build a novel database that includes drugs characterized by high density of DPIs. Next, we comprehensively evaluate a representative set of predictors that are based on each of the three main types of similarities and the corresponding four possible ensembles. Besides evaluating predictive performance at the interaction level, we are the first to perform the drug level assessment and to analyze sensitivity of predictive quality to the intrinsic and extrinsic characteristics of predictors. This work is described in Chapter 5.

# **Chapter 5 Empirical assessment and comparative analysis of similarity-based methods for prediction of drug-protein interactions**

We empirically evaluate seven representative similarity-based DPI predictors. These seven predictors rely on each of the three individually used similarities (DCS, DPS, and PSS) plus four ensembles that combine each pair and all three similarities. We delineate the setup for the assessment by describing the seven predictors and defining measures and a novel high-quality benchmark database of DPIs that we use to assess the predictive performance. Like in the previous studies, we analyze predictive performance at the interaction level. Moreover, we are the first to compare all seven representative methods, to measure and compare predictive performance at the drug level, and to analyze sensitivity of predictive performance to characteristics of input drugs and proteins. We also release a webservice that provides access to the server-size implementations of the seven predictors.

## 5.1 Experimental setup

### 5.1.1 Computation of similarities

The key underpinning concepts that define similarity-based predictors of DPIs is how they quantify and combine the three similarities. We selected one representative approach drawn from previous works to measure each type of similarity. The Tanimoto similarity of chemical structures has been widely applied to quantify DCS [289]. Recent comparative studies have demonstrated that the Tanimoto similarity is one of the best DCS measures [291, 297, 298]. Eleven selected predictors have used the Tanimoto coefficient to quantify DCS [167, 170, 171, 177, 188, 190, 192-194, 198, 200]. The above reasons motivate our choice of this measure to quantify DCS. Tanimoto coefficient is computed based on molecular fingerprint that converts a chemical structure of a given drug into a bit vector of fixed size. For a given compound, the fingerprint represents presence of certain substructures with a bit value of 1 and their absence with a bit value of 0. Similarity of two drug fingerprints is represented by the similarity between their corresponding bit vectors A and B:

$$\text{DCS}(A, B) = a_1 b_1 / (a_1 + b_1 - a_1 b_1)$$

where  $a_1 b_1$  is a count of corresponding positions where both vectors A and B have values 1, and  $a_1$  and  $b_1$  are the counts of positions with value 1 in vectors A and B, respectively. Higher value of the Tanimoto similarity means the two molecules are more structurally similar since they have a higher fraction of similar substructures in common. We use the Chemistry Development Kit software [299-302] to generate 1024-bit molecular fingerprints of drug structures and to compute the Tanimoto similarity between drugs.

We quantify DPS based on a drug side-effect profile similarity introduced in one of the pioneering predictors that utilized this type of similarity for the first time [177]. A given drug is

represented by a profile vector that denotes presence/absence of certain side-effect term with a bit value of 1/0. The profile similarity is computed using the weighted Tanimoto coefficient between the side-effect profiles of a given pair of drugs. Each side-effect term has its own weight. The weight is derived based on an abundance of the corresponding term in a large collection of drugs (all drugs included in the internal database) and a correlation of this term with the other terms. Higher weights are associated with terms that are less frequent (specific to a small number of drugs) and that are dissimilar to other terms (they are infrequently used together with other terms for the same drugs). Consequently, higher value of DPS means that a given pair of drugs share a high fraction of side-effect terms with high values of weights. This approach to quantify DPS is arguably more accurate than the approaches taken by some other methods that use a simpler definition of weights [193] or unweighted Tanimoto coefficients [188].

We use sequence alignment to estimate PSS. This is the most popular approach that was adopted by 18 predictors [170, 176, 179, 180, 182-184, 187, 189, 191-197, 199, 200]. First, we run BLAST [154, 156] with default parameters to perform sequence alignment between a sequence of a protein target of the input drug provided by user and each protein target in the database of known DPIs. BLAST finds the closest protein from the database based on a distance defined as the fraction of identical and similar residues in the pairwise alignment. Therefore, proteins from the database that have high value of sequence similarity are arguably likely to also interact with the input drug by the virtue of being similar to the known target of this drug.

We create the four ensemble models using a linear combination of multiple types of similarities. This approach is in line with a number of published ensemble methods [177, 187-189, 200]. We consider the 3S model that combines the three types of similarities and three 2S ensembles that combine each pair of the three similarities, which we denote as DCS+DPS,

DCS+PSS, and DPS+PSS. Some of the past methods combine similarities using more sophisticated approaches, such as machine learning models and drug-protein networks. A typical machine learning-based predictor uses an algorithm such as SVM to combine multiple kernel functions/matrices derived from two or three similarities [191]. However, SVM requires computationally costly parameterization and this is a black-box method, which means that the model is so complex that it is impossible to understand how predictions are performed. Network-based predictors rely on a linear combination of similarities to quantify weights associated with edges in the network [187]. These predictors require knowledge of drug-drug or drug-target connections (network edges) for an input drug. Consequently, they cannot be utilized to predict DPIs for drugs that are not already integrated in the network [32]. We opt to use the linear combination of similarities which is computationally efficient, white-box (linear function explicitly defines how similarities are combined), and works with novel drugs.

### **5.1.2 Prediction of drug-protein interactions**

To perform the prediction, we screen the query drug against all candidate proteins from the internal database of known DPIs to evaluate how likely they may interact with this drug. Given the three types of similarities, the input information for the query drug may include drug structure, drug profile and/or protein sequences of its known targets. The procedure to perform predictions depends on which inputs are available. If the drug structure is available then for every candidate protein in the database we compute DCS between the query drug and every single drug that is known to bind to that candidate protein (excluding the query structure itself if the candidate protein is already known as a binding partner of this drug). The maximal value among these DCS values is used as the propensity of DPI between the query drug and the candidate protein. A higher propensity indicates that the candidate protein is more likely to bind to the query drug because this

protein is known to be a target of a drug which is structurally similar to the query drug. This is consistent with an observation that similar drug structures share the same protein target [32, 85-87]. A similar procedure is used when the drug profile is available. The propensity of DPI for the input drug and a given candidate protein is computed as the maximal DPS between this drug and all drugs that are known to bind to this candidate protein in the database of known DPIs. Such prediction relies on the assertion that drugs with similar side-effect profiles likely target the same protein [177]. If the protein targets of the input drug are known and their sequences are available then we compute pairwise PSS between each candidate protein and all known targets of this drug (excluding the candidate protein itself if this protein is already known to interact with the query drug in the database). The maximal PSS among all known targets is used as the propensity of DPI for the query drug and the candidate protein. The sequence similarity-based prediction is motivated by an observation that similar proteins tend to interact with the same drug [32, 85-87]. If multiple inputs are available then they are combined together. We assess whether such ensembles of two or three similarities would provide improved quality of predictions when compared to using these similarities individually.

### **5.1.3 Benchmark database of drug-protein interactions**

The DPI predictors rely on the internal database that contains native DPIs. We develop a novel benchmark database that we use as the internal database to evaluate these predictors. The benchmark database integrate three resources: Drug2Gene [247], Therapeutic Target Database (TTD) [43, 103-107], and IUPHAR/BPS Guide to Pharmacology database (GtP) [248, 249, 303-306]. Our database is primarily derived from Drug2Gene that integrates 19 source databases. These sources include four databases, PDSP Ki [202], TTD [43, 103-107], DrugBank [98-102], and ChEMBL [113-116], which are used by the 35 considered predictors to derive their internal



databases. However, we also include 15 other sources: CGDCP [307], ChEBI [308], CTD [238], HGNC [309], GtP [248, 249, 303-306], Ligand Expo [310], MICAD [311], NCBI Gene [312], Pathway Commons DB [313], PDBsum [314], PharmGKB [315], Pubchem Bioassay [239], PubChem Compound [316], PubChem Substance [316], and UniProt [37]. Considering that the 35 predictors adopt no more than six source databases, Drug2Gene provides us with a more complete information about DPIs. Another survey also highlights Drug2Gene as the most comprehensive DPI database [22]. In particular, use of Drug2Gene helps us to acquire high density of DPIs in the benchmark database. However, Drug2Gene (version 5) incorporates older versions of the TTD database (release 2011) and GtP database (release 2012) when compared its other sources. Thus, we combined Drug2Gene with newer versions of TTD (release 2015) and GtP (release 2015). These three resources altogether cover 10,515 compounds, 16,880 proteins, and 161,736 interactions. The density of DPIs for this database is 15 DPIs/drug, before removal of duplicates across these sources (see first row in Table 10).

The seven predictors that we assess rely on quantification of the three types of similarities. Thus, drug structures, drug profiles, and protein sequences are required for every drug/protein entry in the benchmark database. Drug fingerprints were collected from PubChem [316] by querying their compound identifiers (CIDs) that are available in three sources databases. Drug profiles were obtained from SIDER 2 [120, 121], a database of drug side-effects for marketed drugs, by matching PubChem CIDs. Protein sequences were retrieved from UniProt [37] using their UniProt accession numbers (UniProt IDs) which are available in TTD and GtP, and with the Entrez Gene [312] identifiers which are available in Drug2Gene. Consequently, drugs and proteins are respectively indexed by PubChem CIDs and UniProt IDs along with drug structures from PubChem, drug profiles from SIDER, and protein sequences from UniProt in the benchmark

database. We found redundant drug/protein entries because older versions of TTD and GtP have already been imported into Drug2Gene. We removed the duplicate drugs and proteins by comparing PubChem CID and UniProt ID, respectively. SIDER 2 provides side-effects for 996 drugs, which limits the number of drugs in our benchmark database. After collecting information for computing similarities and cleaning the duplicates, the resulting benchmark database contains 965 drugs, 7,565 proteins, 93,015 interactions, and 96 DPIs/drug (see second row in Table 10). Like most of studies in this area [165, 168-172, 176, 177, 179, 180, 182-187, 189-193, 196-200], we focus on the human protein targets. Thus, we eliminated non-human proteins based on their taxonomic identifiers from UniProt. Consequently, 563 drugs, 1,537 proteins, 35,352 interactions, and 63 DPIs/drug are left in the benchmark database (see third row in Table 10). Next, to ensure that sufficient amount of information about drug structure and protein sequence similarities is available to perform empirical assessment and sensitivity analysis, we removed small compounds that have fewer than 10 atoms and drugs that have fewer than five known protein targets, respectively. The final version of the benchmark database is composed of 449 drugs, 1,469 proteins, 34,456 interactions, and includes 76 DPIs/drug (see the last row in Table 10). When compared to the internal databases of the considered 35 predictors, this benchmark database is among the top 11% with respect to the number of DPIs shown in Table 8. Moreover, an arguably key indicator of a high-quality benchmark DPI database is the density of DPIs. High density of interactions facilitates reliable estimates for per-drug assessment of predictive performance. The benchmark database has the highest value of average per-drug density of DPIs at 76 DPIs/drug (median density = 95 DPIs/drug). Moreover, the median per-target density of DPIs is 4 DPIs/protein. This is a direct result of merging the largest number of sources of the DPI data and the fact that we only consider drugs that have at least five protein targets. Figure 9 shows the per-drug and per-target

density of DPIs for the drugs and proteins in the benchmark database, respectively. The top ten drugs that have the highest number of known targets include Imatinib (PubChem: 5291, 485 DPIs), Sorafenib (PubChem: 216239, 388 DPIs), Erlotinib (PubChem: 176870, 385 DPIs), Nilotinib (PubChem: 644241, 385 DPIs), Dasatinib (PubChem: 3062316, 384 DPIs), Gefitinib (PubChem: 123631, 343 DPIs), Chlorpromazine (PubChem: 2726, 168 DPIs), Mitoxantrone (PubChem: 4212, 166 DPIs), Nifedipine (PubChem: 4485, 162 DPIs), and Verapamil (PubChem: 2520, 158 DPIs). The top ten proteins that interact with the largest number of drugs include Cytochrome P450 3A4 (UniProt: P08684, 350 DPIs), Cytochrome P450 2D6 (UniProt: C1ID52, 329 DPIs), Cytochrome P450 2C9 (UniProt: P11712, 307 DPIs), Potassium voltage-gated channel, subfamily H (UniProt: A0A090N7W1, 298 DPIs), Cytochrome P450 1A2 (UniProt: P05177, 296 DPIs), Mitogen-activated protein kinase 1 (UniProt: P28482, 288 DPIs), Dopamine receptor D2, isoform CRA\_c (UniProt: A0A024R3C5, 283 DPIs), Muscarinic acetylcholine receptor (UniProt: A0A024R3S2, 280 DPIs), Muscarinic acetylcholine receptor M1 (UniProt: P11229, 280 DPIs), and Muscarinic acetylcholine receptor (UniProt: A4D1Q0, 279 DPIs). The list of drugs, protein targets, and DPIs of the benchmark database are shown in the Appendixes 1, 2 and 3, respectively.

Table 10. Summary of the benchmark DPI database. The numbers were counted after each major step of the procedure that lead to the completion of the benchmark database. The density of DPIs (DPIs/drug) is calculated by the average number of DPIs per drug.

<b>Procedure of data processing</b>	<b>Drugs</b>	<b>Proteins</b>	<b>DPIs</b>	<b>DPIs/drug</b>
Total counts in original sources databases	10,515	16,880	161,736	15
Filtered by availability of necessary information to compute similarities	965	7,565	93,015	96
Filtered by to include human proteins	563	1,537	35,352	63
Filtered by drug size (> 10 atoms) and number of known targets per drug (> 5 DPIs/drug)	449	1,469	34,456	76

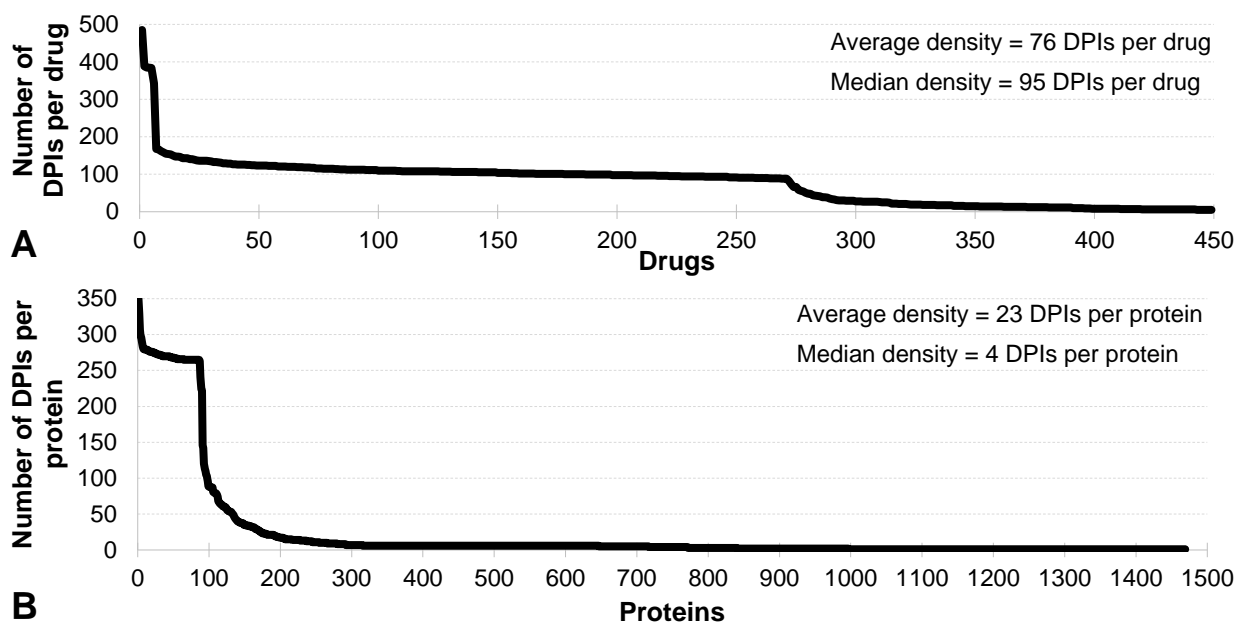


Figure 9. Density of DPIs for the drugs and protein targets in the benchmark database. Panel A shows the numbers of DPIs per drug and sorts the drugs in the descending order by these numbers. Panel B shows the numbers of DPIs per protein and sorts the proteins in the descending order by these numbers.

The source DPI databases include annotations of native interacting drug-protein pairs but they lack the annotations of non-interacting pairs. In the past, these databases were used to assess predictors of DPIs in several ways. A few early studies have assessed predictive performance using only the native interacting pairs [177, 190]. These assessments are incomplete since they measured only the rate of correctly predicted native DPIs while they did not evaluate the predictive performance for the non-interacting pairs, i.e., they did not evaluate the number of false positives. More recent works have assessed predictions using both interacting and non-interacting drug-protein pairs. Most of these studies assume that the drug-protein pairs that are not annotated as interacting are non-interacting. This assumption may result in mislabeling some of the native interacting pairs as non-interacting; in particular, those that were not yet discovered. This commonly applied approach to annotate the non-interacting pairs relies on an assertion that the number of such mislabeled pairs is much smaller than the number of correctly assumed non-

interacting pairs. We are the first to study this assumption empirically. We annotate weak binders among the native drug-protein binding pairs and we compare similarity between the assumed non-interacting drug-protein pairs and the similarity among the weakly binding pairs. We hypothesize that the assumed non-interacting drug-protein pairs can be used to represent the native non-interacting pairs if the difference between similarity of the non-interacting drug-protein pairs and similarity among the native interacting pairs is significantly higher than the difference between similarity of weak interactors and the similarity of the native interacting pairs.

