

Therapeutic target database update 2012: a resource for facilitating target-oriented drug discovery

Feng Zhu¹, Zhe Shi¹, Chu Qin^{1,2}, Lin Tao^{1,2}, Xin Liu¹, Feng Xu^{3,4}, Li Zhang⁴, Yang Song⁴, Xianghui Liu¹, Jingxian Zhang¹, Bucong Han^{1,5}, Peng Zhang⁶ and Yuzong Chen^{1,*}

¹Bioinformatics and Drug Design Group, Department of Pharmacy, and Center for Computational Science and Engineering, National University of Singapore, Singapore 117543, ²NUS Graduate School for Integrative Sciences and Engineering, Singapore 117456, ³College of Pharmacy and Tianjin Key Laboratory of Molecular Drug Research, Nankai University, Tianjin 300071, People's Republic of China, ⁴State Key Laboratory of Medicinal Chemistry & Biology, Tianjin International Joint Academy of Biotechnology & Medicine, Tianjin 300457, ⁵Computation and Systems Biology, Singapore-MIT Alliance, National University of Singapore 117543 and ⁶Computational Biology Program, National University of Singapore, Singapore 117543

Received August 24, 2011; Revised September 8, 2011; Accepted September 9, 2011

ABSTRACT

Knowledge and investigation of therapeutic targets (responsible for drug efficacy) and the targeted drugs facilitate target and drug discovery and validation. Therapeutic Target Database (TTD, <http://bidd.nus.edu.sg/group/ttd/ttd.asp>) has been developed to provide comprehensive information about efficacy targets and the corresponding approved, clinical trial and investigative drugs. Since its last update, major improvements and updates have been made to TTD. In addition to the significant increase of data content (from 1894 targets and 5028 drugs to 2025 targets and 17 816 drugs), we added target validation information (drug potency against target, effect against disease models and effect of target knockout, knockdown or genetic variations) for 932 targets, and 841 quantitative structure activity relationship models for active compounds of 228 chemical types against 121 targets. Moreover, we added the data from our previous drug studies including 3681 multi-target agents against 108 target pairs, 116 drug combinations with their synergistic, additive, antagonistic, potentiative or reductive mechanisms, 1427 natural product-derived approved, clinical trial and pre-clinical drugs and cross-links to the clinical trial information page in the ClinicalTrials.gov database for 770 clinical trial drugs. These updates are useful for facilitating target discovery and validation, drug lead discovery

and optimization, and the development of multi-target drugs and drug combinations.

INTRODUCTION

Modern drug discovery is primarily focused on the search or design of drug-like molecules, which selectively interact and modulate the activity of one or a few selected therapeutic targets (1–3). One challenge in drug development is to choose and explore promising targets from a growing number of potential targets (4). Target selection and validation are important not only for achieving therapeutic efficacy but also for increasing drug development odds, given that few innovative targets have made it to the approved list each year [12 innovative targets in 1994–2005 (5) and 10 new human targets in 2006–2010 (6) for small molecule drugs]. Apart from target selection and validation, drug discovery efforts can be facilitated by enhanced knowledge of bioactive molecular scaffolds (7,8), structure–activity relationships (9), multi-target agents (10,11) and synergistic drug combinations (12) against selected target or multiple targets, and information about the sources of drug leads such as the species origins of natural product-derived drugs (13).

Internet resources such as Therapeutic Target Database (TTD) (14,15) and DrugBank (16) provide comprehensive information about the targets and drugs in different development and clinical stages, which are highly useful for facilitating focused drug discovery efforts and pharmaceutical investigations against the most relevant and proven targets (17–19). In addition to the update of these databases by expanded target and drug data

*To whom correspondence should be addressed. Tel: +65 6516 6877; Fax: +65 6774 6756; Email: cscyz@nus.edu.sg

contents, the usefulness of these databases for facilitating drug discovery efforts can be further enhanced by adding additional information and knowledge derived from the target and drug discovery processes. Therefore, we updated TTD by both significantly expanding the target and drug data and adding new information about target validation, quantitative structure–activity relationship (QSAR) models of a variety of molecular scaffolds active against selected targets and specific types of drugs (multi-target drugs and natural product-derived drugs) and drug combinations (synergistic, additive, antagonistic, potentiative and reductive combinations).

The significantly expanded target and drug data cover 364 successful, 286 clinical trial, 44 discontinued clinical trial and 1331 research targets, and 1540 approved, 1423 clinical trial, 345 discontinued clinical trial, 165 pre-clinical and 14853 experimental drugs linked to their primary targets (14170 small molecule and 652 anti-sense drugs with available structure and sequence data) (Table 1). These are compared to 348 successful, 249 clinical trial, 43 discontinued clinical trial and 1254 research targets, and 1514 approved, 1212 clinical trial and 2302 experimental drugs in our last update (15). To facilitate the access of clinical trial information of the clinical trial drugs, cross-links to the relevant page in ClinicalTrials.gov database are provided for 770 clinical trial drugs. The newly added target validation data includes the experimentally measured potency of 11 810 drugs against 915 targets, the observed potency or effects of 497 drugs against disease models (cell lines, *ex vivo*, *in vivo* models) linked to 393 targets, and the observed effects of target knockout, knockdown or genetic variations for 307 targets (Table 2). The QSAR data consists of 841 QSAR models for active compounds of 228 chemical types against 121 targets (Table 2).

