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Chapter

The Role of Bioinformatics in Drug Discovery: A Comprehensive Overview

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Abstract

Bioinformatics plays a crucial role in various aspects of drug discovery, drug metabolism, and pharmacology. In drug discovery, bioinformatics enables the efficient analysis and interpretation of large-scale biological data, facilitating target identification, lead compound optimization, and prediction of drug-target interactions. It aids in the identification and characterization of potential drug targets through genomic and proteomic analyses. Additionally, bioinformatics assists in the prediction of drug metabolism and pharmacokinetic properties, offering insights into the safety and efficacy of potential drug candidates. Furthermore, it contributes to pharmacology by enabling the analysis of drug-drug interactions, adverse drug reactions, and personalized medicine approaches. The integration of computational tools and algorithms with biological and chemical data has accelerated the drug discovery process, improved success rates, and reduced costs. Bioinformatics has become an indispensable tool in the development of novel therapeutics and the optimization of drug efficacy and safety. This book chapter elucidates the profound impact of bioinformatics in drug metabolism and pharmacology, emphasizing the transformative potential it holds for the future of pharmaceutical research, ultimately improving patient outcomes and bringing innovative therapies.

Keywords: bioinformatics, technology, drug metabolism, pharmacology, innovative, drug discovery

1. Introduction

The process of drug development is a complex and resource-intensive undertaking that is crucial to the pharmaceutical industry's objective of enhancing healthcare outcomes on a global scale. The endeavor encompasses a diverse range of experiences that last over an extended period, encompassing multiple phases, and necessitating significant financial resources [1]. Drug development is primarily motivated by the

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objective of developing therapies that are safer, more effective, and characterized by innovation, with the aim of addressing medical requirements that have not yet been satisfied [2].

The initial step is the identification of a specific chemical or pathway that is associated with a particular disease [3]. The commencement of this preliminary stage frequently arises from comprehensive biological investigation and a profound comprehension of the fundamental causes of the disease [3-6]. After the identification of a target, drug candidates are formulated, manufactured, and subjected to comprehensive laboratory testing. The initial preclinical phases involve evaluating the potential effectiveness and safety of the proposed drugs [7]. After successful selection, candidates progress to the clinical phase, which encompasses a series of human trials specifically designed to assess the safety, dose, and efficacy of the intervention. This phase is comprised of three distinct segments. Phase I trials typically encompass a limited number of individuals who are in good health, Phase II trials thereafter encompass a larger cohort of patients diagnosed with the specific ailment under investigation, and Phase III trials comprise an even more extensive and diverse patient population. Clinical trials are frequently characterized by their lengthy duration, substantial financial investment, and stringent regulatory oversight, all of which are implemented to safeguard the safety and effectiveness of the prospective pharmaceutical compound [8]. The process of regulatory submission is characterized by its stringent nature, necessitating the provision of comprehensive data pertaining to safety, efficacy, and manufacturing quality [9–11]. In conjunction with clinical trials, pharmaceutical corporations allocate significant resources toward research and development (R&D), which involves the employment of extensive teams comprising scientists, physicians, and support workers. In addition, researchers are required to effectively manage a multifaceted network of intellectual property concerns, wherein they engage in the process of patenting their findings as a means to safeguard their investments and establish market exclusivity.

The process from the identification of an objective through the attainment of regulatory approval is replete with many hurdles, encompassing the potential for failure at any given point. The majority of medication candidates fail to successfully complete the entire process, primarily owing to safety concerns, lack of efficacy, or other factors. The attrition rate, when coupled with the substantial expenses associated with clinical development, renders drug development a high-stakes and resource-intensive undertaking. Hence, the process of drug development is complex, time-consuming, and expensive, necessitating the integration of scientific knowledge, financial capital, regulatory supervision, and a steadfast dedication to enhancing worldwide healthcare. Despite the intricate nature and difficulties associated with it, the pharmaceutical sector continues to persist in its endeavor to develop innovative treatments that have the potential to revolutionize the quality of life and mitigate the impact of illnesses on the broader community.

With the rapid progress in technology, it is noteworthy that bioinformatics has emerged as an essential instrument in contemporary biological research. This field empowers scientists to get significant insights from extensive and intricate information. Bioinformatics is an interdisciplinary domain situated at the convergence of biology, computer science, and data analysis. The field encompasses the utilization of computational methodologies and statistical approaches to effectively handle, scrutinize, and elucidate biological information [12, 13]. The aforementioned discipline holds significant importance in multiple domains of biology, encompassing genomics, proteomics, evolutionary biology, and drug development. This book chapter

provides a comprehensive examination of the pivotal role that bioinformatics plays in the realms of drug metabolism and pharmacology.