We map the drug-protein pairs from the benchmark database into the PDSP Ki database that provides binding affinities [202]. A high binding affinity (affinity constant  $K_i < 10 \mu\text{M}$ ) is typically considered to indicate an interacting drug-protein pair [177, 234]. Consequently, we divide the mapped drug-protein pairs into three subsets: the native interacting pairs with  $K_i < 10 \mu\text{M}$ , weak native interacting pairs with  $K_i > 10 \mu\text{M}$ , and the non-interacting pairs that include all pairs that are not annotated as DPIs. We compute DCS, DPS, and PSS for the drug-protein pairs in each subset. Figure 10 compares distributions of the values of three similarities for the native interacting pairs, weak native interacting pairs (borderline pairs), and non-interacting pairs. The distributions are represented by the 5th, 20th, 50th (median), 80th, and 95th percentiles. The results are consistent across the three similarities. The similarity values for the non-interacting drug-protein pairs are significantly lower when compared to the similarities for the weak native interactors ( $p\text{-value} < 0.01$ ). They are also significantly lower when compared to the similarities for the native interacting pairs ( $p\text{-value} < 0.01$ ). In other words, Figure 10 reveals that only a small portion of the non-interacting pairs has DCS, DPS and PSS values that are comparable to the DCS values of the native DPIs. We also observe that the distributions for DPS and PSS for the weak native interactors are similar to the distributions for the native interactors ( $p\text{-value} = 0.11$  and  $0.65$ ,

respectively). While the difference between weak native interactors and native interactors for DCS is significant, the median DCS are 0.65, 0.41, and 0.28 for the native interacting pairs, weak native interacting pairs and non-interacting pairs, respectively. Over 95% / 80% of the native interacting pairs have higher DCS values than at least 50% / 80% of the non-interacting pairs. In agreement with previous studies, these results suggest that the assumed non-interacting pairs can be used to represent non-interacting pairs since their similarity is significantly lower than the similarity of the weak native interactors and the native interactors, while the differences between the latter two sets of drug-protein pairs are substantially smaller. We also observe that the number of non-interacting pairs that have relatively high PSS is greater than those that have relatively high DCS and PSS. This implies that predictions using PSS might be less accurate than the predictions with DCS or DPS.

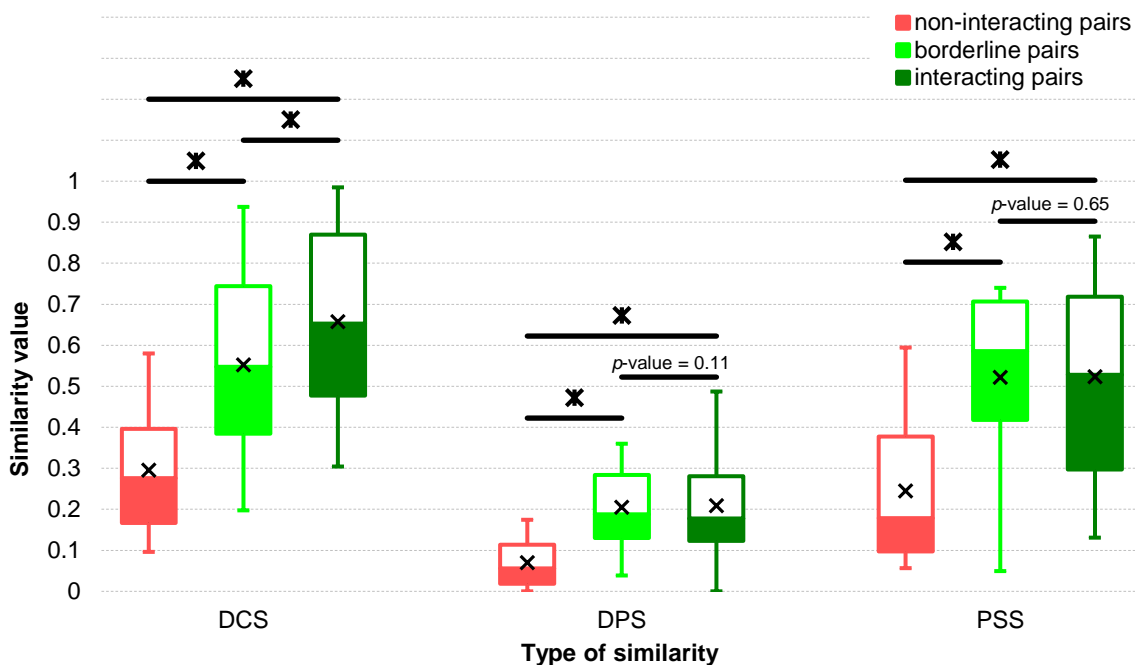


Figure 10. Distributions of values of the three types of similarities for native interacting drug-protein pairs ( $K_i < 10 \mu\text{M}$ ; dark green), weak native interactors ( $K_i > 10 \mu\text{M}$ ; borderline pairs in light green), and non-interacting drug-protein pairs (in red). Boxes and whiskers represent the 5th, 20th, 50th, 80th, and 95th percentiles of the similarity values. Marker  $\times$  represents average similarity value for a given set of drug-protein pairs. We assess significance of differences between the similarity values for each pair of drug-protein pair sets using the Wilcoxon rank sum test [317]; we use the non-parametric test since these data are not normal according to the Anderson-Darling test at 0.01 significance. \* indicates that the difference is statistically significant ( $p\text{-value} < 0.01$ ); otherwise the actual  $p\text{-value}$  is shown.

### 5.1.4 Assessment of predictive performance

Using the benchmark database, we empirically test predictions for each of the 449 drugs by comparing the putative targets generated by a given method with the known native interactors for this drug. When testing predictions for a given drug, we remove information about its known targets from the database. We analyze the results across all drugs and separately for each drug. Like virtually all considered in this review methods we use the receiver operating characteristic (ROC) curve and the area under the ROC curve (AUC) to assess quality of DPI predictions [165, 166, 168-172, 175, 176, 178-189, 191-201]. ROC curve is a plot of True Positive Rates (TPRs) against False Positive Rates (FPRs):  $\text{TPR} = \text{TP} / (\text{TP} + \text{FN})$  and  $\text{FPR} = \text{FP} / (\text{FP} + \text{TN})$ , where the

TP (True Positive) and the TN (True Negative) are the numbers of native interacting pairs and native non-interacting pairs that are predicted correctly, respectively; the FN (False Negative) is the number of native interacting pairs predicted as non-interacting; and the FP (False Positive) corresponds to the number of native non-interacting pairs predicted as interacting. The predicted propensities are transformed into binary predictions (positive vs. negative) using threshold values, which are next used to compute the TPR and FPR. Drug-protein pairs with propensity above the threshold are assumed to bind (positive), otherwise they are assumed to be non-binding (negative). The thresholds are set to be equal to all unique values of the predicted propensities of DPIs in order to derive the most accurate ROC curve. Higher AUC values denote better predictive performance, i.e., they correspond to predictions that offer higher TPRs (more correct predictions of DPIs) for lower FPRs (fewer incorrect predictions of non-interactions as DPIs).

The fraction of the native interacting drug-protein pairs among all drug-protein pairs in the benchmark database is at about 5%. Thus, for example, if  $FPR = 10\%$  then the number of predicted putative DPIs is about twice the number of actual native interacting pairs. This corresponds to a substantial over-prediction of putative DPIs. Moreover, the AUC values are determined primarily by the part of the curve where FPR is high, focusing on the over-prediction, i.e., area under the curve for the low FPR values is much smaller than for high FPR values. Thus, motivated by recent works [318-321] we focus the lower part of ROC with FPR less than 5% ( $ROC_{low}$ ) where the number of incorrectly predicted DPIs is not larger than the number of native DPIs. Accordingly, we calculate the corresponding area under  $ROC_{low}$  curve ( $AUC_{low}$ ). Moreover, to ease interpretation of this index, we report  $Ratio_{AUC_{low}} = AUC_{low} / AUC_{low-random}$ , where  $AUC_{low-random}$  is  $AUC_{low}$  for a random predictor. A random predictor generates TPRs that are equal to FPRs, resulting in a diagonal line in the TPR-FPR space.  $Ratio_{AUC_{low}}$  measures to what degree a given



predictor is better than a random predictor.  $\text{Ratio}_{\text{AUC}_{\text{low}}} > 1$  means the method is better than random. An alternative to measuring the ROC for dataset with low numbers of positive samples is to use Precision-Recall curves. However, we opt to use  $\text{ROC}_{\text{low}}$  because this is the most frequently used measure in this area [165, 166, 168-172, 175, 176, 178-189, 191-201].

## 5.2 Empirical analysis of predictive performance

We perform evaluation of the predictive quality of the three 1S predictors as well as their 2S and 3S ensembles. We assess predictive performance for each drug by removing it from the benchmark database, predicting its interactions with each proteins target in that database, and evaluating these predictions against the removed native interactions of this drug. We aggregate these results over all the drugs and 659,581 drug-protein pairs. A query drug might be dissimilar to the drugs in the benchmark database in terms of its structure and side-effect profile. To simulate a practical scenario, we limit the similarity between the query drug and the drugs in database. Specifically, given a query drug, we not only remove this drug but we also remove the drugs with above median DCS and DPS from the benchmark database when performing the evaluations. Use of the median represents an average case. Note that the protein sequences are easy to collect and all of them are available for every prediction. The complete set of sequences for human proteins can be obtained from UniProt. Thus, the predictions for a given query drug are generated based on the drugs with the below-median DCS and DPS, and the complete set of protein sequences.

### 5.2.1 Assessment of predictive performance at the drug-protein interaction level

Figure 11 shows the ROCs and  $\text{ROC}_{\text{low}}$  that measure the predictive quality at the interaction level over all drug-protein pairs in the benchmark database for the three 1S, three 2S, and one 3S predictors. The 3S model has the highest AUC,  $\text{AUC}_{\text{low}}$  and  $\text{Ratio}_{\text{AUC}_{\text{low}}}$  values, which are given

in the legend for Figure 11. The 1S models register a modest drop in predictive quality when compared to the 2S models. Specifically, the relative difference in AUC (in  $AUC_{low}$ ) between 3S and the best 2S model equals  $[0.926-0.913]/0.913 = 1.4\%$  ( $[0.0285-0.0274]/0.0274 = 4.0\%$ ) (Figure 11A). The corresponding relative difference when comparing 3S and 1S models are at least  $[0.926-0.883]/0.883 = 4.9\%$  for AUC and  $[0.0285-0.0231]/0.0231 = 23.4\%$  for  $AUC_{low}$ . These results consistently demonstrate that the use of ensembles results in improvement in predictive quality. Moreover, our results show that adoption of the 3S, the three 2S, and DCS and DPS models provides high-quality predictions. The only relatively low results for PSS could be perhaps explained by the larger overlap of similarities between the native DPIs and non-DPIs observed in Figure 10. Although DCS provides more accurate predictions in terms of AUC when compared to DPS and PSS, the ensemble of DPS+PSS outperforms the two 2S predictors that rely on DCS. Combining DPS and PSS provides the largest improvement over these similarities used individually. Specifically, the relative difference in AUC (in  $AUC_{low}$ ) is 4.8% (13.7%) and 20.4% (130%) when comparing DPS+PSS with DPS and PSS, respectively. The corresponding improvements for the other two 2S models are more modest. DCS+PSS provides a relative increase in AUC (in  $AUC_{low}$ ) when compared to DCS and PSS by 2.6% (9.5%) and 19.5% (143%), respectively. Similarly, the value of AUC ( $AUC_{low}$ ) for DCS+DPS is better by 1.9% (18.6%) and 3.3% (29.9%) than the values for DCS and DPS, respectively. One possible explanation for these differences is that each of the three similarities offers good predictive performance while DPS and PSS are lack any correlation (Spearman correlation coefficient [SCC] = 0.05), DCS and PSS are weakly correlated (SCC = 0.14), and DCS and DPS are modestly correlated (SCC = 0.30). Therefore, PSS and DPS complement each other the most which results in the largest improvement in the quality of predictions.

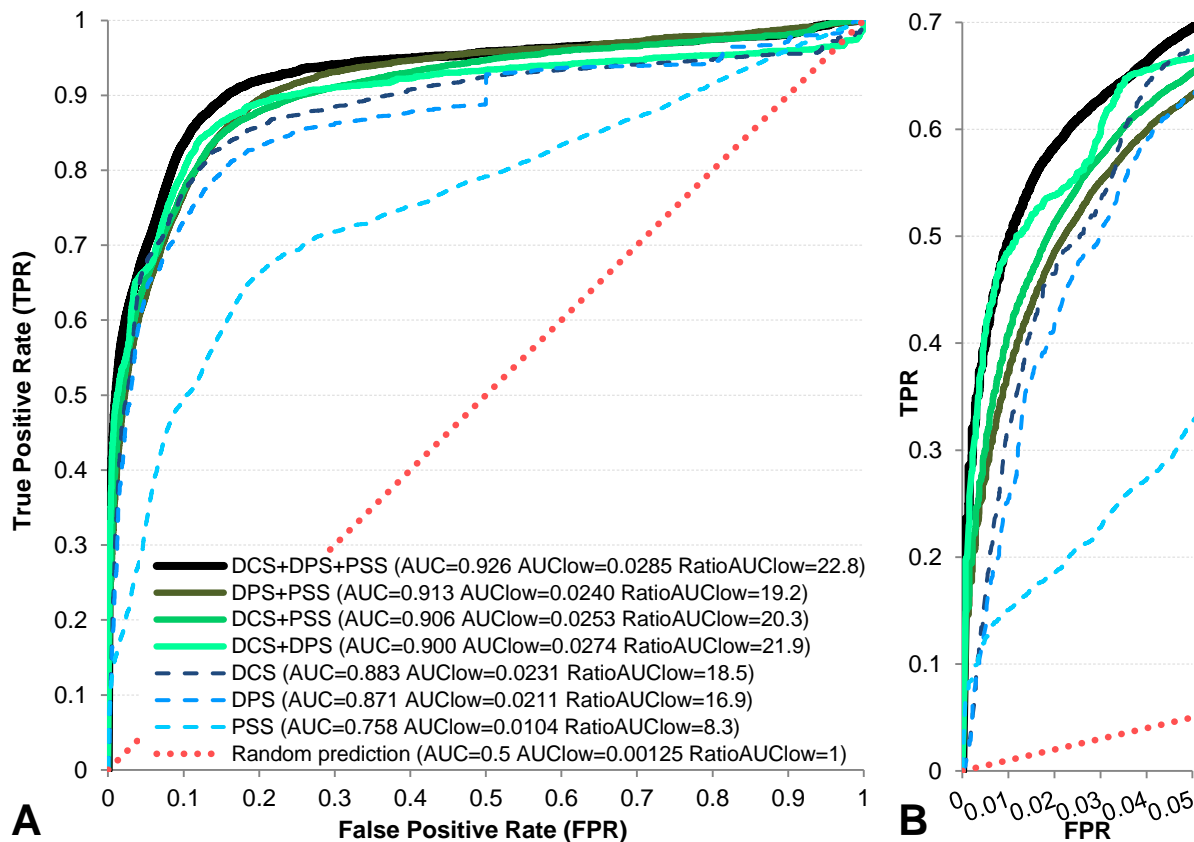


Figure 11. Comparison of predictive performance for the 1S, 2S, and 3S DPI predictors measured at the interaction level. Panel A shows ROC curves and panel B shows ROC<sub>low</sub> for which FPRs  $\leq 0.05$ . Diagonal dotted line denotes the ROC curve for a random predictor for which TPR = FPR. Values of AUC, AUC<sub>low</sub> and RatioAUC<sub>low</sub> are shown in the legend for panel A.