Moreover, we added the data partly derived from our previous studies of multi-target drugs (20,21), drug combinations (12) and natural product derived drugs (13)

Table 1. Statistics of drug targets, drugs and structure and sequence data in TTD database

Data Category	2012 update	2010 update
Statistics of drug targets		
Number of all targets	2025	1894
Number of successful targets	364	348
Number of clinical trial targets	286	249
Number of discontinued targets	44	43
Number of research targets	1331	1254
Statistics of drugs		
Number of all drugs	17 816	5028
Number of approved drugs	1540	1514
Number of clinical trial drugs	1423	1212
Number of discontinued drugs	345	274
Number of pre-clinical drugs	165	142
Number of experimental drugs	14 853	2302
Statistics of drugs with available structure or sequence data		
Number of small molecular drugs with available structure	14 170	3382
Number of antisense drugs with available sequence data	652	649

(Table 2). The multi-target drug data is composed of 3681 multi-target agents active against 108 target pairs together with their potencies against the target pairs. The drug combination data includes 72, 14 and 4 pharmacodynamically synergistic, additive and antagonist combinations, and 19 and 7 pharmacokinetically potentiative and reductive combinations together with their mode of actions and combination mechanisms. The natural product-derived drug data includes the drug names and their species origins and species families for 939 approved, 369 clinical-trial and 119 pre-clinical drugs.

NEW TARGET AND DRUG DATA COLLECTION

Additional target and drug data, including the approved, clinical trial and experimental drugs and their primary targets, were collected by using the same methods described in our previous publications (14,15). In particular, all TTD targets are primary targets (i.e. efficacy targets) directly responsible for the claimed therapeutic efficacies (in

Table 2. Summary and statistics of newly added data in 2012 version of TTD

Data Category	Number of Information
Target validation data	
Experimentally measured potency of drugs against targets	
Number of drugs	11 810
Number of targets	915
Drug potency against disease model (cell-lines, <i>ex vivo</i> , <i>in vivo</i> models)	
Number of drugs	497
Number of targets	393
The observed effects of target knockout, knockdown or genetic variations	
Number of targets	307
QSAR models	
Number of QSAR models	841
Number of Chemical types	228
Number of targets	121
Structure and potency information of multi-target agents against target pairs	
Number of multi-target agents	3681
Number of target pairs	108
Drug combination data	
Pharmacodynamically synergistic drug combinations	
Number of drug combinations due to anti-counteractive actions	22
Number of drug combinations due to complementary actions	30
Number of drug combinations due to facilitating actions	20
Number of pharmacodynamically additive drug combinations	14
Number of pharmacodynamically antagonistic drug combinations	4
Number of pharmacokinetically potentiative drug combinations	19
Number of pharmacokinetically reductive drug combinations	7
Natural product-derived drugs and their species origins	
Number of natural product-derived approved drugs	939
Number of natural product-derived clinical trial drugs	369
Number of natural product-derived pre-clinical drugs	119

drug approval, clinical trial or investigations) of the corresponding drugs as confirmed by biochemical assay and strong cell based and/or *in vivo* evidence linking the target to drug (15,17,22). The status of approved drugs and clinical trial drugs is up-to-date as of December 2010. The discontinued clinical trial drugs are based on the report from US National Institutes of Health (NIH, <http://clinicaltrials.gov/>). The discontinued clinical trial targets are those clinical trial targets that no longer have an active clinical trial drug at the end of 2010. Pre-clinical drugs are drug candidates that have passed discovery stages and started such pre-clinical studies as safety, PK/ADME, active pharmaceutical ingredient preparation and formulation (23). The newly added experimental drugs were selected based on a potency cut-off value of $\leq 20 \mu\text{M}$ against their targets.

TARGET VALIDATION DATA

Target validation has been routinely performed to demonstrate the functional role of the potential target in disease phenotype and the ability of drug-like molecules to modulate the activities of the target to achieve therapeutic efficacies (24,25). Target validation normally requires the determination that the target is expressed in the disease-relevant cells/tissues, it can be directly modulated by a drug or drug-like molecule with adequate potency in biochemical assay, and that target modulation in cell and/or animal models ameliorates the relevant disease phenotype (24,26). *In vivo* target validation has been conducted mostly in knockout mice, transgenic *in vivo* models, and also in RNA interference, antibody and antisense treated *in vivo* models (26,27). We therefore searched the PubMed database (28) to collect from literature three types of

target validation data: experimentally determined potency of drugs against their primary target or targets, observed potency or effects of drugs against disease models (cell lines, *ex vivo*, *in vivo* models) linked to their primary target or targets, and the observed effects of target knockout, knockdown, transgenic, RNA interference, antibody or antisense-treated *in vivo* models. Target validation data can be retrieved by clicking the 'Target Validation' field in the TTD home page, which lead to the TTD target validation information page wherein a user can select the relevant data for a particular target from the target name list (Figure 1).