2. Bioinformatics in drug metabolism

The process of drug metabolism holds significant importance in the field of pharmaceutical research and development, as it governs the ultimate disposition of pharmaceuticals within the human body. The field of bioinformatics assumes a pivotal function in comprehending and enhancing the mechanisms of drug metabolism. Bioinformatics plays a pivotal role in advancing drug metabolism research through several significant avenues (**Figure 1**) [12, 13].

The prediction of metabolic pathways involves the utilization of bioinformatics techniques and databases to anticipate the potential metabolic transformations that a medication may undergo within the physiological context of the human body [14–18]. The aforementioned is crucial in evaluating the safety and effectiveness



Figure 1. Application of bioinformatics in drug metabolism.

of a pharmaceutical compound under consideration [12, 19–24]. The utilization of bioinformatics facilitates the identification of distinct enzymes that play a role in the process of drug metabolism. The identification of the specific enzymes involved in the metabolism of a drug is of utmost importance in the anticipation of drug-drug interactions and the potential manifestation of adverse effects. The utilization of bioinformatics tools facilitates the process of identifying and characterizing drug metabolites. Metabolites possess distinct pharmacological characteristics in comparison to the original drug, and their identification is crucial for assessing the comprehensive effects of a medication. The utilization of bioinformatics models enables the prediction of probable harmful metabolites or drug metabolism products, hence facilitating the evaluation of the safety profile of drug candidates by researchers.

The field of pharmacogenomics investigates genetic differences in drug-metabolizing enzymes across diverse populations. The aforementioned data is used to individualize pharmaceutical interventions, hence guaranteeing that individuals are administered the most efficacious and secure medications in accordance with their genetic characteristics [25].

Bioinformatics tools play a crucial role in the analysis of high-throughput screening data for drug discovery. These tools assist in the identification of prospective medication candidates and the prioritization of compounds for subsequent testing, utilizing their metabolic profiles. Drug repurposing, a process facilitated by bioinformatics, involves the analysis of metabolic pathways and the identification of potential off-target effects of existing medications, leading to the discovery of novel therapeutic applications. The implementation of this approach has the potential to expedite the process of medication development while simultaneously mitigating financial expenditures [26–28].

In summary, the discipline of drug metabolism has been significantly transformed by the advent of bioinformatics, which has introduced robust tools and procedures for the analysis and interpretation of data. The consideration of individual genetic differences in medication response plays a pivotal role in optimizing drug development processes, enhancing drug safety, and promoting the progress of personalized medicine. The ongoing progression of technology necessitates the further integration of bioinformatics within the realm of drug research and development, hence fostering innovation and enhancing patient outcomes within the pharmaceutical sector.

3. Pharmacology and bioinformatics integration

The amalgamation of pharmacology and bioinformatics exemplifies a potent synergy between conventional pharmacological methodologies and state-of-theart computational tools [23, 25, 29–32]. The integration of bioinformatics in drug development pipeline has greatly improved our capacity to identify, create, and refine pharmaceuticals with heightened accuracy and effectiveness. This part of the chapter provides an overview of the integration of pharmacology and bioinformatics, highlighting its transformative impact on the domain of drug discovery and development (**Figure 2**).

First, bioinformatics tools facilitate the methodical examination of biological data encompassing genomes, proteomics, and transcriptomics, with the aim of identifying and validating new therapeutic targets [33–36]. Through the examination of extensive datasets, researchers have the ability to identify particular genes, proteins, or pathways that assume critical functions in the development and progression of diseases.



Figure 2.

Application of bioinformatics in pharmacology.

Subsequently, these targets undergo a comprehensive pharmacological validation process to verify their significance and appropriateness for therapeutic intervention.

Second, bioinformatics-driven computational techniques, such as molecular docking and molecular dynamics simulations, are utilized for the purpose of virtual screening and the generation of prospective drug candidates. This enables researchers to rapidly examine a wide range of chemical compounds, hence optimizing time and resource use throughout the initial phases of drug discovery. Bioinformatics plays a crucial role in the prioritization of candidate drugs based on their binding affinity and specificity toward target proteins through the utilization of predictive models [29, 35, 37–39]. In addition, the utilization of bioinformatics models enables the anticipation of pharmacokinetic characteristics and toxicity of potential drug candidates, encompassing absorption, distribution, metabolism, and excretion. Moreover, these models evaluate the possible toxicity and unwanted effects, assisting in the identification of safer and more efficacious medication candidates prior to their advancement into expensive experimental stages.