When FPR is greater than 0.05, the number of native non-DPIs that are incorrectly predicted as DPIs is larger than the total number of native DPIs. In other words, we over-predict DPIs. Therefore, we utilize AUC<sub>low</sub> that considers the ROC curve for FPR < 0.05. The advantages of using multiple similarities, i.e., 3S vs 2S and 2S vs 1S, are maintained for AUC<sub>low</sub> (Figure 11B). The RatioAUC<sub>low</sub> reveals that 3S model is about 23 times more accurate than random predictions while 2S and 1S models are up to 22 and 19 times more accurate when compared to the random predictions. In particular, 3S predictor identifies 70% and the best 2S model finds 67% of native DPIs while they incorrectly recognize 5% of non-DPIs as DPIs (FPR = 0.05). Almost all predictors

successfully detect over 63% of native DPIs ( $\text{TPR} > 0.6$ ) at 5% level of FPR, except PSS which finds 33% of native DPIs. Similar to the evaluations based on the overall AUC, predictor based on DCS is the most accurate 1S model in terms of  $\text{AUC}_{\text{low}}$ . Therefore, DCS drives the predictive quality of the ensembles. Moreover, PSS has the lowest performance of the three similarities, which is still eight times better than the random predictions. Moreover, PSS is helpful for the ensemble models given its lack of correlation with the other two similarities. The  $\text{AUC}_{\text{low}}$  for the 2S ensembles that include PSS register relative improvement by 9.5% and 13.7% when contrasted with DCS and DPS, respectively.

We also evaluate statistical significance of the differences in predictive quality between the 3S model, the three 2S models, and the three 1S models. To do that, we evaluate the differences over a diverse collection of 100 datasets drawn from the benchmark database. Each dataset includes 10% of randomly selected (without replacement) drugs from the benchmark database. Therefore, overlap between these datasets is minimal resulting in a large and diverse sampling of subsets of the benchmark datasets. We measure the AUC,  $\text{AUC}_{\text{low}}$ , and  $\text{Ratio}_{\text{AUC}_{\text{low}}}$  for each dataset. The corresponding averages and standard deviations quantified over the 100 datasets are given in Table 11. These averages are consistent with the results on the entire benchmark database that we give in Figure 11A. The  $p$ -values that measure significance of differences between all pairs of the considered seven methods are below 0.01, which mean that the differences in the predictive quality are statistically significant. This reveals that the benefits brought by the use of multiple similarities and the higher predictive performance of DCS compared to other 1S models are consistent over a diverse sampling of datasets. Overall, we show that 3S is the most accurate and significantly more accurate than the 2S predictors, while the 2S predictors are significantly better than the 1S models.

DCS is significantly more accurate when compared to DPS and PSS. These observations provide useful hints for future users and designers of the DPI predictors.

Table 11. Significance of differences in the predictive performance of DPI predictors measured at interaction level. The distribution of AUC,  $AUC_{low}$ , and  $Ratio_{AUC_{low}}$  values quantified over 100 different datasets (randomly selected 10% of drugs from the benchmark database) are represented by average  $\pm$  standard deviation. The *italic* and underlined fonts represent results of tests of significance of difference in AUC and in  $AUC_{low}$ , respectively, for each pair of predictors. We quantify the corresponding  $p$ -values by running  $t$ -test (for measurement with normal distribution) or Wilcoxon signed-rank test (for non-normal data) between each pair of predictors. We test the normality with the Anderson-Darling test at 0.01 significance.

Method	Predictive quality (average $\pm$ standard deviation)			Statistical significance (p-value) of the differences between all pairs of predictors						
	AUC	$AUC_{low}$	$Ratio_{AUC_{low}}$	3S	DPS+PSS	DCS+PSS	DCS+DPS	DCS	DPS	PSS
3S	0.925 $\pm$ 0.005	0.0284 $\pm$ 0.0005	22.7 $\pm$ 0.4		<i>5.4E-26</i>	<i>4.0E-77</i>	<i>2.3E-46</i>	<i>3.7E-59</i>	<i>1.6E-54</i>	<i>8.5E-104</i>
DPS+PSS	0.912 $\pm$ 0.004	0.0240 $\pm$ 0.0005	19.2 $\pm$ 0.4	<u>1.0E-69</u>		<i>3.3E-10</i>	<i>1.9E-12</i>	<i>1.0E-30</i>	<i>5.5E-51</i>	<i>5.8E-105</i>
DCS+PSS	0.905 $\pm$ 0.005	0.0252 $\pm$ 0.0005	20.2 $\pm$ 0.4	<u>4.7E-64</u>	<u>3.9E-14</u>		<i>7.4E-07</i>	<i>4.1E-37</i>	<i>5.8E-34</i>	<i>4.8E-98</i>
DCS+DPS	0.899 $\pm$ 0.006	0.0273 $\pm$ 0.0007	21.9 $\pm$ 0.6	<u>1.3E-08</u>	<u>1.3E-30</u>	<u>1.7E-18</u>		<i>8.2E-45</i>	<i>8.4E-32</i>	<i>5.5E-81</i>
DCS	0.882 $\pm$ 0.006	0.0230 $\pm$ 0.0006	18.4 $\pm$ 0.5	<u>2.0E-56</u>	<u>3.0E-05</u>	<u>3.2E-22</u>	<u>5.2E-58</u>		<i>3.3E-08</i>	<i>5.1E-74</i>
DPS	0.869 $\pm$ 0.008	0.0210 $\pm$ 0.0007	16.8 $\pm$ 0.6	<u>2.9E-69</u>	<u>3.7E-34</u>	<u>7.9E-39</u>	<u>5.7E-78</u>	<u>8.2E-23</u>		<i>1.5E-66</i>
PSS	0.759 $\pm$ 0.012	0.0100 $\pm$ 0.0029	8.0 $\pm$ 2.3	<u>3.2E-92</u>	<u>9.2E-87</u>	<u>2.0E-88</u>	<u>2.1E-72</u>	<u>1.6E-65</u>	<u>1.2E-57</u>	

We study relationship between the predictive performance and similarity values by comparing predictions between the 3S and 1S models to understand how the predictive performance benefits from combining multiple similarities. We divide values of DCS, DPS, and PSS into 20 equally sized intervals and utilize these intervals to partition the benchmark database into subsets in which the drug-protein pairs have comparable similarity values. Figure 12 deconstructs the 3S model into two dimensional plots of two similarities, each divided into 20 intervals for the total of 400 data points. This figure compares the predictive quality of the 3S model (shown inside of the first quadrant) with the three 1S models (left most vertical set of points and bottom most horizontal set of points, which are outside of the quadrant). The predictive quality is measured with accuracy defined as a fraction of correctly identified DPIs and non-DPIs to total number of drug-protein pairs in a given data point; we denote that by the bubble size in Figure 12. We could not use AUC because some of these data points may not have either native DPIs or native non-DPIs. We use colors to denote relative enrichment of native DPIs and non-DPIs for

each data point where dark red denotes enrichment in non-DPIs and dark green is for enrichment in DPIs. The enrichment is defined as the difference between the fractions of DPIs and non-DPIs, which are computed by dividing the number of native DPIs (non-DPIs) in a given data point by the total number of DPIs (non-DPIs) in the benchmark database. For instance, a light red point for  $DCS \in [0.25, 0.3]$  and  $PSS \in [0, 0.05]$  in Figure 12B. shows that a modest majority of drug-protein pairs with these values of the two similarities are non-DPIs (which is denoted by the light red color) and accuracy of the 3S model for this data point is 100% (which is denoted by the large size of the bubble).

Figure 12A shows that the predictive accuracy for 3S model is separated into two distinct regions. The first region includes red data points for  $DCS \in [0.05, 0.45]$  and  $DPS \in [0, 0.15]$ . This region is enriched in native non-DPIs (red color) and has high predictive accuracy (large bubble). The second region includes green data points for  $DCS \in [0.45, 1]$  and  $DPS \in [0.1, 0.3]$ . This region is enriched in native DPIs (green color) and has lower predictive accuracy (smaller bubble) when compared to the red region. As expected, the colors reveal that the native non-DPIs are concentrated in the drug-protein pairs with low values of DCS and DPS while the native DPIs are more enriched in the drug-protein pairs with high similarities. This demonstrates that similarities could be used to discriminate DPIs from non-DPIs. The bubble sizes reveal that it is easier to provide high predictive performance for non-DPIs because they contain many drug-protein pairs and most of them include drugs which are very dissimilar to drugs which are known to bind the same protein. Such dissimilar drugs are easy to be correctly predicted as the non-interacting pairs. On the other hand, the predictions are less accurate for the green bubbles. This is because they cover drug-protein pairs for which drug structures are similar to the drugs that interact with the same proteins. Moreover, some of the pairs in these bubbles are still non-DPIs and they are difficult

to differentiate from the native DPIs. Most importantly, Figure 12A explains why 3S model is better than the corresponding two 1S models that rely on DCS and DPS. DCS values can be used to reliably separate non-DPIs (dark red bubbles in the bottom horizontal line where  $DCS < 0.4$ ) from DPIs (dark green bubbles where  $DCS > 0.5$ ). However, drug-protein pairs for DCS between 0.4 and 0.5 cannot be easily separated. The separation of these drug-protein pairs into DPIs and non-DPIs can be improved by adding the values of DPS. Specifically, drug-protein pairs with  $DCS \in [0.4, 0.5]$  and  $DPS \in [0, 0.1]$  are mostly non-DPIs (red bubbles) while the drug-protein pairs with  $DCS \in [0.4, 0.5]$  and  $DPS > 0.1$  are mostly DPIs (green bubbles). Moreover, the bubble sizes also suggest that the accuracy of the 3S model is better than DCS model. The bubble for  $DCS \in [0.45, 0.5]$  has moderate accuracy = 78%. The corresponding column for the 3S model at  $DCS \in [0.45, 0.5]$  has includes much larger bubbles that correspond to higher accuracies. The accuracy for the 3S model is high (between 89% and 98%) when  $DPS < 0.2$  and  $DCS \in [0.45, 0.5]$ . On average, accuracy of the 3S model for  $DCS \in [0.45, 0.5]$  equals 84% when compared to 78% when DCS is employed alone. Similar observations can be made for Figure 12B. Overall, the 3S model improves over the 1S models in the interface between the red and green regions.

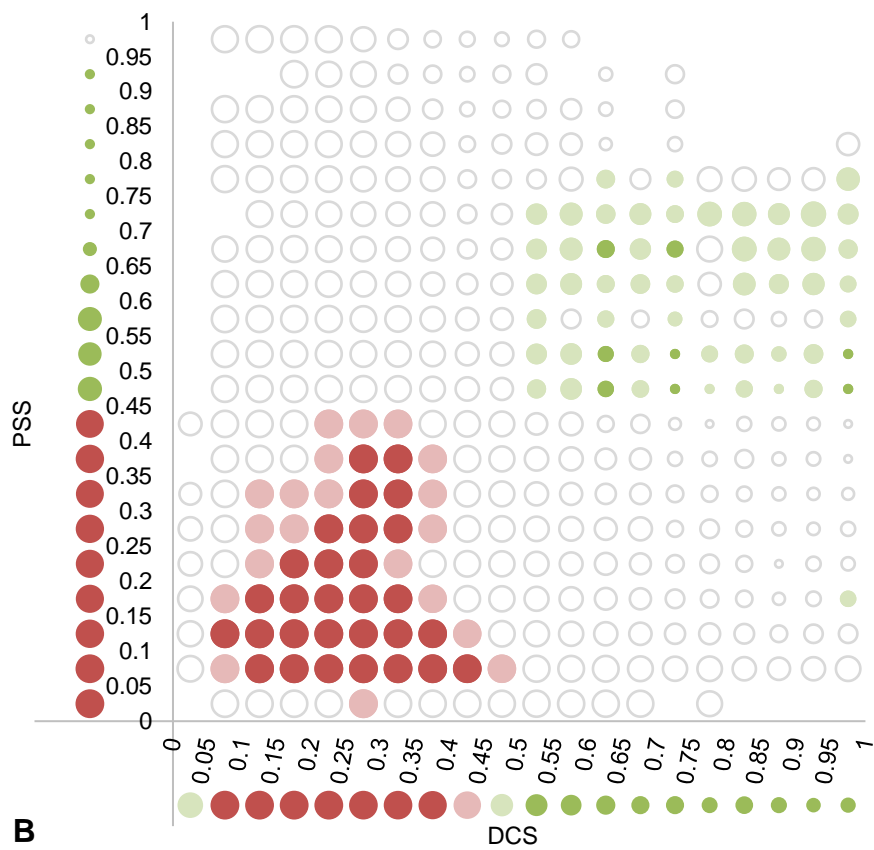
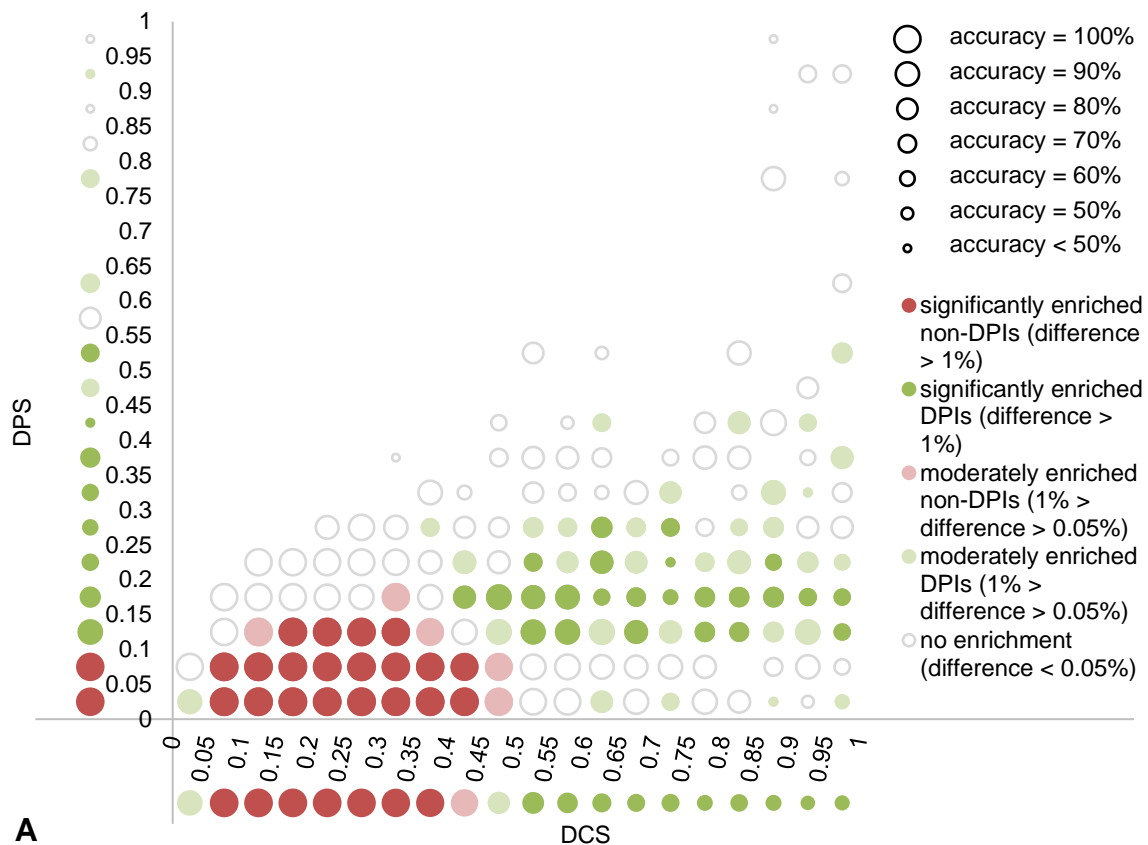




Figure 12. Comparison of predictive performance between 3S and 1S models in the function of values of the three similarities. The values of the three similarities are divided into 20 equally sized intervals. The comparison of the 3S vs the three 1S models is divided into two panels that compare the 3S model vs. two sets of 1S models each. Panel A shows the comparison of 3S vs. DCS and DPS. Panel B shows the comparison of 3S vs. DCS and PSS. Accuracy for the 3S model is shown inside the first quadrant while 1S models are given as a horizontal line below x-axis and a vertical line to left from the y-axis. Each bubble represents the drug-protein pairs in a given interval. Bubble sizes denote accuracy, which is defined as the fraction of correctly identified DPIs and non-DPIs to total number of drug-protein pairs in that bubble. Color denotes enrichment in native DPIs/non-DPIs, which is defined as the difference between the fractions of native DPIs and non-DPIs. These are computed by dividing the number of DPIs (non-DPIs) in a given bubble by the total number of DPIs (non-DPIs) in the benchmark database. We discretize the enrichment into five levels: dark green (dark red) bubble denotes significant enrichment in DPIs (non-DPIs) if the difference  $\geq 1\%$ ; light green (light red) bubble indicates moderate enrichment in DPIs (non-DPIs) if the difference  $\geq 0.5\%$ ; and white hollow bubble means no enrichment for which the difference  $< 0.5\%$ . White space in the figure denotes bubbles that we removed because they contain fewer than 100 drug-protein pairs; this is to ensure that statistics are robust.

### 5.2.2 Assessment of predictive performance at drug level

All previous studies evaluate predictive performance at the interaction level, which measures accuracy of the DPI predictions over drug-protein pairs that span across multiple drugs. Considering the fact that different drugs may share different levels of similarity to the benchmark database, it would be useful to evaluate these drugs individually. We provide first-of-its-kind assessment of predictive performance for DPI predictions at the drug level. The drug-level assessment provides further insight into complementarity and differences between various 1S, 2S, and 3S predictors. We measure the AUC over the DPI predictions for each individual drug ( $AUC_{\text{drug}}$ ), which evaluates the quality of associations that are predicted between a given drug and all of the 1469 druggable proteins. We ensure that each drug in the benchmark database has at least five protein targets, which allows us to provide relatively robust estimates of the  $AUC_{\text{drug}}$  values.