QUANTITATIVE STRUCTURE–ACTIVITY RELATIONSHIP MODELS AGAINST SPECIFIC TARGET

QSAR models for active compounds against many different targets have been developed and explored for drug lead discovery and optimization (9,29). These models elucidate the chemical characteristics favorable to the modulation of the activity of specific target at sufficient potency by establishing quantitative correlations between molecular properties and biological activities (e.g. 50% inhibition concentration or binding affinities) (30). In drug lead optimization projects, QSAR models against specific target can be recursively developed and used for guiding the design or search of more potent compounds or compounds with more desired drug-like properties as the new activity or drug-like property data from newly synthesized compounds become available (9,29). Therefore, knowledge of developed QSAR models for different molecular scaffolds active against different targets is highly useful for facilitating further drug

The image shows the 'Therapeutic Targets Database' (TTD) website interface. At the top, there is a banner with the text 'Therapeutic Targets Database' and the logo for 'BIDD Bioinformatics and Drug Design group'. Below the banner is a navigation bar with several tabs: 'HOME', 'Customized Search', 'Target Similarity Search', 'Drug Similarity Search', 'Download', 'QSAR Models', 'Target Validation', 'Multi Target Agents', 'Drug Combinations', and 'Nature-derived Drugs'. The 'Target Validation' tab is highlighted. Below the navigation bar is a search section titled 'Search Target with Target Validation Information'. It contains a label 'Search by target name:' followed by a dropdown menu with the text 'Select from the target name List' and a search button, and a 'Reset' button.

Figure 1. The target validation information page of TTD.

development and lead optimization efforts. In addition to the QSAR models, we have collected in our previous analysis of QSAR models of bioactive compounds (31), we searched PubMed database (28) to collect 309 papers that describe 841 ligand-based QSAR models for active compounds of 228 chemical types against 121 targets. While there are also a high number of papers describing receptor-based QSAR models, these models were not included in TTD because they are not easily displayed in explicit form in a database setting without obtaining copyrights from the relevant journals. The included QSAR models can be accessed by clicking the 'QSAR Models' field in the TTD home page, which lead to the TTD QSAR model page wherein a user can select the relevant model for a particular chemical class against a specific target either from the target name list or the chemical type list (Figure 2). The retrieved QSAR model page (Figure 3) contains the information about target and ID, target species, chemical type, compound mode of action, QSAR models, the molecular descriptors in the QSAR models, references and hyperlinks to the molecular descriptor computation web servers MoDeL (32) and e-dragon (33).

MULTI-TARGET AGENTS

Therapeutic agents directed at an individual target frequently show reduced efficacies, undesired safety profiles and drug resistances due to network robustness,

redundancy, cross-talk, compensatory and neutralizing actions, anti-target and counter-target activities (34–36). Multi-target agents directed at selected multiple targets have been increasingly explored for enhanced therapeutic efficacies, improved safety profiles and reduced resistance activities by simultaneously modulating the activity of a primary target and the counteractive elements (3,37,38). In addition to the multi-target agents we have collected in our previous studies of multi-target drugs (20,21), we further searched PubMed (28) using such keywords as 'multi-target', 'dual target' and 'dual inhibitor'. Multi-target agent against a target pair refers to a compound active against both targets at potency values of $\leq 20 \mu\text{M}$ regardless of their possible activities against other targets. The 3D structures of these multi-target agents were generated by using CORINA (39) from the 2D structures manually drawn based on the literature provided structures or the structures found in such chemical databases as BindingDB (40), ChEMBL (41) and PubChem (28). These multi-target agents can be retrieved by clicking the 'Multi-Target Agents' field in the TTD home page, which lead to the TTD multi-target agents page wherein a user can download the multi-target agents against a specific target pair from the target pair list (Figure 4).

DRUG COMBINATIONS

Apart from multi-target agents, drug combinations have also been extensively explored for enhanced therapeutic

The image shows the user interface of the Therapeutic Targets Database (TTD). At the top, there is a banner with the text "Therapeutic Targets Database" and the logo for "BIDD Bioinformatics and Drug Design group". Below the banner is a navigation menu with buttons for "HOME", "Customized Search", "Target Similarity Search", "Drug Similarity Search", and "Download". A secondary menu includes "QSAR Models", "Target Validation", "Multi Target Agents", "Drug Combinations", and "Nature-derived Drugs". The main section is titled "Search Quantitative Structure-Activity Relationship (QSAR) Models". It contains two search sections: "Search by drug target name:" with a dropdown menu labeled "Select from the target name List" and "Search" and "Reset" buttons; and "Search by chemical type:" with a dropdown menu labeled "Select from the chemical type List" and "Search" and "Reset" buttons.

Figure 2. QSAR model page of TTD.