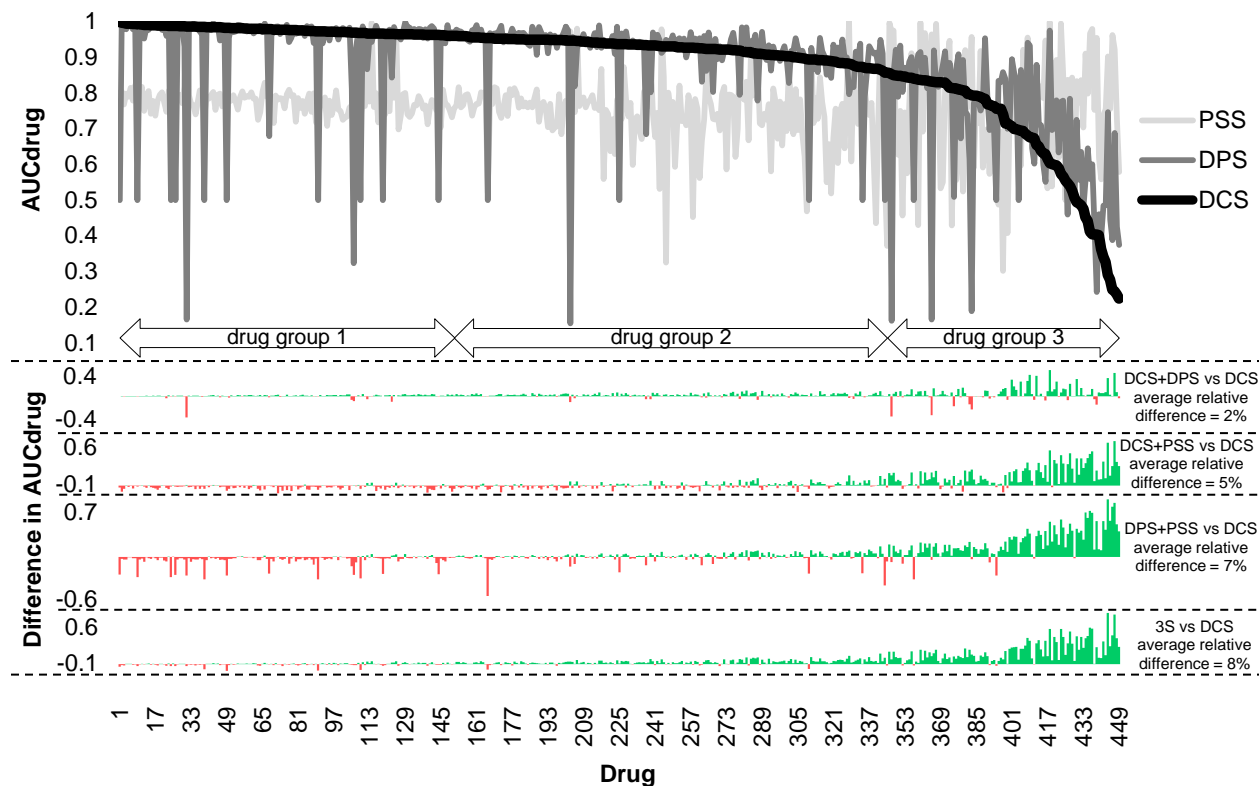


Figure 13. Comparison of predictive performance for the considered DPI predictors at the drug level. Black and gray lines at the top of the figure show the AUC measured per drug ( $AUC_{drug}$ ) for each of the three 1S models. Drugs are sorted by their AUC produced by the most accurate DCS model. The four sets of bar charts at the bottom of the figure show the difference in drug-level AUC between each ensemble model and DCS. Green bar (red bar) means improvement (decline) in the  $AUC_{drug}$  values.

The upper half of Figure 13 shows the  $AUC_{drug}$  for the three 1S predictors over each of the 449 drugs. The drugs are sorted by the corresponding  $AUC_{drug}$  values of DCS, which is the most accurate 1S model when measured at the interaction level (Figure 11). We divide the drugs into three groups. The *first group* of 150 drugs has  $AUC_{drug}$  for DCS  $> 0.96$ . The  $AUC_{drug}$  for DPS and PSS is virtually always lower than  $AUC_{drug}$  for DCS for this group. The *second group* of 195 drugs has  $AUC_{drug}$  for DCS between 0.96 and 0.86. The values of  $AUC_{drug}$  for PSS are almost always lower than DCS while  $AUC_{drug}$  for DPS and DCS are similar for these 195 drugs. The *third group* of the remaining 104 drugs has  $AUC_{drug}$  values for DCS that are on average lower than DPS and PSS. Although DCS and DPS are much better than PSS for the first two drug groups, the  $AUC_{drug}$

for PSS (0.752) for the *third group* of drugs is on average higher than the  $AUC_{\text{drug}}$  for DCS and DPS (0.674 and 0.709). This reveals that although overall PSS provides lower predictive performance, it outperforms the other two measures of similarity for  $60/449 = 13\%$  of drugs. The lists of drugs for each of the three groups are shown as three separate columns in the Appendix 1.

The interaction-level AUC of DCS across the 449 drugs is 0.883 (Figure 11). DCS achieves  $AUC_{\text{drug}} > 0.883$  for  $324/449 = 72\%$  of drugs. Moreover,  $AUC_{\text{drug}}$  for either DPS or PSS  $> AUC_{\text{drug}}$  for DCS for 100 out of the 125 drugs for which  $AUC_{\text{drug}}$  for DCS  $< 0.883$ . These drugs should be of particular focus for the designers of future DPI predictors since they should be predicted with the help of the DPS and PSS rather than the most accurate at the interaction level DCS. This reflects trade-offs between the three measures of similarity and motivates the development of predictors that use consensus of multiple similarities.

We also compare the drug-level performance for the three 2S and the one 3S predictor with the most accurate 1S predictor, DCS. The lower half of Figure 13 shows the difference in  $AUC_{\text{drug}}$  between DCS and each of the four ensemble predictors. Overall, the ensemble models are more accurate than DCS for most of the drugs (green bars in Figure 13). Specifically, DCS is outperformed by DCS+DPS, DCS+PSS, DPS+PSS, and 3S model for 370, 222, 244, and 349 drugs, respectively. We measure relative difference in  $AUC_{\text{drug}}$ , which is defined as the absolute difference in  $AUC_{\text{drug}}$  divided by the  $AUC_{\text{drug}}$  for DCS. The average relative differences in  $AUC_{\text{drug}}$  over the 449 drugs between DCS and the four ensembles are 2% (when compared to DCS+DPS), 5% (DCS+PSS), 7% (DPS+PSS), and 8% (3S). Thus, as expected based on the interaction-level results, the 3S model is also the most accurate predictor at the drug level. The drug-level results for the 2S models are also consistent with the evaluations at the interaction level. DPS+PSS is the most accurate 2S predictor that secures 7% improvement over the DCS model. In particular, it

benefits from PSS for the drugs in the third drug group.  $AUC_{drug}$  for DCS and DPS are correlated for the third drug group ( $SCC = 0.58$ ). On the other hand,  $AUC_{drug}$  for PSS is not correlated with either DCS or DPS ( $SCC = 0.07$  and  $0.05$ ) and it secures relatively high  $AUC_{drug}$  values. This implies that PSS is a strong predictive input that compliments the other two similarities, which explains why the ensemble predictors outperform DCS for the third group of drugs.

Our novel drug-level assessment of predictive performance shows that no single similarity could provide accurate DPI predictions across all drugs. DCS is the most accurate 1S model and the primary driver of the ensemble-based predictors for the first two group of drugs. For 23% of drugs (the third drug group) for which DCS does not provide higher predictive quality, the use of the other two similarities substantially increases the predictive performance. The 1S models are strongly dependent on the assumption that similar drugs share the same targets and similar proteins tend to interact with the same drug. The complementarity between PSS and DCS/DPS allows us to accurately cover a wider range of drugs for which only some of these similarities work individually.

### **5.3 Sensitivity of predictive performance to characteristics of predictors**

The predictive performance can be influenced by two factors: 1) intrinsic characteristics of the similarity-based predictors of DPIs, which are defined based on similarity of the query drug or its known targets to the benchmark database; and 2) extrinsic characteristics that are defined solely based on properties of the query drug and its known targets. For instance, if the query drug is similar to many of the drugs from the benchmark database then we anticipate it might be more likely to accurately find its protein targets when compared to a drug that is dissimilar to the drugs in the database. Also, a query drug that has a large number of known targets might be easier to

predict, irrespective of the predictive system used. This is because its targets can be exploited to find more potential new targets from the database when compared to a query drug with no or few known targets. We are the first to assess the sensitivity of predictive quality to a set of practical intrinsic and extrinsic characteristics of predictors.

### **5.3.1 Sensitivity to intrinsic characteristics**

Similarity-based DPI predictors rely on finding drugs that are similar to a query drug and proteins that are similar to the known targets of the query drug. The quality of DPI predictions depends on the values of the similarities between query drug/protein and the benchmark database, which in turn are dependent on the size and coverage of the database. In principle, the benchmark database is incomplete as it only covers the currently known drug structures, drug profiles, and druggable human sequences. In a typical practical scenario, a query drug might be dissimilar to all the drugs in the benchmark database. This reduces the chance that a DCS- or DPS-based predictor successfully identifies potential DPIs for the query drug, even if the query drug actually shares targets with the drugs in the benchmark database. We simulate such scenarios by excluding drugs (proteins) that share certain levels of similarity to the query drug (target) from the benchmark database when making predictions for the query drug (target). We partition the drugs and proteins from the benchmark databases into clusters using average-linkage hierarchical clustering [322]. As a result, the average similarity of drugs or proteins between any two clusters is lower than a predefined similarity threshold used for the clustering. In other words, the drugs (proteins) from one cluster are dissimilar to drugs (proteins) from another cluster. Subsequently, given a query drug (protein), we exclude the drugs (proteins) that belong to its cluster and use the only remaining drugs (proteins) to compute DCS/DPS/PSS for prediction. Thus, the predictions are based on drugs and proteins that are dissimilar to the inputs. Specifically, we use the 80<sup>th</sup>, 50<sup>th</sup> (median), and 20<sup>th</sup>

percentile of similarity values over all the drug-protein pairs in the benchmark database as the clustering thresholds. We also consider a scenario where all drugs and proteins are utilized for the predictions except for the query drug or protein itself. This scenario is equivalent to the clustering using the 100<sup>th</sup> (maximal) percentile of similarity values. Additionally, random predictions that correspond to the 0<sup>th</sup> percentile are also considered. We use these five scenarios to study the sensitivity of the predictive performance to the similarities between the query drug (protein) and the benchmark database. The predictive performance is quantified with the interaction-level AUCs.

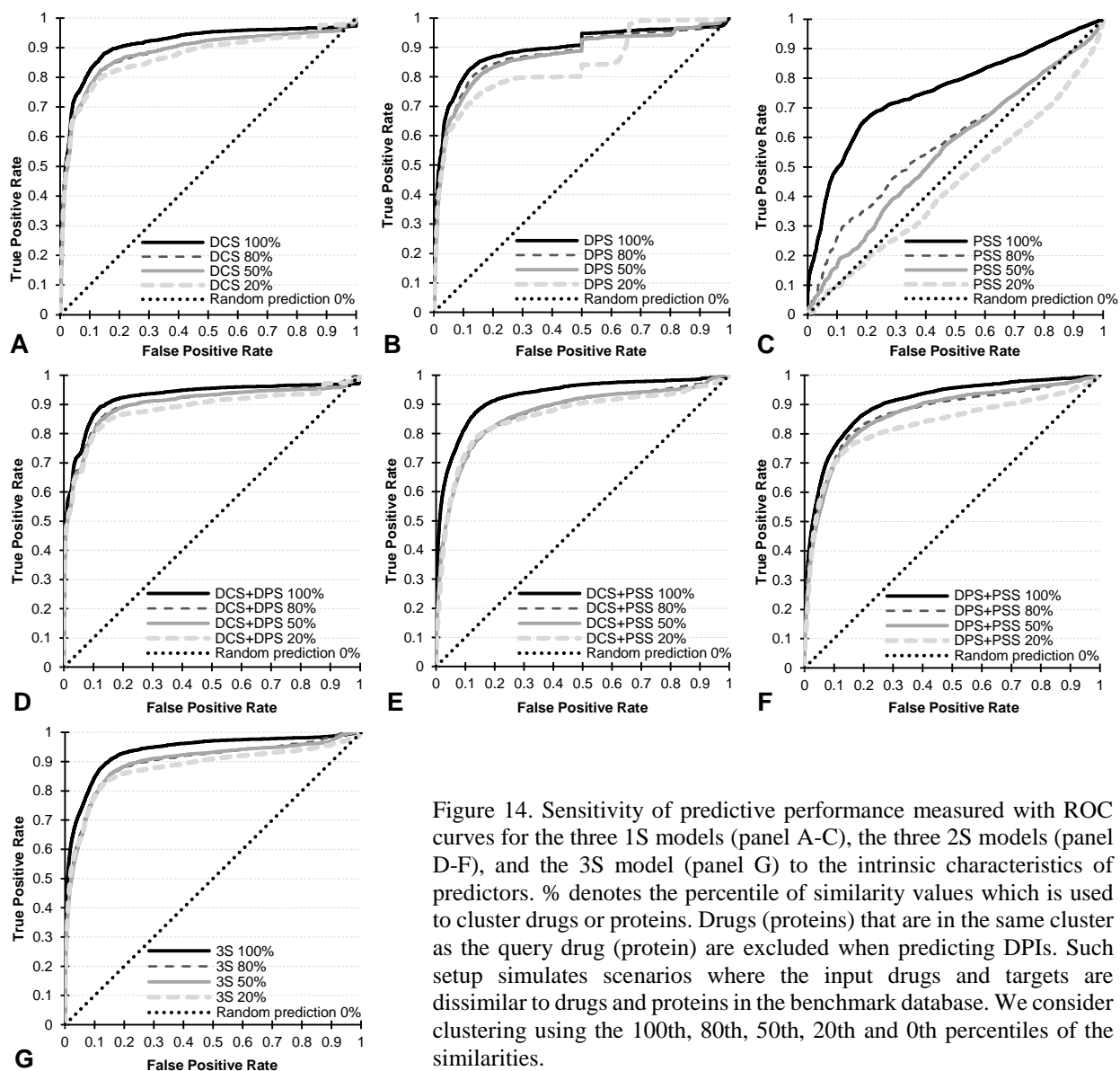


Figure 14. Sensitivity of predictive performance measured with ROC curves for the three 1S models (panel A-C), the three 2S models (panel D-F), and the 3S model (panel G) to the intrinsic characteristics of predictors. % denotes the percentile of similarity values which is used to cluster drugs or proteins. Drugs (proteins) that are in the same cluster as the query drug (protein) are excluded when predicting DPIs. Such setup simulates scenarios where the input drugs and targets are dissimilar to drugs and proteins in the benchmark database. We consider clustering using the 100th, 80th, 50th, 20th and 0th percentiles of the similarities.

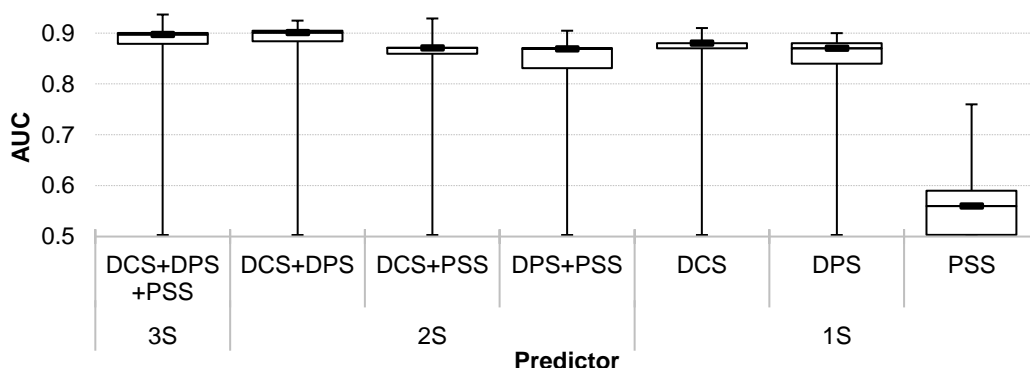


Figure 15. Sensitivity of predictive performance to the intrinsic characteristics of predictors. The box-plots denotes the AUC values for the scenarios where drugs (proteins) similar to the query drug (protein) are excluded from predictions based on clustering using the 100<sup>th</sup>, 80<sup>th</sup>, 50<sup>th</sup>, and 20<sup>th</sup> percentile of the similarities. The bottom bar denotes random predictions that corresponds to the 0<sup>th</sup> percentile (AUC = 0.5).

Figure 14 shows the ROC curves for the five scenarios and the three 1S, three 2S, and one 3S model. Figure 15 summarizes the corresponding AUC values. In general, all but one model are not sensitive to the three intrinsic characteristics. The range of AUC values between 100<sup>th</sup> and 20<sup>th</sup> percentiles of similarities for the 3S, the three 2S, DCS, and DPS models is narrow. This means that predictive quality drops by only between 0.04 (DCS+DPS and DCS) and 0.07 (DCS+PSS and DPS+PSS) with the decrease in similarities by 80%. Consequently, the six models offer high predictive quality even when dealing with the input drugs that have low similarity to the benchmark database. The one exception is the PSS model for which the predictive performance is sensitive to the degree of similarity to the targets in the database. Its AUC value substantially drops from 0.76 (100<sup>th</sup> percentile; clustering threshold for PSS = 0.4 which corresponds to 40% pairwise sequence similarity) to 0.56 (50<sup>th</sup> percentile; threshold = 19% pairwise sequence similarity). The results for the 20<sup>th</sup> percentile of PSS (threshold = 10% pairwise sequence similarity) are equivalent to random predictions. This is consistent with previous studies which unveiled that protein sequences with identity < 0.25 are likely to have different functions and structures [323, 324]. This is also related to our observations in the Figure 10 where the distributions of the PSS values overlap

between interacting and non-interacting drug-protein pairs, in particular when compared to DCS and DPS.

This analysis also confirms that use of a larger set of similarities in general results in an improved predictive performance. In particular, for the 100<sup>th</sup> percentile scenario, the AUC of the best 1S model is 0.91, the best 2S model is 0.93, and the 3S model is 0.94. Because the adoption of low PSS similarities results in lower predictive performance, combining it with DCS or DPS into a 2S model does not enhance predictive performance (compare DCS+PSS vs DCS, and DPS+PSS vs DPS plots in Figure 15).

The results of analysis of sensitivity to the intrinsic characteristics of predictors reveal that the predictive performance is not sensitive to the values of DCS and DPS, while it is sensitive to the values of PSS. Moreover, combining PSS with DCS and/or DPS makes the predictors robust to the low values of PSS. We conclude that use of PSS only model is risky when the known targets of query drug are dissimilar to the targets in the benchmark database.

### **5.3.2 Sensitivity to extrinsic characteristics**

Predictive performance could also be sensitive to extrinsic characteristics that describe known a priori input drug structure, drug profile, and protein target. We are the first to investigate several extrinsic characteristics for each of the three types of similarities. They include surface area, charge, shape, weight, size, lipophilicity, number of similar drugs, number of similar drugs sharing targets, and similarity to the most similar drugs which are computed from the drug structure. We also considered three markers of drug profiles: number of side-effects, similarity of the profile to the most similar profile, and number of similar profiles. Finally, we investigated three markers of the input drug targets: number of known targets, number of known targets that interact with similar drugs, and known targets that interact with the most similar drug. We discuss one “best” marker



for each type of similarity, which we selected based on the fact that it significantly affects the predictive performance and is easy to quantify. These markers include the number of similar drug structures that share targets with the input drug, the number of side-effects, and the number of known targets.

We study sensitivity of predictive quality to these extrinsic markers by partitioning the considered drugs into two groups for which we observe large differences in predictive performance. For the best DCS marker, we compare 177 drugs that share targets with  $< 50$  similar drugs (which corresponds to the median level of DCS) vs the remaining drugs that share targets with a larger number of similar drugs. Similarly, for the best DPS characteristic, we contrast 55 drugs that have relatively small side-effects profile ( $<40$ ) vs the remaining drugs that have a larger profile. Finally, for the best PSS marker, we compare 128 drugs with  $< 20$  native targets vs the remaining more promiscuous drugs. Figure 16 compares distributions of  $AUC_{\text{drug}}$  values between these groups of drugs when considering the corresponding 1S models and the 3S model.

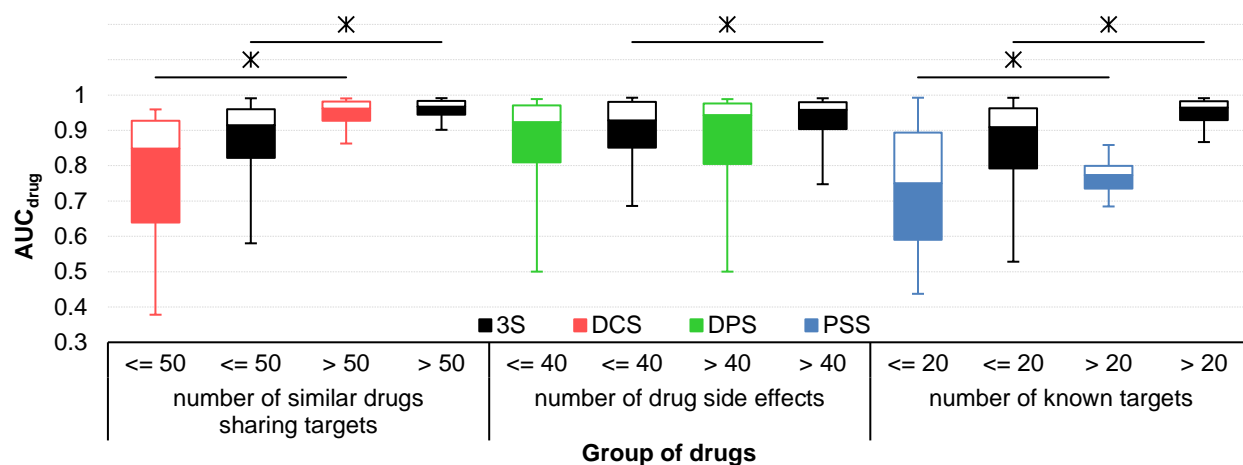


Figure 16. Sensitivity of predictive quality to extrinsic characteristics of predictors. The boxplots denote the 5th, 20th, 50th, 80th, and 95th percentiles of  $AUC_{drug}$  values for the 1S and 3S model over the corresponding two groups of drugs separated with help of a given marker that characterizes the input drug/targets. The asterisk indicates that the difference in the  $AUC_{drug}$  is significant ( $p$ -value  $< 0.05$ ) between drug groups. We assess significance of differences between the corresponding two groups of drugs using the Wilcoxon rank sum test [317]; we use the non-parametric test since these data are not normal according to the Anderson-Darling test at 0.01 significance.

Figure 16 shows that the  $AUC_{drug}$  for DCS varies substantially between 0.38 and 0.96 with a median = 0.85 for the drugs that share targets with fewer similar drugs. For the remaining drugs that share targets with the larger number of similar drugs, the  $AUC_{drug}$  for DCS is always  $> 0.86$  with a median = 0.96. These drugs have lower variation and significantly higher values for  $AUC_{drug}$  ( $p$ -value  $< 0.05$ ) when compared to the drug that share targets with fewer similar drugs. Similarly, the 3S model also has significantly higher  $AUC_{drug}$  values with narrower spread for the drugs with larger number of similar drugs sharing targets. These observations reveal that the predictive quality is significantly higher when working with drugs that share targets with a larger number of similar drugs in the benchmark database. Based on the assertion that similar drugs tend to target the same proteins, that makes it easier to accurately identify targets for such drugs when using DCS. In contrast, the drugs that share targets with a low number of similar drugs are harder to accurately predict.

The  $AUC_{drug}$  for DPS is lower for the drugs that have a smaller profile (median  $AUC_{drug} = 0.92$ ) than for the drugs that have larger profile (median  $AUC_{drug} = 0.94$ ), but this difference is not statistically significant ( $p$ -value = 0.17). The corresponding difference for the 3S model is slightly higher and statistically significant ( $p$ -value < 0.05): median  $AUC_{drug} = 0.93$  vs 0.96, respectively. The sensitivity to the size of the drug profile is expected since a larger profile offers more information that in turn result in a more accurate quantification of DPS.

The differences in  $AUC_{drug}$  between the less vs more promiscuous drugs are significant for the PSS and 3S models ( $p$ -value < 0.05). The median  $AUC_{drug}$  for the 3S model is 0.91 for the less promiscuous drugs while it equals 0.96 for the more promiscuous drugs. Similarly, for the 1S model that relies on PSS the median  $AUC_{drug} = 0.75$  vs 0.77. This trend could be explained by an observation that the drugs which interact with many targets are more likely to have targets that are highly similar to the proteins in the benchmark database. This is supported by the assertion that similar proteins tend to interact with the same drugs.

The results of the analysis of sensitivity to the extrinsic characteristics reveal that the predictive performance is sensitive to several easy to estimate characteristics of the input drug structures, drug profiles, and drug targets. As expected, we find that it is more likely to secure higher predictive quality when a more comprehensive information is available for the input drugs, such as a larger number of similar drugs sharing targets, a larger drug profile, and a higher number of known targets.

## **5.4 CONNECTOR webservice**

CONNECTOR (prediCtOr of compouNd-proteiN intEraCTiOn based on ensemble of similaRities) is a webservice that implements the seven predictors that we evaluate in this review.

The webserver and the benchmark database are freely available at <http://biomine.cs.vcu.edu/servers/CONNECTOR/>. Figure 17 shows the interface of the webserver.

**CONNECTOR - prediCtOr of compouNd-proteiN intEraCTiOn based on ensemble of similaRities**

Materials | References | Acknowledgments | Disclaimer | Biomine

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CONNECTOR webserver

CONNECTOR is a webserver that predicts propensity of putative drug-protein interactions based on similarity between the input drug structure, drug profile, and/or protein sequence and the experimental drug-protein interactions that are included in the internal database. This webserver facilitates prediction for any combination of inputs including any individual input (drug structure, drug profile, and protein sequence), any pair of inputs, and all three inputs.

The internal database of CONNECTOR integrates drug-protein interactions that were collected from Therapeutic Target Database, IUPHAR/BPS Guide to Pharmacology database and Drug2Gene that combines data from CGDCP, ChEBI, ChEMBL, CTD, DrugBank, HGNC, Ligand Expo, MICAD, NCBI Gene, Pathway Commons DB, PDBsum, PDSP Ki, PharmGKB, Pubchem Bioassay, PubChem Compound, PubChem Substance, and UniProt.

The current version of the internal database includes 449 drugs, 1469 protein targets, and 34456 drug-protein interactions

**Please follow the three steps below to make predictions.**

**Step 1. Provide at least one of the three inputs listed below**

Enter structure of a query drug in the SMILES format.

C(CC(=O)O)CN

ExampleClear input

List side-effects of the query drug in the CSV format. The side-effect terms must come from this fixed list of terms.

anaphylaxis,urticaria,angioedema,tenderness,pain

ExampleClear input

Enter amino acids sequence of a known protein target in one line.

MSHHWGYGKHNGPEHWHKDFPIAKGE  
RQSPVDIDTHTAKYDPSLKLPLSVSYDQA  
TSLRILNNGHAFNVEFDSDQKAVLKGK  
PLDGTYRLIQFHHWGLDGGGSEHTV  
DKKKYAAELHLVHWNTKYGDFGKAVQQ

ExampleClear input

**Step 2. Provide your email address (optional)**

Please enter your email address in the following text area. A link to prediction results will be sent to your email address once they are ready.

**Step 3. Click button to launch prediction**

Run CONNECTOR

## Materials

The benchmark database

- Internal database of CONNECTOR

The db.zip file includes four files:

- drug\_structures.tsv - tab-separated list of PubChem identifiers and structures of the 449 drugs in the SMILES format.
- drug\_profiles.tsv - tab-separated list of PubChem identifiers and profiles of the 449 drugs. The profiles are based on the list of terms that are available from [here](#).
- protein\_sequences.fasta - the FASTA formatted list of UniProt accession numbers and sequences for the 1469 drug targets.
- drug\_protein\_interactions.tsv - tab-separated list of 34456 drug-protein interactions where drugs are identified using PubChem identifiers and drug targets are identified using UniProt accession numbers.

Figure 17. The interface of the CONNECTOR webserver.

CONNECTOR facilitates prediction for any combination of the three inputs including any individual input (drug structure, drug profile, and protein sequence), any pair of inputs, and all three inputs. CONNECTOR uses the benchmark dataset as its internal database. The computations are performed on the server side and thus the end user only needs to access the webserver page via any major web browser and provide the inputs. The prediction is performed in three steps: 1) provide any combination of the three inputs including drug structure in the SMILES format, comma separated list of side effects (drug profile), and/or protein sequences in the FASTA format; 2) provide email address where a unique link to the results will be sent once the predictions are ready; and 3) click “Run CONNECTOR” (see Figure 17). Each submitted job is entered into a FIFO queue of jobs on the server. User is notified via the browser window about the current placement in the queue and when the job reaches the front of the queue. The results are displayed in the browser window and the unique link to the page with the results is sent to the user-identified email address. We provide four views of the results:

- All DPis, which shows all putative drug-protein pairs that include query drug and target(s) and similar compounds and proteins.
- DPis that include the query drug structure, which cover interactions between the query drug structure and its putative protein targets (if drug structure was provided as one of the inputs)
- DPis that include the query drug profile, which include interactions between the query drug represented by its profile and its putative protein targets (if drug profile was provided as one of the inputs)
- DPis that include the query protein sequence, which gives interactions between the query target sequence and the drugs that are predicted to interact with this target (if target sequence was provided as one of the inputs)

Each putative interaction is coupled with the corresponding value of similarity. Drugs are linked to their entries in the PubChem databases and target sequences are linked to their UniProt entries. For user's convenience, similarities between query drug/target and the drug/target used to make prediction and the propensities of putative drug-protein interactions are color-coded. Dark green/green/light green/pale green/red denotes that the corresponding drug-protein pair is very likely/likely/moderately likely/unlikely/very unlikely to interact. We annotate these five colors based on the values of the similarity that belong to the top 20%, 20 to 40%, 40 to 60%, 60 to 80%, and the bottom 20% of the distribution of these values. We also provide a text-based version of the results for download. We will store the page with the results for at least three months.

## **5.5 Conclusions**

We have developed a novel benchmark database that includes drugs characterized by high density of interactions and we use it to evaluate a representative set of 1S, 2S, and 3S predictors. This database integrates data coming from three resources (19 source databases) and includes 449 drugs, 1469 druggable human proteins, and 34456 native DPIs, resulting in high density of native DPIs per drug that equals 76. We observe that most of the surveyed methods have evaluated predictive performance on both DPIs and non-DPIs, which allowed for computation of TPR, FPR, and the resulting AUC values. However, these methods assessed predictive performance only at the interaction level that spans multiple drugs which may differ in structure, profile, and the number and type of protein partners that they bind to. We are the first to perform both interaction- and drug-level assessments and to comprehensively and side-by-side compare all 1S, 2S, and 3S models.

At the interaction level, we reveal that the use of ensembles results in improved predictive quality. Specifically, the 3S model significantly outperforms the 1S and 2S models, while the 2S models are significantly more accurate than the 1S models. We empirically analyze reasons for these improvements and we show that they stem from an improved handling of interactions characterized by modest levels of similarities. Among the three 1S models, DCS and DPS are more accurate than PSS. We also find a modest level of correlation between DCS and DPS while correlations between PSS and DCS as well as PSS and DPS are low. The modest or low levels of correlations further explain why the ensembles benefit from the integration of multiple similarities and why the majority of current predictors are ensembles.

At the drug level, we demonstrate that the predictive quality varies widely between drugs and these differences depend on the type of similarity used. We show that no single 1S model could provide accurate DPI predictions across all the drugs. Moreover, we demonstrate that ensembles improve over the 1S models. The average relative improvements in  $AUC_{drug}$  over the 449 drugs between the best 1S model, DCS, and the four ensembles are: 2% (compared to DCS+DPS), 5% (DCS+PSS), 7% (DPS+PSS), and 8% (3S). We divide drugs into three groups: group one includes 150 drugs with high  $AUC_{drug}$  for DCS; group two includes 195 drugs with moderate  $AUC_{drug}$  for DCS; and group three with 104 drugs for which  $AUC_{drug}$  for DCS is on average lower than DPS and PSS. We found that the use of 3S ensemble provides particularly large improvements by on average 29% in  $AUC_{drug}$  over the use of DCS for the 23% of drugs which constitute the third group. Our empirical analysis also reveals that although per-interaction PSS provides the lowest predictive performance, it outperforms the other two 1S models for 13% of drugs when assessed at the drug level. These drugs should be of particular focus for the development of future DPI predictors because more accurate predictions could be obtained with the help of the DPS and PSS

rather than with the overall most accurate at the interaction-level DCS that dominates the current methods.