Target Name	HIV-1 protease
Target TTD ID	TTDS00319

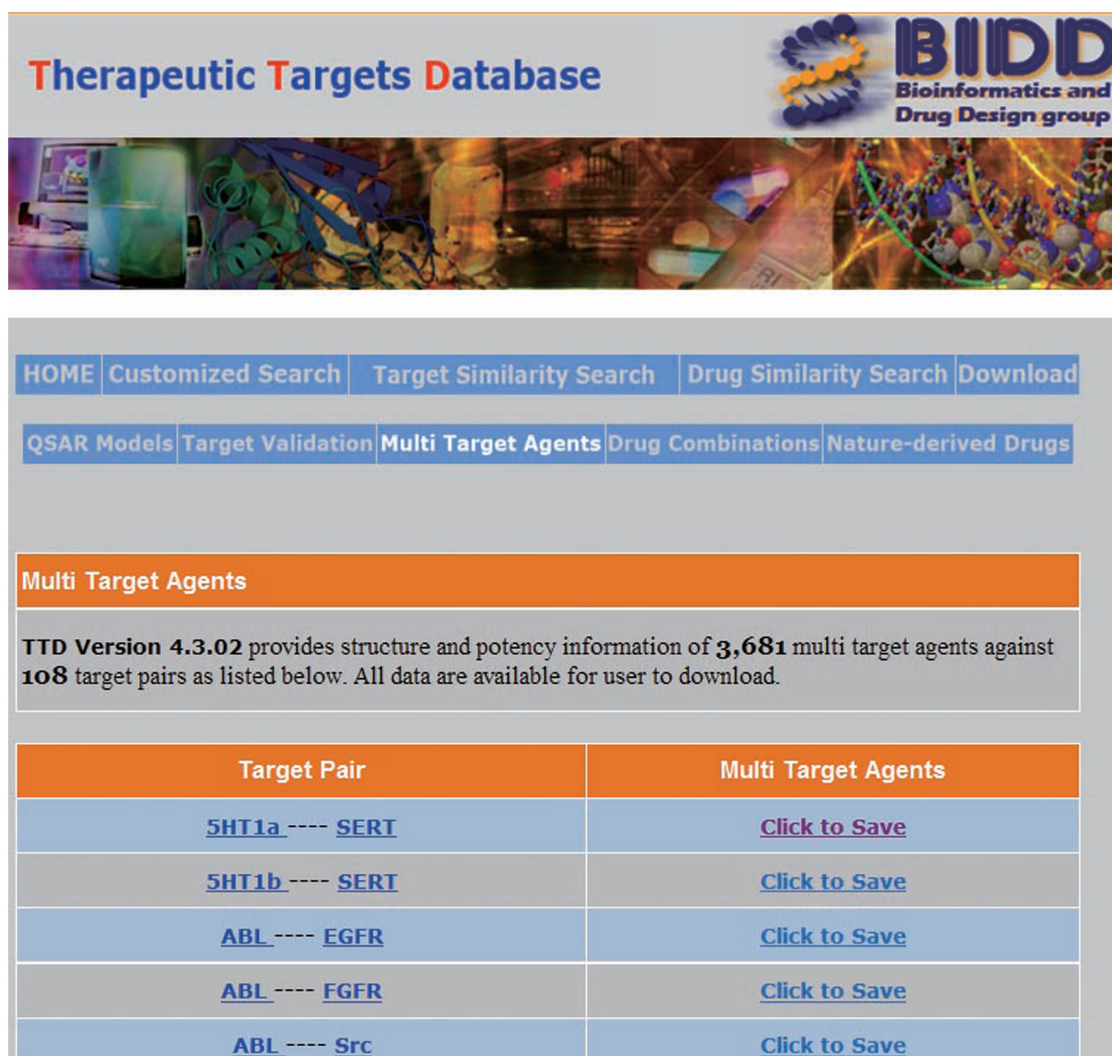
Target Species	Human immunodeficiency virus 1
Chemical Type	N-Aryl Heteroarylisopropanolamines
Mode of Action	Inhibitor
QSAR Model 1	$pIC_{50} = -4.284 - (0.659)*Sfit + (0.010)*Dip-mom - (0.340)*HOMO + (0.008)*MW + (0.008)*Volume - (0.053)*G_CDS_aq$
Molecular Descriptor	Access the following web-servers to compute molecular descriptors: MoDel and e-dragon Parameter - description: Sfit - Steric fit between ligand and receptor; Dip-Mom - Dipole moment (AMSOL); HOMO - HOMO ligand energy (AMSOL); MW - Molecular weight (AMSOL); Volume - Molecular volume (AMSOL); G_CDS_aq - Cavity-dispersion-solvent free energy (AMSOL).
Reference	Design, Synthesis and QSAR Studies on N-Aryl Heteroarylisopropanolamines, a New Class of Non-Peptidic HIV-1 Protease Inhibitors. <i>Bioorganic & Medicinal Chemistry</i> 10 (2002) 2511–2526

Figure 3. The page of the QSAR models for a particular chemical class against a specific target in TTD.

efficacies, improved safety profiles and reduced resistance activities (12,38,42). When two drugs produce the same broad therapeutic effect, their combination collectively produces the same effects of various magnitudes in contrast to the summed response of the individual drugs. A drug combination is pharmacodynamically synergistic, additive or antagonistic if the effect is greater than, equal to or less than the summed response of the individual drugs (43). Drug combinations may also produce pharmacokinetically potentiative or reductive effects such that the therapeutic activity of one drug is enhanced or reduced by another drug via regulation of the first drug's ADME (43). In our earlier studies of drug combinations (12), we have searched PubMed (28) to select those literature-reported drug combinations evaluated by rigorous combination analysis methods and with known molecular mechanism of combination retrievable from PubMed by using combinations of the keywords 'drug combination', 'drug interaction', 'multi-drug', 'additive', 'antagonism', 'antagonistic', 'infra-additive', 'potentiated', 'potentiative', 'potentiation', 'reductive', 'supra-additive', 'synergism', 'synergistic' and 'synergy'.

All major classes of drug combinations can be further divided into groups of specific action types (12). Pharmacodynamically synergistic drug combinations can

be divided into three groups: each one with anti-counteractive, complementary and facilitating actions, respectively. Anti-counteractive actions reduce network's counteractive activities against a drug's therapeutic effect. Complementary actions positively regulate a target or process by interactions with multiple target/pathway sites, different target subtypes and states, and competing mechanisms (3). Facilitating actions are secondary actions of one drug in enhancing the activity or level of another drug. Pharmacodynamically additive drug combinations can be divided into two groups, one with equivalent or overlapping actions, and the other with independent actions of the drugs involved. Pharmacodynamically antagonistic drug combinations can also be divided into two groups, one with mutually interfering actions at the same target, another with mutually counter-active actions at different targets of related pathways that regulate the same target. Pharmacokinetically potentiative drug combinations can be divided into three groups, each one with positive modulation of drug transport or permeation, drug distribution or localization and drug metabolism, respectively. Pharmacokinetically reductive drug combinations can be divided into three groups, each one with negative modulation of drug transport or permeation, drug distribution or localization and drug metabolism, respectively.



Therapeutic Targets Database

BIDB
Bioinformatics and Drug Design group

HOME | Customized Search | Target Similarity Search | Drug Similarity Search | Download

QSAR Models | Target Validation | **Multi Target Agents** | Drug Combinations | Nature-derived Drugs

Multi Target Agents

TTD Version 4.3.02 provides structure and potency information of **3,681** multi target agents against **108** target pairs as listed below. All data are available for user to download.

Target Pair	Multi Target Agents
5HT1a ---- SERT	Click to Save
5HT1b ---- SERT	Click to Save
ABL ---- EGFR	Click to Save
ABL ---- FGFR	Click to Save
ABL ---- Src	Click to Save

Figure 4. Multi-target agents page of TTD.

These drug combinations and their combination mechanisms can be accessed by clicking the 'Drug Combinations' field in the TTD home page, which lead to the TTD drug combinations page wherein a user can download the relevant drug combination data from the drug combination type list (Figure 5).

NATURAL PRODUCT-DERIVED DRUGS


Many of the approved and clinical trial drugs are derived from natural products (44,45). Although drug discovery focus has been shifted from natural products to synthetic chemicals, natural product-derived drugs still constitute a substantial percentage of recently approved drugs (26% of the 46 FDA approved new molecular entities in 2009–2010 are natural product derived) (13). There is a renewed interest in natural products as sources for drug discovery (46). Knowledge of the natural sources of drugs, the species origins of the natural product-derived approved, clinical trial and pre-clinical drugs, are highly useful for

facilitating the search and development of new drug leads. In our earlier analysis of the species origins of natural product-derived drugs, we have collected the species origins and species families of natural product-derived approved, clinical trial and pre-clinical drugs (13).


The species-origins of these drugs have been identified as follows. First the literature-reported approved drugs (44), clinical trial (45,47) and pre-clinical (13) drugs of natural origin were evaluated with respect to the drugs in our TTD database (15) to check their current approval or clinical trial status. Then the species-origin of every drug was searched from books, review and regular articles by using combinations of such keywords as drug name and alternative names, species, natural product and nature. The species-origin of a drug is confirmed if it is specifically mentioned that it 'originates from', 'derived from', 'isolated from' or 'comes from' a species or species-group (e.g. genus or family). For drugs of semi-synthetic derivatives, mimics and peptidomimetics, their parent natural product leads were first searched followed by the search of host

Drug Combinations	
<p>TTD Version 4.3.02 provides drug-combination data which include 72, 14 and 4 pharmacodynamically synergistic, additive, and antagonist combinations, and 18 and 7 pharmacokinetically potentiative and reductive combinations together with their mode of actions and combination mechanisms. All data are available for user to download.</p>	
Types of Drug Combinations	Download
Pharmacodynamically synergistic drug combinations due to anti-counteractive actions	Click to Save
Pharmacodynamically synergistic drug combinations due to complementary actions	Click to Save
Pharmacodynamically synergistic drug combinations due to facilitating actions	Click to Save
Pharmacodynamically additive drug combinations	Click to Save
Pharmacodynamically antagonistic drug combinations	Click to Save
Pharmacokinetically potentiative drug combinations	Click to Save
Pharmacokinetically reductive drug combinations	Click to Save

Figure 5. Drug combination page of TTD.