DPI prediction relies on accurate values of similarities between the query drug (its known target) and the drugs (proteins) in the benchmark database. The quality of these values is likely affected by the intrinsic characteristics of predictors, such as the similarity between inputs and the benchmark database. We provide the first-of-its-kind sensitivity analysis of predictive quality for each of the three similarities. We find that the predictive quality is not sensitive to the values of DCS and DPS, which means that the predictive performance of the methods that utilize DCS/DPS does not substantially change when the input drug structures or profiles are dissimilar to the structures and profiles in the internal database. In contrast, the predictive quality for PSS drops significantly when the input protein sequences are dissimilar to the sequences in the database. However, such sensitivity to low values of PSS is mitigated when using methods that combine PSS with other similarities. These observations demonstrate that the ensembles are not only accurate at the interaction and drug levels but they are also robust to low values of similarities.

We are also the first to investigate sensitivity of predictive quality to extrinsic characteristics of the predictive models. These extrinsic characteristics are intrinsic to the inputs and include information extracted directly from drug structures, drug profiles, and drug targets. We find that the 3S model and the corresponding three 1S models are more likely to provide accurate predictions when the input drugs share targets with a larger number of similar drugs in the benchmark database, when the input drugs have larger side-effect profiles, and when the input drugs are more promiscuous. This suggests that a larger amount of available data (number of known targets and/or side-effects) leads to calculations of higher quality and higher values of similarities, which in turn results in higher predictive performance.



## Chapter 6 Summary and conclusions

This dissertation has three goals that focus on the prediction and analysis of the DPIs in the druggable human proteome. In Chapter 2 we provide a brief introduction to the related background to explain and motivate our goals. This chapter includes information about protein and drug-protein complex structures that define molecular-level details of the therapeutic and off-target effects of drugs, as well as a summary and classification of current publications related to the computational predictions of DPIs. This is followed by the subsequent three chapters which detail methods and results for each of the three goals. My original contributions in this dissertation that are organized under each of the three goals include:

**Goal 1: Evaluation of protein structure-based DPI predictors and development of DPI database.**

- We provide empirical comparative analysis of the protein structure-based DPI predictors: eFindSite, SMAP and ILbind.
- We develop and deploy the PDID database that stores 1.1 million predictions and 17 thousand high-confidence putative DPIs for the entire structure human proteome and provides interface for drug-based, protein-based, and target sequence-based data queries.

**Goal 2: Review of the similarity-based DPI predictors.**

- We review a comprehensive set of 35 high-impact similarity-based DPI predictors spanning from the three pioneering methods in this area which were published a decade ago to eight most recent approaches which have never been covered by other surveys.
- We define the categorization of similarity-based DPI predictors based on the types and numbers of similarities that they use.
- We review the 12 source databases that are used to derive the internal databases of predictors and we comprehensively explain connections between the internal and source databases.
- We investigate impact and describe internal databases of the 35 considered methods including the recent approaches.
- We analyze the use of similarities and ensembles in the considered set of 35 predictors.
- We critically analyze drawbacks of current reviews and methods in this area.

**Goal 3: Empirical assessment and comparative analysis of similarity-based DPI predictors.**

- We develop and release a novel benchmark database that covers large-scale drug-protein data and high-density DPIs. This database is particularly suitable for comparative empirical assessment of DPI predictors.
- We are the first to compare all seven representative predictors including three individual predictors that rely on each of the three main types of similarities and four ensemble predictors that combine two or three similarities.
- We are the first to assess predictive quality at the drug level. This novel drug-level assessment of predictive performance provides additional insights.

- We provide a first-of-its-kind sensitivity analysis of predictive performance to the intrinsic characteristics of DPI predictors which describe the similarities between the inputs and the benchmark database.
- We are also the first to analyze the sensitivity of predictive performance to the extrinsic characteristics that are the priori known properties of the input drug structures, drug profiles, and protein targets.
- We develop and release at <http://biomine.cs.vcu.edu/servers/CONNECTOR/> the CONNECTOR webserver that implements seven similarity-based DPI predictors that we assessed.

Following, we summarize the work done and list major conclusions for each of the three goals. In the context of the *first goal*, we empirically assess the predictive quality of three representative protein structure-based approaches for the prediction of the DPIs. This is done for dozens of representative drugs over the structural human proteome. Our tests show that these three methods provide relatively accurate predictions. Relying on the putative DPIs that were accurately predicted by these approaches and the native DPIs collected from PDB, DrugBank and BindingDB, we develop and deploy a large-scale database of putative and native DPIs. This PDID database stores 1.1 million predictions that cover 51 popular and representative drugs and the entire structural human proteome, which includes 9652 protein structures. PDID maps the drugs to their target proteins, where these interactions may correspond to therapeutic effects and/or adverse events. The database helps to comprehensively catalog drug targets, facilitates repurposing and repositioning of existing drugs, and unveils an opportunity to systematically analyze molecular-level DPIs at a proteome scale. The research related to this goal was published in Ref. [29].

For the *second goal*, we completed a comprehensive review for 35 selected high-impact similarity-based DPI predictors. These similarity-based methods offer the opportunity to perform prediction when protein structures are unavailable, complementing the protein-structure based methods that are studied in our first goal. We systematically summarize the key aspects of these similarity-based predictors including their methodological underpinnings, volume and coverage of their internal databases, information about source databases, inclusion of empirical analysis, timeline of development, and their impact. Majority of them were published in high-impact journals and are highly cited, suggesting that they are of substantial value to the community. Our review shows that combining more source databases would likely further increase the completeness of information about drug promiscuity in the internal databases. This would benefit predictive quality of the similarity-based predictors and would also enable the development of higher-quality benchmark databases. Additionally, we note that regular update and dissemination would help to increase the effectiveness, completeness, and impact of the source databases. Periodic publications and peer review will also boost quality of underlying data and features. Given the fact that three main types of similarities are used by these methods, we categorize the 35 tools based on the number of similarities that they apply and combine together. We find that most of these methods ensemble two or three similarities. Recently, DCS and PSS are frequently employed and combined to constitute ensemble predictors while DPS is infrequently utilized due to the incompleteness and difficulty in acquiring side-effect profiles of drugs. Moreover, we unveil drawbacks of current reviews and methods: lack of a systematic empirical analysis of predictive quality for individual drugs; lack of an in-depth analysis of sensitivity of predictive performance to intrinsic and extrinsic characteristics of predictors is missing; and lack of a comprehensive

comparative analysis that includes the three single-similarity-based predictors and the four ensembles.

The *third goal* was motivated by the drawbacks of the current reviews and similarity-based methods which we uncovered in our second goal. To overcome these drawbacks, we implement, empirically evaluate, and compare all seven representative similarity-based DPI predictors. We develop a novel benchmark database that stores a comprehensive collection of high-quality DPIs which we harvested from 19 data sources. The benchmark database also encompasses essential information for the development of similarity-based methods, including chemical structures and side-effect profiles of drugs and protein sequences of drug targets. Like in the previous studies we assess the predictive performance of the seven representative predictors at the interaction level. We also provide the first-of-its-kind assessment of predictive quality at the drug level. This drug-level analysis shows that different combination of similarities should be used for different drugs to obtain more accurate predictions. Moreover, we reveal that ensembles of multiple similarities offer higher predictive quality than models that rely on single or fewer similarities. This result is consistent for evaluations at both interaction and drug levels. We are the first to analyze the sensitivity of predictive quality to the intrinsic and extrinsic characteristics of predictors. Our analysis reveals sensitivity to lower values of PSS while the predictive quality is not sensitive to values of DCS and DPS. This suggests that the approach using PSS only would not provide accurate predictions when the input proteins are dissimilar to the proteins in the internal database. However, ensemble models are robust to low values of similarities. The sensitivity analysis also demonstrates that the predictive quality could benefit from a larger amount of information for the inputs, including a larger a larger number of similar drugs sharing targets in the internal database,

a larger side-effect profile, and a larger number of known targets. These conclusions arguably offer a useful guidance for the selection of similarity-based predictors for specific drugs and protein targets.

The studies and conclusions summarized above inspire several possible directions for future works. Combining a larger and more diverse set of source databases would likely further improve quality of the internal databases, which in turn would further boost the predictive quality. Authors of future predictors should consider to integrate recent and comprehensive resources, such as the DGIdb database [245, 246] and Pharos database [243], to expand our benchmark database and/or the internal databases of their algorithms. Additionally, since the size of the benchmark database is primarily limited by the availability of drug profiles in the SIDER database, we recommend that future works should also consider combining related information about drug side-effects from the MetaADEDDB [296] and IntSide database [128]. Moreover, most of the current development efforts focus on protein targets that are structured [20]. However, about 30% of eukaryotic proteins are either fully disordered or have long regions of intrinsic disorder [83, 325]. These disordered proteins are implicated in a wide range of diseases [326-333]. Moreover, certain protein families are enriched in the intrinsic disorder, such as nuclear receptors, kinases, and various enzymes [20, 83, 84, 334-336]. These protein families include important therapeutic drug targets and druggable proteins [1, 2, 18, 19, 44]. This prompts our recommendation that future works should invest into the development of disorder-specific DPI databases and methods, which by definition cannot rely on the protein structure-based computations.

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## **Vita**

Chen Wang was born on July 21, 1986, in Baoding, Hebei, China. He received the M.Sc. degree in Information and Communication Engineering and the B.Sc. degree in Electronics and Information Engineering from the Harbin Institute of Technology, China, in 2011 and 2009, respectively. He is currently a Ph.D. Candidate and Research Assistant in the Computer Science Department at the Virginia Commonwealth University. Before joining Virginia Commonwealth University, he was a Research Assistant at the University of Alberta and the Harbin Institute of Technology between 2012 and 2015.



# Appendix 1 List of drugs included in the benchmark database for Goal 3

The list of PubChem CIDs and names for the 449 drugs that are included in the benchmark database from Chapter 5.

Drug group 1		Drug group 2		Drug group 3	
CID	Drug name	CID	Drug name	CID	Drug name
3366	5-fluorocytosine	5419	Tetrahydrozoline	3080	2,3-dimercaptopropanol
3385	5-fluorouracil	3406	4-methylpyrazole	4075	5-aminosalicylic acid
4114	8-methoxyypsoralen	667490	6-mercaptopurine	71158	Acamprosate
1978	Acebutolol	2723601	6-thioguanine	60164	Adapalene
71771	Aceclofenac	1983	Acetaminophen	5493444	Aliskiren
2094	Allopurinol	1986	Acetazolamide	3007	Amphetamine
2099	Alosetron	2022	Acyclovir	2179	Amsacrine
3125	Alpha-methyl-p-tyrosine	2082	Albendazole	2182	Anagrelide
2118	Alprazolam	2088	Alendronate	166548	Anidulafungin
2130	Amantadine	51263	Alfentanil	60795	Aripiprazole
2145	Aminoglutethimide	2092	Alfuzosin	2266	Azelaic acid
2170	Amoxapine	123606	Almotriptan	82146	Bexarotene
3698	Amrinone	2141	Amifostine	104865	Bosentan
2187	Anastrozole	2160	Amitriptyline	2441	Bromazepam
2249	Atenolol	2162	Amlodipine	2471	Bumetanide
2284	Baclofen	2216	Apraclonidine	60953	Capecitabine
2337	Benzocaine	2244	Aspirin	2551	Carbachol
2366	Betahistine	148192	Atazanavir	2678	Cetirizine
2375	Bicalutamide	2265	Azathioprine	2713	Chlorhexidine
2391	Bisacodyl	2267	Azelastine	8612	Chloroprocaine
444	Bupropion	2578	BCNU	2719	Chloroquine
2477	Buspirone	7699	Benzonatate	2789	Clobazam
2478	Busulfan	12555	Benzydamine	25419	Clodronate
2484	Butenafine	2369	Betaxolol	119182	Clofarabine
2541	Candesartan	2370	Bethanechol	151171	Conivaptan
2708	Chlorambucil	39042	Bezafibrate	5625	Delavirdine
2725	Chlorpheniramine	2381	Biperiden	137	Delta-aminolevulinic acid
2749	Ciclopirox	2405	Bisoprolol	2973	Desferrioxamine
2764	Ciprofloxacin	2435	Brimonidine	42113	Desflurane
2802	Clonazepam	68844	Brinzolamide	125017	Desvenlafaxine
2907	Cyclophosphamide	60726	Bromfenac	3009	DFMO
2913	Cyproheptadine	6834	Brompheniramine	3117	Disulfiram
2972	Deferiprone	2474	Bupivacaine	71329	Dofetilide
124087	Desloratadine	2519	Caffeine	681	Dopamine
2140	Diatrizoate	2554	Carbamazepine	4510	DWP-401
3042	Dicyclomine	2576	Carisoprodol	60877	Emtricitabine
3059	Diflunisal	2583	Carteolol	3226	Enflurane
3100	Diphenhydramine	2585	Carvedilol	176870	Erlotinib
36811	Dobutamine	2662	Celecoxib	60198	Exemestane
3151	Domperidone	2726	Chlorpromazine	150311	Ezetimibe
3158	Doxepin	2727	Chlorpropamide	3331	Felbamate
3168	Droperidol	2732	Chlorthalidone	3345	Fentanyl
3198	Econazole	2733	Chlorzoxazone	119	Gamma-aminobutyric acid

3241	Epinastine	2756	Cimetidine	10413	Gamma-hydroxybutyrate
564	Aminocaproic acid	2762	Cinoxacin	123631	Gefitinib
59768	Esmolol	2771	Citalopram	774	Histamine
3261	Estazolam	2801	Clomipramine	3647	Hydroflumethiazide
3291	Ethosuximide	2803	Clonidine	60852	Ibandronate
3305	Etidronate	2812	Clotrimazole	60753	Ibutilide
3308	Etodolac	2895	Cyclobenzaprine	104741	ICI 182,780
3324	Famciclovir	2955	Dapsone	5311181	Iloprost
3325	Famotidine	3062316	Dasatinib	3763	Isoflurane
3339	Fenofibrate	2995	Desipramine	27661	Isosorbide-5-mononitrate
3342	Fenopropfen	30623	Dexrazoxane	219078	Lacosamide
6918558	Fesoterodine	3016	Diazepam	612	Lactate
3354	Flavoxate	3019	Diazoxide	216326	Lenalidomide
3365	Fluconazole	679	Dimethyl sulphoxide	3915	Levocabastine
3373	Flumazenil	3105	Dipivefrin	4004	Malathion
3372	Fluphenazine	3108	Dipyridamole	4057	Mepenzolate methylbromide
3393	Flurazepam	3114	Disopyramide	4058	Meperidine
3410	Formoterol	3152	Donepezil	4064	Meprobamate
3446	Gabapentin	3156	Doxapram	6476	Methsuximide
3478	Glipizide	3157	Doxazosin	4139	Methylene blue solution
3510	Granisetron	3182	Dyphylline	4189	Miconazole
3516	Guaifenesin	77993	Eletriptan	51634	Miglustat
2123	Hexamethylmelamine	838	Epinephrine	47641	Naftifine
3637	Hydralazine	3278	Ethacrynic acid	4421	Nalidixic acid
3652	Hydroxychloroquine	2761171	Ethionamide	4436	Naphazoline
3690	Ifosfamide	3292	Ethotoin	50294	Nedocromil sodium
5291	Imatinib	6049	Eteic Acid	4493	Nilutamide
57469	Imiquimod	3333	Felodipine	4499	Nisoldipine
3767	Isoniazid	3348	Fexofenadine	41684	Nitazoxanide
3825	Ketoprofen	3386	Fluoxetine	4616	Oxazepam
3826	Ketorolac	3394	Flurbiprofen	60843	Pemetrexed
3869	Labetalol	3397	Flutamide	4768	Phenoxybenzamine
3883	Lansoprazole	3440	Furosemide	750	Polyglycine
3914	Levobunolol	3454	Ganciclovir	4993	Pyrimethamine
3948	Lomefloxacin	5379	Gatifloxacin	104758	Raltitrexed
3950	Lomustine	3463	Gemfibrozil	56959	Ranolazine
3957	Loratadine	3488	Glibenclamide	449193	Roflumilast
3961	Losartan	3475	Gliclazide	446157	Rosuvastatin
453	Mannitol	3494	Glycopyrrolate	129228	Rufinamide
4053	Melphalan	3519	Guanfacine	5206	Sevoflurane
8271	Mephobarbital	3559	Haloperidol	5312125	Silodosin
4062	Mepivacaine	3598	Hexachlorophene	4369359	Sitagliptin
598	Mesna	3639	Hydrochlorothiazide	216239	Sorafenib
1349907	Methimazole	785	Hydroquinone	5314	Succinylcholine
4107	Methocarbamol	3658	Hydroxyzine	41693	Sufentanil
4171	Metoprolol	3672	Ibuprofen	110635	Tadalafil
4173	Metronidazole	3696	Imipramine	5381	Tazarotene
4174	Metyrapone	3702	Indapamide	5391	Temazepam
4197	Milrinone	3715	Indomethacin	6018	Tetrabenazine
5746	Mitomycin C	3739	Iodipamide	1130	Thiamine
4211	Mitotane	3749	Irbesartan	2720	Thiazide
4236	Modafinil	3759	Isocarboxazid	853	Thyroxine
7638	Monobenzone	3779	Isoproterenol	216237	Tolvaptan
4409	Nabumetone	3783	Isosuprine	110634	Vardenafil
4456	Neostigmine	3821	Ketamine	170361	Varenicline
644241	Nilotinib	3827	Ketotifen	2520	Verapamil
4539	Norfloxacin	3878	Lamotrigine	5665	Vigabatrin
4543	Nortriptyline	3899	Leflunomide	1054	Vitamin B6
4595	Ondansetron	3902	Letrozole	68740	Zoledronic acid
4601	Orphenadrine	59708	Levetiracetam	5734	Zonisamide
4614	Oxaprozin	3676	Lidocaine	5735	Zopiclone
4634	Oxybutynin	3958	Lorazepam		
4678	Panthenol	3964	Loxapine		
4723	Pemoline	3998	Mafenide acetate		
4725	Penciclovir	4032	Mecamylamine		
4748	Perphenazine	4044	Mefenamic acid		
4763	Phenobarbital	4046	Mefloquine		
4828	Pindolol	4054	Memantine		
4891	Praziquantel	4060	Mephenytoin		
4906	Prilocaine	4078	Mesoridazine		
4909	Primidone	4086	Metaproterenol		
4915	Procarbazine	4091	Metformin		
4917	Prochlorperazine	4095	Methadone		
4927	Promethazine	4158	Methylphenidate		
4932	Propafenone	4168	Metoclopramide		
4935	Proparacaine	4170	Metolazone		
657298	Propylthiouracil	4178	Mexiletine		
1046	Pyrazinamide	4192	Midazolam		
5002	Quetiapine	4195	Midodrine		
5029	Rabeprazole	4205	Mirtazapine		
5039	Ranitidine	4212	Mitoxantrone		