Therapeutic Targets Database



HOME
Customized Search
Target Similarity Search
Drug Similarity Search
Download

QSAR Models
Target Validation
Multi Target Agents
Drug Combinations
Nature-derived Drugs

Nature-derived Drugs

TTD Version 4.3.02 provides **939**, **369** and **119** nature-derived approved, clinical trial and preclinical drugs together with their species origin information. All data are available for user to download.

Drug Status	Data of Nature-derived Drugs
Nature-derived Approved Drugs	Click to Save
Nature-derived Clinical Trial Drugs	Click to Save
Nature-derived Preclinical Drugs	Click to Save

Figure 6. Natural product-derived drugs page of TTD.

species as described above. The corresponding species-families of the host-species of these drugs as well as all the known species-families in the nature are from the NCBI taxonomy database (28). These natural product-derived drugs and their species origins and families can be retrieved by clicking the 'Nature-Derived Drugs' field in the TTD home page, which lead to the TTD natural product-derived drugs page wherein a user can download the relevant data from the drug status list (Figure 6).

REMARKS

A goal in updating TTD is to make it into a more useful target and drug discovery resource in complement to other related databases. Continuous efforts will be made to provide the latest and comprehensive information about the primary (efficacy) targets of approved, clinical trial, pre-clinical and experimental drugs and other relevant data for these drugs. Intensive efforts in drug and target discovery have led to and will continue to enable the generation of new information, knowledge and models from existing targets (18), drugs (9,29,48,49), multi-target drugs (20) and drug combinations (12,38,42). Drug discovery efforts have benefited and are continuing to be benefited from the exploration of multiple lead sources including synthetic chemicals (1–3), biologics (50–53) and natural products (13,44,45). Inclusion of these information, knowledge and models into TTD and other databases will further enable these databases to better serve the drug discovery and research communities in their efforts for discovering new targets and new drugs from different sources.

FUNDING

Fundamental Research Funds for the Central Universities of China and the Singapore Academic Research Fund R-148-000-141-750 and R-148-000-141-646. Funding for open access charge: Fundamental Research Funds for the Central Universities of China.

Conflict of interest statement. None declared.