5071	Rimantadine	23897	Molindone
5245	Risedronate	4034	Monamine
2083	Salbutamol	4440	Naratriptan
5152	Salmeterol	4449	Nefazodone
5161	Salsalate	4463	Nevirapine
5193	Secobarbital	4485	Nifedipine
5210	Sibutramine	4497	Nimodipine
5253	Sotalol	4506	Nitrazepam
5318	Sulconazole	4033	Nitrogen mustard
5215	Sulfadiazine	4583	Ofloxacin
5344	Sulfisoxazole	130881	Olmesartan medoxomil
5401	Terazosin	4594	Omeprazole
5403	Terbutaline	34312	Oxcarbazepine
5426	Thalidomide	115237	Paliperidone
5430	Thiabendazole	4679	Pantoprazole
5452	Thioridazine	4680	Papaverine
5479	Tinidazole	4649	Para-aminosalicylic acid
41781	Torasemide	4737	Pentobarbital
5523	Tramadol	4740	Pentoxifylline
5533	Trazodone	3675	Phenelzine
5556	Triazolam	4771	Phentermine
5572	Trihexyphenidyl	5775	Phentolamine
5593	Tropicamide	1775	Phenytoin
119607	Valdecoxib	16362	Pimozide
5656	Venlafaxine	4829	Pioglitazone
5719	Zaleplon	27400	Pizotifen
		4893	Prazosin
		4908	Primaquine
		4911	Probenecid
		4913	Procaïnamide
		4914	Procaine
		4934	Propantheline
		4943	Propofol
		10100	Propoxyphene
		4946	Propranolol
		4976	Protriptyline
		4991	Pyridostigmine
		5035	Raloxifene
		5070	Riluzole
		5073	Risperidone
		5078	Rizatriptan
		5090	Rofecoxib
		5095	Ropinirole
		77999	Rosiglitazone
		338	Salicylic acid
		65863	Sertaconazole
		5212	Sildenafil
		54454	Simvastatin
		5320	Sulfacetamide
		5358	Sumatriptan
		5359	Suprofen
		1935	Tacrine
		65999	Telmisartan
		5411	Tetracaine
		2153	Theophylline
		5453	Thiotepa
		5472	Ticlopidine
		5487	Tizanidine
		5503	Tolazamide
		5546	Triamterene
		5566	Trifluoperazine
		6256	Trifluorothymidine
		861	Triiodothyronine
		5578	Trimethoprim
		6503	Tris-HCl
		5591	Troglitazone
		3121	Valproic acid
		5978	Vincristine
		71616	Voriconazole
		5717	Zafirlukast
		5732	Zolpidem

## Appendix 2 Druggable human proteome included in the benchmark database for Goal 3

The list of UniProt accession numbers for the 1469 druggable human proteins that are included in the benchmark database from Chapter 5.

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Q8IZS8	Q8N1C3	Q8N1Q1	Q8N4C8	Q8N568	Q8N5S9	Q8N695	Q8N752	Q8N8N7	Q8NDX3	Q8NE62	Q8NE63	Q8NER1	Q8NEV4
Q8NFD2	Q8TCT1	Q8TCU5	Q8TD08	Q8TD43	Q8TDC3	Q8TDR2	Q8TDS4	Q8TE04	Q8WTQ7	Q8WUI4	Q91ZY1	Q91ZY2	Q923Y7
Q92630	Q92731	Q92736	Q92769	Q92830	Q92887	Q92918	Q92952	Q92959	Q96BD0	Q96CX2	Q96FI4	Q96FL8	Q96GD4
Q96L34	Q96LB2	Q96NT5	Q96NX5	Q96Q40	Q96QE3	Q96RJ0	Q96RP8	Q96SB4	Q99246	Q99250	Q99418	Q99527	Q99549
Q99571	Q99643	Q99683	Q99700	Q99714	Q99808	Q99816	Q99928	Q99BP9	Q9BR01	Q9BRL5	Q9BRS2	Q9BVS4	Q9BX84
Q9BXA5	Q9BXC0	Q9B4C1	Q9BY49	Q9BY64	Q9BYC2	Q9BYV1	Q9BZL6	Q9C007	Q9D6N1	Q9EQ60	Q9ERZ4	Q9GVZ3	Q9H015
Q9H1D0	Q9H1R3	Q9H221	Q9H222	Q9H244	Q9H2G2	Q9H2K8	Q9H2C1	Q9H2X6	Q9H2X9	Q9H3N8	Q9H3Y6	Q9H4B4	Q9H598
Q9HAB3	Q9HAZ1	Q9HB55	Q9HBH1	Q9HC16	Q9HC97	Q9HCF6	Q9HCG7	Q9HCR9	Q9JIS7	Q9NP56	Q9NPA1	Q9NPA2	Q9NPD5
Q9NQA5	Q9NR96	Q9NR97	Q9NRP7	Q9NS40	Q9NS75	Q9NS85	Q9NSA0	Q9NSY1	Q9NTF0	Q9NVH6	Q9NVA1	Q9NY47	Q9NY57
Q9NYB5	Q9NYG8	Q9NYK1	Q9NYX4	Q9NZK7	Q9NZQ8	Q9P0X4	Q9P0Z9	Q9P289	Q9P2K8	Q9QYN8	Q9UBC3	Q9UBF8	Q9UBS5
Q9UEE5	Q9UEW8	Q9UHC3	Q9UHC9	Q9UHD2	Q9UHL4	Q9UI33	Q9UIF8	Q9UIG8	Q9UK23	Q9UK32	Q9UKE5	Q9UL54	Q9UL62
Q9ULX7	Q9UM07	Q9UN88	Q9UNA4	Q9UPE1	Q9UPY5	Q9UQB9	Q9UQD0	Q9UQL6	Q9WUD2	Q9Y233	Q9Y251	Q9Y271	Q9Y2H1
Q9Y2H9	Q9Y2I1	Q9Y468	Q9Y5K3	Q9Y5N1	Q9Y5Y4	Q9Y5Y9	Q9Y616	Q9Y666	Q9Y694	Q9Y6L6	Q9Y6M4	Q9Z0U4	Q9Z0V1
Q9Z2J6	V9GXZ4	A0A024QYT5	A0A024QYW7	A0A024QYX0	A0A024QZ12	A0A024QZ15	A0A024QZ20	A0A024QZ20	A0A024QZ20	A0A024QZ20	A0A024QZ20	A0A024QZ20	A0A024QZ20
A0A024QZ30	A0A024QZ70	A0A024QZA8	A0A024QZM9	A0A024QZS4	A0A024QZU0	A0A024QZV1	A0A024QZV1	A0A024QZV1	A0A024QZV1	A0A024QZV1	A0A024QZV1	A0A024QZV1	A0A024QZV1
A0A024QZ25	A0A024QZ27	A0A024R040	A0A024R049	A0A024R0C0	A0A024R0C6	A0A024R0H1	A0A024R0H9	A0A024R0I0	A0A024R0J1	A0A024R0L5	A0A024R0Q9	A0A024R125	A0A024R136
A0A024R1I3	A0A024R1V0	A0A024R222	A0A024R230	A0A024R230	A0A024R244	A0A024R276	A0A024R2B3	A0A024R2H8	A0A024R2M7	A0A024R2N2	A0A024R2Q0	A0A024R2W7	A0A024R2Y6
A0A024R3C5	A0A024R3C7	A0A024R3D5	A0A024R3G7	A0A024R3H7	A0A024R3K6	A0A024R3S2	A0A024R3S2	A0A024R3S3	A0A024R3T2	A0A024R3W4	A0A024R3Z2	A0A024R426	A0A024R440
A0A024R4X8	A0A024R4Z5	A0A024R567	A0A024R5B6	A0A024R5C5	A0A024R5E6	A0A024R5H1	A0A024R5I4	A0A024R5K6	A0A024R5P0	A0A024R5S8	A0A024R5W3	A0A024R5X5	A0A024R5X5
A0A024R6L5	A0A024R6N2	A0A024R6Q6	A0A024R6R2	A0A024R6R4	A0A024R6T9	A0A024R704	A0A024R718	A0A024R720	A0A024R728	A0A024R730	A0A024R7C0	A0A024R7E4	A0A024R7J0
A0A024R8E2	A0A024R8J3	A0A024R8K3	A0A024R8S3	A0A024R8U1	A0A024R8U8	A0A024R906	A0A024R909	A0A024R913	A0A024R928	A0A024R964	A0A024R980	A0A024R9A7	A0A024R9A7
A0A024R9Q5	A0A024R9X6	A0A024R9X9	A0A024R9Y0	A0A024R9Z8	A0A024RA31	A0A024RA66	A0A024RA96	A0A024RAE8	A0A024RAG0	A0A024RAH0	A0A024RAH7	A0A024RAP2	A0A024RAP4
A0A024RAV2	A0A024RAV7	A0A024RAY5	A0A024RB10	A0A024RB43	A0A024RB59	A0A024RB99	A0A024RBB2	A0A024RBB6	A0A024RBG4	A0A024RBG6	A0A024RBH0	A0A024RBL3	A0A024RBN1
A0A024RC53	A0A024RC61	A0A024RC92	A0A024RCE9	A0A024RCJ0	A0A024RCN9	A0A024RCW6	A0A024RD04	A0A024RD15	A0A024RD18	A0A024RD21	A0A024RD25	A0A024RD33	A0A024RD58
A0A024RDA5	A0A024RDD4	A0A024RDH4	A0A024RDJ4	A0A024RDK3	A0A024RDL4	A0A024RDM3	A0A024RE05	A0A024RF658	A0A024R7B7B4	A0A087WSY1	A0A087WT22	A0A087WT64	A0A087WTS4
A0A087WW79	A0A087WWV0	A0A087WV4	A0A087WY0	A0A087WY24	A0A087WZ06	A0A087WZ88	A0A087WZL8	A0A087X090	A0A087X0I6	A0A087X0W8	A0A087X1B1	A0A088AWN0	A0A088QCU6
A0A090N8Y0	A0A090N8Z1	A0A0A0MQR8	A0A0A0MQX8	A0A0A0MR48	A0A0A0MR60	A0A0A0MR67	A0A0A0MRG0	A0A0A0MRG2	A0A0A0MRL7	A0A0A0MRV2	A0A0A0MS52	A0A0A0MSE3	A0A0A0MSK3
A0A0A0MTJ0	A0A0A0NOL2	A0A0A06YYA8											

# Appendix 3 Benchmark database of drug-protein interactions for Goal 3

The list of 34456 drug-protein interactions that are included in the benchmark database from Chapter 5. We provide PubChem CIDs and names for drugs (highlighted in gray color) and UniProt accession numbers for protein targets for each drug.

CID 119: gamma-aminobutyric acid  
A0A024QZ17 A0A024R4E2 A0A024R909 A0A024R9X6 A0A024RC9N A0A090N8Z1 A0A0A0MTJ0 A0A0A6YYA8 A8K177 B4DN83 B4E398 B7ZKN7 F1D8N7 O75899 O88871 P02545 P13612 P21728 P23415 P24046 P31644 P34903 P50440 Q03164 Q16445 Q68D08 Q6ZWB6 Q92830 Q96CX2 Q96QE3 Q9UBS5 Q9UIF8 Q9Z0U4

CID 137: delta-aminolevulinic acid  
A0A024QZ17 B2CQT6 P02545 P13716 P24046 Q16348 Q9UIF8

CID 338: salicylic acid  
A0A024QZ17 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R5I4 A0A024R6R4 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RBW9 A0A024RD15 A0A087WU84 A0A090N7W1 A0A090N7X8 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1D2 A4D1Q0 A8K1F6 A8K249 A8K3J4 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B2R807 B2RXH2 B3KUB4 B4DN15 B4DUH8 B7Z1L9 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O60656 P00352 P00533 P00915 P00918 P02768 P05177 P05181 P06133 P06239 P06241 P07451 P07550 P08173 P08236 P08246 P08254 P08311 P08588 P08684 P08913 P09917 P11229 P11509 P11712 P14780 P14902 P15428 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P22748 P22894 P23219 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P30872 P30874 P31391 P32238 P32245 P32745 P33032 P35218 P35346 P35354 P35367 P36537 P37288 P41143 P41595 P41968 P43166 P49146 P50052 P50406 P51681 Q01959 Q04828 Q08209 Q16790 Q38Q88 Q4U2R8 Q92830 Q9NSA0 Q9UHC3

CID 444: bupropion  
A0A024QZ17 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R5I4 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RAU7 A0A024RC9N A0A024RD15 A0A087WU84 A0A090N7W1 A0A0A0MQX8 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0A0A0MTJ0 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K5W4 A8K7N8 A8KAF4 A8KAG8 B0ZBD3 B0ZBE0 B2R7Y7 B3KP78 B4DN15 B7Z1L9 B7Z242 B7ZKN7 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O94782 P00352 P00533 P00918 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P17252 P17405 P18825 P20813 P21397 P21452 P21554 P21728 P21917 P22303 P23975 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P32297 P33032 P35354 P35367 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 P83916 Q01959 Q08209 Q38Q88 Q92830 Q92887 Q9UIF8

CID 453: mannitol  
A0A024QZ17 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R4E2 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RD15 A0A087WU84 A0A090N7W1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1D2 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B4DN15 B7Z1L9 B7Z242 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O15245 P00533 P00918 P02545 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P39748 P41143 P41595 P41968 P49146 P50052 P50406 P51681 P83916 Q01959 Q08209 Q16236 Q38Q88 Q92830 Q9Y468

CID 564: epsilon-aminocaproic acid  
A0A024QZ17 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R6T9 A0A024R909 A0A024R9I2 A0A024RAP2 A0A024RAV2 A0A024RC9N A0A024RD15 A0A087WU84 A0A090N7W1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B4DN15 B7Z1L9 B7Z242 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O15245 P00533 P00918 P02545 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P16050 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 P83916 Q01959 Q08209 Q13526 Q38Q88 Q92830 Q96QE3

CID 598: mesna  
A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R6T9 A0A024R9I2 A0A024R9Y0 A0A024RAP2 A0A024RD15 A0A087WU84 A0A090N7W1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B2RXH2 B4DN15 B7Z1L9 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O15375 O95907 P00533 P00915 P00918 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P16050 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P22748 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 Q01959 Q08209 Q38Q88

CID 612: lactate  
A0A024R0H1 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R5C5 A0A024R5I4 A0A024R5Z9 A0A024R6T9 A0A024R8J3 A0A024R8U1 A0A024R9I2 A0A024R9I5 A0A024RAP2 A0A024RBB2 A0A024RD15 A0A087WT22 A0A087WU84 A0A090N7W1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B3KU60 B4DF30 B4DN15 B4DPF4 B7Z1L9 B7ZM24 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O15375 O95907 P00533 P00915 P00918 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11717 P11229 P11509 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P22748 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35218 P35354 P35367 P36021 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 P80404 Q01959 Q08209 Q16790 Q38Q88 Q92959 Q9BYV1 Q9HX29 Q9Y666

CID 679: dimethyl sulfoxide  
A0A024QY75 A0A024QZ25 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RD15 A0A087WU84 A0A090N7W1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0YJ76 B0ZBE0 B2R7Y7 B4DN15 B7Z1L9 B8K2Q5 C1ID52 E5KQF5 E9KL36 F1D8N3 F1D8Q5 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O60885 P00533 P00918 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P17252 P18825 P21397 P21452