REFERENCES

- Ohlstein,E.H., Ruffolo,R.R. Jr and Elliott,J.D. (2000) Drug discovery in the next millennium. *Annu. Rev. Pharmacol. Toxicol.*, **40**, 177–191.
- Zambrowicz,B.P. and Sands,A.T. (2003) Knockouts model the 100 best-selling drugs—will they model the next 100? *Nat. Rev. Drug Discov.*, **2**, 38–51.
- Keith,C.T., Borisy,A.A. and Stockwell,B.R. (2005) Multicomponent therapeutics for networked systems. *Nat. Rev. Drug Discov.*, **4**, 71–78.
- Hewitt,D.J., Hargreaves,R.J., Curtis,S.P. and Michelson,D. (2009) Challenges in analgesic drug development. *Clin. Pharmacol. Ther.*, **86**, 447–450.
- Zheng,C., Han,L., Yap,C.W., Xie,B. and Chen,Y. (2006) Progress and problems in the exploration of therapeutic targets. *Drug Discov. Today*, **11**, 412–420.
- Rask-Andersen,M., Almen,M.S. and Schioth,H.B. (2011) Trends in the exploitation of novel drug targets. *Nat. Rev. Drug Discov.*, **10**, 579–590.
- Duarte,C.D., Barreiro,E.J. and Fraga,C.A. (2007) Privileged structures: a useful concept for the rational design of new lead drug candidates. *Mini Rev. Med. Chem.*, **7**, 1108–1119.
- Zhao,H. (2007) Scaffold selection and scaffold hopping in lead generation: a medicinal chemistry perspective. *Drug Discov. Today*, **12**, 149–155.
- Sproul,D.G., Palmer,R.K., Swanson,J.T. and Lawless,M. (2010) QSAR in the pharmaceutical research setting: QSAR models for broad, large problems. *Curr. Top. Med. Chem.*, **10**, 619–637.
- Youdim,M.B. and Buccafusco,J.J. (2005) Multi-functional drugs for various CNS targets in the treatment of neurodegenerative disorders. *Trends Pharmacol. Sci.*, **26**, 27–35.
- Bilanges,B., Torbett,N. and Vanhaesebroeck,B. (2008) Killing two kinase families with one stone. *Nat. Chem. Biol.*, **4**, 648–649.
- Jia,J., Zhu,F., Ma,X., Cao,Z., Li,Y. and Chen,Y.Z. (2009) Mechanisms of drug combinations: interaction and network perspectives. *Nat. Rev. Drug Discov.*, **8**, 111–128.
- Zhu,F., Qin,C., Tao,L., Liu,X., Shi,Z., Ma,X., Jia,J., Tan,Y., Cui,C., Lin,J. et al. (2011) Clustered patterns of species origins of nature-derived drugs and clues for future bioprospecting. *Proc. Natl Acad. Sci. USA*, **108**, 12943–12948.
- Chen,X., Ji,Z.L. and Chen,Y.Z. (2002) TTD: therapeutic target database. *Nucleic Acids Res.*, **30**, 412–415.
- Zhu,F., Han,B., Kumar,P., Liu,X., Ma,X., Wei,X., Huang,L., Guo,Y., Han,L., Zheng,C. et al. (2010) Update of TTD: therapeutic target database. *Nucleic Acids Res.*, **38**, D787–D791.
- Knox,C., Law,V., Jewison,T., Liu,P., Ly,S., Frolkis,A., Pon,A., Banco,K., Mak,C., Neveu,V. et al. (2011) DrugBank 3.0: a comprehensive resource for 'omics' research on drugs. *Nucleic Acids Res.*, **39**, D1035–D1041.
- Zheng,C.J., Han,L.Y., Yap,C.W., Ji,Z.L., Cao,Z.W. and Chen,Y.Z. (2006) Therapeutic targets: progress of their exploration and investigation of their characteristics. *Pharmacol. Rev.*, **58**, 259–279.
- Zhu,F., Han,L., Zheng,C., Xie,B., Tammi,M.T., Yang,S., Wei,Y. and Chen,Y. (2009) What are next generation innovative therapeutic targets? Clues from genetic, structural, physicochemical, and systems profiles of successful targets. *J. Pharmacol. Exp. Ther.*, **330**, 304–315.
- Knowles,J. and Gromo,G. (2003) A guide to drug discovery: target selection in drug discovery. *Nat. Rev. Drug Discov.*, **2**, 63–69.
- Ma,X.H., Shi,Z., Tan,C., Jiang,Y., Go,M.L., Low,B.C. and Chen,Y.Z. (2010) In-silico approaches to multi-target drug discovery: computer aided multi-target drug design, multi-target virtual screening. *Pharm. Res.*, **27**, 739–749.
- Ma,X.H., Wang,R., Tan,C.Y., Jiang,Y.Y., Lu,T., Rao,H.B., Li,X.Y., Go,M.L., Low,B.C. and Chen,Y.Z. (2010) Virtual screening of selective multitarget kinase inhibitors by combinatorial support vector machines. *Mol. Pharm.*, **7**, 1545–1560.
- Overington,J.P., Al-Lazikani,B. and Hopkins,A.L. (2006) How many drug targets are there? *Nat. Rev. Drug Discov.*, **5**, 993–996.
- Steinmetz,K.L. and Spack,E.G. (2009) The basics of preclinical drug development for neurodegenerative disease indications. *BMC Neurol.*, **9**(Suppl. 1), S2.
- Lindsay,M.A. (2003) Target discovery. *Nat. Rev. Drug Discov.*, **2**, 831–838.
- Overall,C.M. and Kleifeld,O. (2006) Tumour microenvironment opinion: validating matrix metalloproteinases as drug targets and anti-targets for cancer therapy. *Nat. Rev. Cancer*, **6**, 227–239.
- Vidalin,O., Muslmani,M., Estienne,C., Echchakir,H. and Abina,A.M. (2009) In vivo target validation using gene invalidation, RNA interference and protein functional knockout models: it is the time to combine. *Curr. Opin. Pharmacol.*, **9**, 669–676.
- Stumpf,W.E. (2007) Memo to the FDA and ICH: appeal for in vivo drug target identification and target pharmacokinetics Recommendations for improved procedures and requirements. *Drug Discov. Today*, **12**, 594–598.
- Sayers,E.W., Barrett,T., Benson,D.A., Bolton,E., Bryant,S.H., Canese,K., Chetvernin,V., Church,D.M., DiCuccio,M., Federhen,S. et al. (2011) Database resources of the national