P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288  
P41143 P41595 P41968 P47712 P49146 P50052 P50406 P51681 Q01959 Q02790 Q08209 Q38Q08

CID 681: dopamine  
A0A024QZ7 A0A024R276 A0A024R3C5 A0A024R6L5 A0A024R6T9 A0A024R9Y0 A0A024RAP4 A0A024RAV2 A0A024RBW9 A0A024RCN9 A0A087WT22 A1A4V4  
A8K3J4 A8K5W4 B2R7Y7 B2RXH2 B3KUB4 B4DUH8 B4E398 B7Z242 B7ZKN7 B7ZWS5 C1ID52 D0VY79 F8W6L1 L8B082 O15244 O15245 O43704 O75160 O94925  
P00352 P00915 P00918 P02545 P07451 P07550 P08588 P09172 P10253 P16050 P16662 P21397 P21728 P21917 P21918 P21964 P22309 P22310 P22748  
P27695 P28482 P30729 P35218 P35462 P39748 P42345 P43166 P43220 P50225 P61169 P83916 Q01453 Q01959 Q16790 Q16853 Q5DSZ7 Q5DT02 Q99549  
Q99700 Q99714 Q9UIF8 Q9UN44

CID 750: polyglycine  
A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R4Z5 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RB99 A0A024RD15 A0A087WU84 A0A090N7M1  
A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0A0A6YYA8 A0N0Q1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K228 A8K249 A8K7N8 A8KAF4 A8KAG8 A9ZM15  
B0ZBE0 B2CQT6 B2R7Y7 B4DN15 B4E398 B7Z1L9 B7Z3W8 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 H9NIM1 K9J958 L7RSL3 L7RXH5 O15399  
O60391 O75311 P00533 P00918 P05177 P05181 P06239 P06241 P07550 P07741 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712  
P13196 P14780 P17252 P18825 P21397 P21452 P21549 P21554 P21728 P21917 P22303 P22309 P22557 P23378 P23415 P23416 P23434 P25021 P25024  
P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P34896 P35354 P35367 P37288 P41143 P41250 P41595 P41968 P48167  
P48637 P49146 P50052 P50406 P50440 P51681 Q01098 Q01959 Q05586 Q08209 Q12879 Q13126 Q13224 Q14032 Q14749 Q38Q08 Q4VAM5 Q5T6X5 Q61B77  
Q9BY49 Q9BVV1 Q9H598 Q9P0Z9

CID 774: histamine  
A0A024QZ7 A0A024R909 A0A024RBW9 A0A024RCN9 A0A0A0MR48 A0A0A0MTJ0 A8K3J4 B2KJ49 B3KUB4 B4DUH8 B4DWC1 B4E398 B7ZKN7 O15244 O15245  
O75751 O94782 P00915 P00918 P02545 P07451 P22748 P25021 P25102 P27695 P28223 P34969 P35218 P35367 P43166 P58406 Q16790 Q91Z1 Q91Z2  
Q9H3N8 Q9QYN8 Q9UIF8 Q9UN44 Q9Y5N1

CID 785: hydroquinone  
A0A024QZ7 A0A024R909 A0A024R9Y0 A0A024R9Z8 A0A024RAV2 A0A024RBV5 A0A024RCN9 A0A024RCW6 A0A024RDA5 A0A024RDJ4 A8K3J4  
A8KAF4 B2RXH2 B3KUB4 B4DUH8 B6ZGS9 B7ZKN7 D0VY79 D9YZU5 E5KQF5 F1D8N5 F1D8P8 F1D8P9 H6VQ59 O15245 O43704 O60656 O75604 O94782 P00352 P02545 P02768 P05543  
P02545 P07451 P08684 P15428 P16050 P22748 P35218 P39748 P42345 P43166 P83916 Q01453 Q13526 Q16790 Q5DSZ7 Q5DT02 Q96QE3 Q99549 Q99700  
Q99714

CID 838: epinephrine  
A0A024QZ7 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R6L5 A0A024R6T9 A0A024R9I2 A0A024R9Y0 A0A024RAP2 A0A024RAP4 A0A024RAV2  
A0A024RB4 A0A024RBW9 A0A024RCN9 A0A024RD15 A0A087WU84 A0A090N7M1 A0A090N8Z1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0A0A0MTJ0 A0N0Q1  
A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K3J4 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B2RXH2 B3KUB4 B4DN15 B4DUH8 B7Z1L9 B7ZKN7  
B8K2Q5 C1ID52 D0VY79 E5KQF5 E9PG18 F1D8N3 F1D8P4 F1D8P8 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O15245 O15296 O75164 O94782 P00352  
P00533 P00915 P00918 P05177 P05181 P06239 P06241 P07451 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P13945  
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CID 853: thyroxine  
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B3K7F8 B6ZGS9 B7Z1L9 B7ZWS5 D2KUA6 E9KL36 F1D8N7 F1D8P8 F1D8P9 H6VQ59 O15245 O43704 O60656 O75604 O94782 P00352 P02545 P02768 P05543  
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CID 861: triiodothyronine  
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CID 1046: pyrazinamide  
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P41595 P41968 P47989 P49146 P49327 P50052 P50406 P51681 P83916 Q01959 Q08209 Q38Q08 Q96QE3

CID 1054: vitamin B6  
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CID 1130: thiamine  
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CID 1775: phenytoin  
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P20813 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P27695 P28223 P28482 P29772 P30411 P31644 P32238  
P32245 P33032 P34903 P35354 P35367 P35498 P37288 P39748 P41143 P41595 P41968 P42898 P49146 P50052 P50406 P51681 P83916 Q01453 Q01959  
Q03164 Q08209 Q15858 Q16236 Q16445 Q38Q08 Q92830 Q92887 Q99250

CID 1935: tacrine  
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C1ID52 E5KQF5 E9PG18 F1D8N3 F1D8N7 F1D8L4 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O00519 O15245 P00352 P00533 P00918 P02545 P02768  
P04775 P05177 P05181 P06239 P06241 P06280 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P12004 P14780 P15428 P17252  
P20813 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P27695 P28223 P28482 P29772 P30411 P31644 P32238  
P32245 P33032 P34903 P35354 P35367 P35498 P37288 P39748 P41143 P41595 P41968 P42898 P49146 P50052 P50406 P51681 P83916 Q01453 Q01959  
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CID 1978: acebutolol  
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B4DN15 B7Z1L9 B8K2Q5 C1ID52 D0VY79 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O15245 P00533 P00918 P02545 P05177 P05181  
P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P10827 P11229 P11509 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728  
P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P34969 P35367 P37288 P41143 P41595  
P41968 P49146 P50052 P50406 P51681 Q01959 Q08209 Q38Q08

CID 1983: acetaminophen  
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A8K1F6 A8K249 A8K3J4 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B2ZGL7 B3KUB4 B4DN15 B4DUH8 B7Z1L9 B7Z242 B7ZKN7 B8K2Q5 C1ID52 E5KQF5 F1D8N3 F1D8P6  
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P33032 P35218 P35354 P35367 P36537 P37288 P41143 P41595 P41968 P43166 P49146 P50052 P50225 P50406 P51681 P83916 Q01959 Q08209 Q16790  
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CID 1986: acetazolamide  
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P50406 P51681 Q01959 Q08209 Q38Q08 Q8N1Q1 Q92769 Q9P6N1 Q9ULX7

CID 2022: acyclovir  
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P11509 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 Q01959 Q08209 Q38Q88 Q4U2R8 Q99714

CID 2082: alendazole  
A0A024QZ7 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RCN9 A0A024RD15 A0A087WU84 A0A090N7M1 A0A090N8Z1 A0A0A0MQX8 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0NOQ1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B4DN15 B4DN83 B7Z1L9 B8K2Q5 C1D52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O75874 P00533 P00918 P02545 P05177 P05181 P06239 P06241 P07437 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P41143 P41595 P41968 P43220 P49146 P50052 P50406 P51681 P53582 P68371 P83916 Q01959 Q08209 Q16236 Q38Q88 Q71U36 Q96QE3 Q9HC16

CID 2083: salbutamol  
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CID 2088: alendronate  
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CID 2092: alfuzosin  
A0A024RCN9 A0A068F658 A0A090N7M1 B0ZBD3 B0ZBE0 B2RXH2 O94782 P00352 P02545 P06280 P06864 P10253 P15428 P25100 P35348 P35368 P39748 Q99714

CID 2094: allopurinol  
A0A024QZ7 A0A024R2N2 A0A024R2Q0 A0A024R3C5 A0A024R3S2 A0A024R4E2 A0A024R5I4 A0A024R6T9 A0A024R9I2 A0A024RAP2 A0A024RAU7 A0A024RBV5 A0A024RCN9 A0A024RD15 A0A024RDA5 A0A087WU84 A0A090N7M1 A0A0A0MRG0 A0A0A0MSK3 A0A0A0MT22 A0A0A0MTJ0 A0NOQ1 A1A4V4 A2A3U5 A2RUS0 A4D1Q0 A8K1F6 A8K249 A8K7N8 A8KAF4 A8KAG8 B0ZBE0 B2R7Y7 B4DN15 B4DN83 B4E398 B7Z1L9 B8K2Q5 C1D52 E5KQF5 F1D8N3 F5H1T4 G5E9C5 H6VQ59 K9J958 L7RSL3 L7RXH5 O0533 P00918 P05177 P05181 P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P39748 P41143 P41595 P41968 P46098 P49146 P50052 P50406 P51681 Q01959 Q08209 Q38Q88 Q9GZV3

CID 2099: alossetron  
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CID 2118: alprazolam  
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CID 2123: hexamethylmelamine  
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CID 2130: amantadine  
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CID 2140: diatrizoate  
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CID 2141: amifostine  
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CID 2145: aminoglutethimide  
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CID 2153: theophylline  
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P06239 P06241 P07550 P08173 P08246 P08311 P08588 P08684 P08913 P11229 P11509 P11712 P14780 P17252 P17405 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P33534 P35367 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 Q00975 Q01668 Q01959 Q06432 Q08209 Q08289 Q38Q88 Q8TZS8 Q92830

CID 2170: amoxapine  
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P14780 P14842 P17252 P18505 P18507 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P23975 P25021 P25024 P25025 P25101 P25103 P25929  
P28222 P28223 P28482 P30411 P31388 P31644 P31645 P32238 P32245 P33032 P33032 P33032 P34903 P34969 P35354 P35367 P35368 P37288 P41143 P41595  
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Q99549 Q99700 Q99928 Q9UN88

CID 2179: amsacrine  
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A0A0A0MRL7 A0A0A0MTJ0 A4D1D2 A8K249 A8K459 A8K987 A8K996 B2RXH2 B4DN83 B7Z1F9 B7Z2G8 B7ZKN7 C1ID52 DOVY79 F1D8P8 F8W6L1 O15245  
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Q02880 Q03164 Q06278 Q16236 Q96QE3 Q99549 Q99700 Q99714 Q9UIF8 Q9UN44

CID 2182: anagrelide  
A0A024QZ7 A0A024RCN9 O75164 P05177 P27695 Q14432

CID 2187: anastrozole  
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P08311 P08588 P08684 P08842 P08913 P11229 P11509 P11511 P11712 P14780 P17252 P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021  
P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P35354 P35367 P37288 P41143 P41595 P41968 P49146 P50052  
P50406 P51681 Q01959 Q08209 Q38Q88

CID 2216: apraclonidine  
A0A024R909 A0A024RCN9 A0A024RDJ4 A0A068F658 A0A090N7W1 A0A0A0MTJ0 B0ZBD3 B7ZKN7 O94925 P08913 P18825 Q99714

CID 2244: aspirin  
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Q9UHC3 Q9UN44

CID 2249: atenolol  
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CID 2265: azathioprine  
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CID 3105: dipivefrin  
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CID 3108: dipyrindamole  
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Q9Y233

CID 3114: disopyramide  
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CID 3121: valproic acid  
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CID 3151: domperidone  
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P25929 P27695 P28223 P28482 P30411 P32238 P32245 P33032 P35318 P35354 P35367 P35462 P37288 P41143 P41595 P41968 P42345 P49146 P50052  
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CID 3152: donepezil  
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Q13627 Q92630

CID 3156: doxapram  
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Q01959 Q08209 Q38Q88

CID 3157: doxazosin  
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CID 3158: doxepin  
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CID 3168: droperidol  
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CID 3182: dyphylline  
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CID 3198: econazole  
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CID 3226: enflurane  
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CID 3241: epinastine  
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CID 3261: estazolam  
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Q8N1C3 Q99928 Q9UN88

CID 3278: ethacrynic acid

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CID 3291: ethosuximide  
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CID 3305: etidronate  
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CID 3324: famciclovir  
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CID 3325: famotidine  
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CID 3331: felbamate  
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CID 3333: felodipine  
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CID 3339: fenofibrate  
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CID 3342: fenpropfen  
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CID 3345: fentanyl  
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CID 3348: fexofenadine  
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CID 3354: flavoxate  
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CID 3366: 5-fluorocytosine  
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CID 3372: fluphenazine  
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CID 3373: flumazenil  
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CID 3385: 5-fluorouracil  
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CID 3386: fluoxetine  
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CID 3393: flurazepam  
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CID 3394: flurbiprofen  
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CID 3410: formoterol  
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CID 3446: gabapentin  
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CID 3475: gliclazide  
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CID 3488: glibenclamide  
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CID 3516: guaifenesin  
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CID 3519: guanfacine  
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CID 3559: haloperidol  
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CID 3647: hydroflumethiazide  
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CID 3652: hydroxychloroquine  
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CID 3658: hydroxyzine  
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CID 3672: ibuprofen  
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CID 3675: phenelzine  
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CID 3676: lidocaine  
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CID 3690: ifosfamide  
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CID 3696: imipramine



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P41143 P41595 P41968 P42858 P49146 P50052 P50406 P51681 Q01959 Q07343 Q08209 Q13370 Q13526 Q14432 Q38Q88 Q96QE3 Q99714 Q9UN44

CID 3702: indapamide  
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CID 3715: indomethacin  
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CID 3739: iodipamide  
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CID 3749: irbesartan  
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CID 3759: isocarboxazid  
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CID 3763: isoflurane  
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CID 3767: isoniazid  
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CID 3779: isoproterenol  
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CID 4543: nortriptyline  
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CID 4583: ofloxacin  
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CID 4594: omeprazole  
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CID 4601: orphenadrine  
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CID 4614: oxaprozin  
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CID 4616: oxazepam  
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P30411 P32238 P32245 P33032 P35354 P35367 P37288 P39748 P41143 P41595 P41968 P43220 P49146 P50052 P50406 P51681 Q01453 Q01959 Q08209  
Q38Q88 Q99700 Q9UNA4

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CID 4678: panthenol  
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CID 4679: pantoprazole  
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CID 4680: papaverine  
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CID 4723: pemoline  
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Q08209 Q38Q88

CID 4725: penciclovir  
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Q38Q88

CID 4737: pentobarbital  
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CID 4740: pentoxifylline  
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CID 4748: perphenazine  
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CID 4763: phenobarbital  
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CID 4768: phenoxybenzamine  
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CID 4771: phentermine  
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CID 4828: pindolol  
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CID 4829: pioglitazone  
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CID 4891: praziquantel  
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P18825 P21397 P21452 P21554 P21728 P21917 P22303 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032  
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CID 4893: prazosin  
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CID 4906: prilocaine  
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P07550 P08173 P08246 P08311 P08588 P08684 P08913 P10253 P11229 P11509 P11712 P14780 P15428 P17252 P18825 P21397 P21452 P21554 P21728  
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CID 4908: primaquine  
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CID 4909: primidone  
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CID 4911: probenecid  
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P22309 P25021 P25024 P25025 P25101 P25103 P25929 P28223 P28482 P30411 P32238 P32245 P33032 P33527 P35354 P35367 P37288 P41143 P41595 P41968 P49146 P50052 P50406 P51681 P83916 Q01959 Q08209 Q38Q88 Q4U2R8 Q5DSZ6 Q5DSZ7 Q5DT02 Q92887 Q9NSA0 Q9NYB5 Q9WUD2 Q9Y694

CID 4913: procainamide  
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A8KAG8 B0ZBE0 B2R7Y7 B3KP78 B4DN15 B4E398 B7Z1L9 B7ZKN7 B8K2Q5 C1ID52 D3DNN4 E5KQF5 E9PG18 F1D8N3 F5H1T4 G5E9C5 H6VQ59 I6L9H2 K9J958 L7RSL3  
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CID 4915: procarbazine  
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CID 4917: prochlorperazine  
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CID 4927: promethazine  
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CID 4932: propafenone  
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CID 4935: proparacaine  
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CID 4991: pyridostigmine  
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CID 5002: quetiapine  
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CID 5318: sulconazole

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CID 5320: sulfacetamide

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CID 5344: sulfisoxazole

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CID 5358: sumatriptan

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CID 5359: suprofen

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CID 5401: terazosin

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CID 5403: terbutaline

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CID 5411: tetracaine

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CID 5430: thيابendazole

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