- center for biotechnology information. *Nucleic Acids Res.*, **39**, D38–D51.
29. Mittal, R.R., McKinnon, R.A. and Sorich, M.J. (2009) Comparison data sets for benchmarking QSAR methodologies in lead optimization. *J. Chem. Inf. Model.*, **49**, 1810–1820.
 30. Dudek, A.Z., Arodz, T. and Galvez, J. (2006) Computational methods in developing quantitative structure-activity relationships (QSAR): a review. *Comb. Chem. High Throughput Screen.*, **9**, 213–228.
 31. Yap, C.W., Li, H., Ji, Z.L. and Chen, Y.Z. (2007) Regression methods for developing QSAR and QSPR models to predict compounds of specific pharmacodynamic, pharmacokinetic and toxicological properties. *Mini Rev. Med. Chem.*, **7**, 1097–1107.
 32. Li, Z.R., Han, L.Y., Xue, Y., Yap, C.W., Li, H., Jiang, L. and Chen, Y.Z. (2007) MODEL-molecular descriptor lab: a web-based server for computing structural and physicochemical features of compounds. *Biotechnol. Bioeng.*, **97**, 389–396.
 33. Tetko, I.V., Gasteiger, J., Todeschini, R., Mauri, A., Livingstone, D., Ertl, P., Palyulin, V.A., Radchenko, E.V., Zefirov, N.S., Makarenko, A.S. *et al.* (2005) Virtual computational chemistry laboratory—design and description. *J. Comput. Aided Mol. Des.*, **19**, 453–463.
 34. Pilpel, Y., Sudarsanam, P. and Church, G.M. (2001) Identifying regulatory networks by combinatorial analysis of promoter elements. *Nat. Genet.*, **29**, 153–159.
 35. Sergina, N.V., Rausch, M., Wang, D., Blair, J., Hann, B., Shokat, K.M. and Moasser, M.M. (2007) Escape from HER-family tyrosine kinase inhibitor therapy by the kinase-inactive HER3. *Nature*, **445**, 437–441.
 36. Overall, C.M. and Kleifeld, O. (2006) Validating matrix metalloproteinases as drug targets and anti-targets for cancer therapy. *Nat. Rev. Cancer*, **6**, 227–239.
 37. Smalley, K.S., Haass, N.K., Brafford, P.A., Lioni, M., Flaherty, K.T. and Herlyn, M. (2006) Multiple signaling pathways must be targeted to overcome drug resistance in cell lines derived from melanoma metastases. *Mol. Cancer Ther.*, **5**, 1136–1144.
 38. Larder, B.A., Kemp, S.D. and Harrigan, P.R. (1995) Potential mechanism for sustained antiretroviral efficacy of AZT-3TC combination therapy. *Science*, **269**, 696–699.
 39. Sadowski, J., Gasteiger, J. and Klebe, G. (1994) Comparison of automatic three-dimensional model builders using 639 x-ray structures. *J. Chem. Inf. Comput. Sci.*, **34**, 1000–1008.
 40. Liu, T., Lin, Y., Wen, X., Jorissen, R.N. and Gilson, M.K. (2007) BindingDB: a web-accessible database of experimentally determined protein-ligand binding affinities. *Nucleic Acids Res.*, **35**, D198–D201.
 41. Overington, J. (2009) ChEMBL. An interview with John Overington, team leader, chemogenomics at the european bioinformatics institute outstation of the european molecular biology laboratory (EMBL-EBI). Interview by Wendy A. Warr. *J. Comput. Aided Mol. Des.*, **23**, 195–198.
 42. Zimmermann, G.R., Lehar, J. and Keith, C.T. (2007) Multi-target therapeutics: when the whole is greater than the sum of the parts. *Drug Discov. Today*, **12**, 34–42.
 43. Chou, T.C. (2006) Theoretical basis, experimental design, and computerized simulation of synergism and antagonism in drug combination studies. *Pharmacol. Rev.*, **58**, 621–681.
 44. Newman, D.J. and Cragg, G.M. (2007) Natural products as sources of new drugs over the last 25 years. *J. Nat. Prod.*, **70**, 461–477.
 45. Butler, M.S. (2008) Natural products to drugs: natural product-derived compounds in clinical trials. *Nat. Prod. Rep.*, **25**, 475–516.
 46. Li, J.W. and Vederas, J.C. (2009) Drug discovery and natural products: end of an era or an endless frontier? *Science*, **325**, 161–165.
 47. Saklani, A. and Kutty, S.K. (2008) Plant-derived compounds in clinical trials. *Drug Discov. Today*, **13**, 161–171.
 48. Lipinski, C.A., Lombardo, F., Dominy, B.W. and Feeney, P.J. (2001) Experimental and computational approaches to estimate solubility and permeability in drug discovery and development settings. *Adv. Drug Deliv. Rev.*, **46**, 3–26.
 49. Vistoli, G., Pedretti, A. and Testa, B. (2008) Assessing drug-likeness—what are we missing? *Drug Discov. Today*, **13**, 285–294.
 50. Saladin, P.M., Zhang, B.D. and Reichert, J.M. (2009) Current trends in the clinical development of peptide therapeutics. *IDrugs*, **12**, 779–784.
 51. Woodcock, J., Griffin, J., Behrman, R., Cherney, B., Crescenzi, T., Fraser, B., Hixon, D., Joneckis, C., Kozlowski, S., Rosenberg, A. *et al.* (2007) The FDA's assessment of follow-on protein products: a historical perspective. *Nat. Rev. Drug Discov.*, **6**, 437–442.
 52. Nelson, A.L., Dhimolea, E. and Reichert, J.M. (2010) Development trends for human monoclonal antibody therapeutics. *Nat. Rev. Drug Discov.*, **9**, 767–774.
 53. Melnikova, I. (2007) RNA-based therapies. *Nat. Rev. Drug Discov.*, **6**, 863–864.