The merging of pharmacogenomics and bioinformatics facilitates the advancement of personalized medicine strategies. The utilization of bioinformatics enables the prediction of an individual's pharmacological response by examining their genetic composition. This data enable healthcare practitioners to customize pharmacological therapies based on the distinct genetic characteristics of individual patients, thereby enhancing therapeutic results while avoiding adverse reactions [19, 25, 40–43]. Interestingly, the vast amount of biological and clinical data produced in contemporary drug development is substantial. Bioinformatics encompasses a range of technologies and methodologies that are essential for the effective storage, management, and analysis of biological Big-Data. The utilization of sophisticated data analytics and machine learning algorithms has the ability to reveal latent patterns, biomarkers, and potential correlations between drugs and diseases that may go unnoticed when employing conventional methodologies [44].

It is noteworthy that the utilization of bioinformatics is of paramount importance in the field of drug repurposing, which involves the exploration of existing medications for novel therapeutic purposes. Through the examination of data from diverse sources, such as clinical records and molecular databases, the field of bioinformatics possesses the capability to discern innovative applications for approved pharmaceuticals. This ability expedites the process of incorporating these drugs into newer treatment approaches.

Furthermore, the field of network pharmacology employs network-based methodologies in the realm of bioinformatics, allowing scientists to examine diseases and the effects of drugs within the intricate framework of biological networks [32, 35, 45–47]. The adoption of a holistic perspective facilitates a more profound comprehension of the interrelatedness of biological mechanisms and assists in the recognition of multi-target medications capable of regulating several elements within a disease network. In essence, the amalgamation of pharmacology and bioinformatics has revolutionized the field of drug research and development, rendering it a data-centric and increasingly accurate discipline. The integration of experimental pharmacology and computational biology holds promise for enhancing drug safety and efficacy, expediting the drug development process, and ultimately enhancing patient care through personalized treatment approaches. The ongoing progress of technology will ensure that the partnership between these two fields remains a prominent aspect of pharmaceutical research and innovation.

4. Bioinformatics for toxicology and safety assessment

The field of bioinformatics plays a crucial role in the domain of toxicology and safety assessment. Bioinformatics has become an indispensable instrument in the realm of toxicology and safety assessment, facilitating the evaluation of possible dangers linked to chemical substances, medicines, and environmental factors (**Figure 3**) [48]. The below part provides the main applications of bioinformatics in the field of toxicology and safety evaluation.

The utilization of bioinformatics techniques facilitates the field of chemo-informatics, which encompasses the examination of chemical structures and their correlation with toxicity. Machine learning models that have been trained using extensive chemical databases possess the capability to forecast the toxicity of novel compounds by leveraging their structural resemblances to established dangerous substances [49]. Predictive models play a crucial role in the timely detection of potentially hazardous compounds, hence optimizing efficiency and conserving resources in the field of toxicological testing [49].



Figure 3.

On the other hand, toxico-genomics is an interdisciplinary field that integrates genomics and toxicology to investigate the impact of toxic chemicals on genes and gene expression. The field of bioinformatics is of utmost importance in the analysis of high-throughput gene expression data obtained from microarray and RNA sequencing investigations [50]. Through the identification of genes and pathways impacted by hazardous substances, toxicologists are able to get valuable knowledge regarding the underlying processes of toxicity, as well as prospective biomarkers that could be utilized for the early detection of such toxicity. Bioinformatics techniques are utilized to evaluate adverse event reports derived from clinical trials and post-market surveillance databases, with the aim of identifying patterns of toxicity that are linked to medications and other items. The aforementioned analyses have the potential to facilitate the discovery of safety risks that were previously unknown, hence motivating regulatory interventions or alterations in product labeling [51].

Metabolomics, a branch of bioinformatics, is dedicated to the investigation of small chemicals known as metabolites that are generated by cells and organisms. The identification of alterations in metabolite profiles resulting from toxin exposure is

Application of bioinformatics in toxicology and safety assessment.

of paramount importance in the field of toxicology. Bioinformatics technologies are utilized for the purpose of analyzing this data and establishing connections between modifications in metabolic pathways and distinct harmful consequences [12, 52–56]. The field of in silico toxicology encompasses the application of computer simulations to forecast the toxicological characteristics of chemical substances. Bioinformatics models have the capability to predict the toxicity of a chemical by the simulation of its interactions with biological molecules, including proteins and enzymes. This methodology facilitates the prioritization of substances for subsequent testing and diminishes the necessity for animal experiments. Hence, Bioinformatics plays a pivotal role in the quantitative assessment of risks by effectively integrating various datasets pertaining to exposure, toxicity, and biological response.

In summary, the field of bioinformatics has brought about a significant transformation in the realm of toxicology and safety assessment. This transformation is primarily attributed to the provision of data-driven, cost-effective, and efficient tools that enable the evaluation of possible dangers associated with diverse chemicals and compounds. The capacity to combine and analyze extensive datasets from various sources facilitates the generation of more precise toxicity predictions, expedites the discovery of dangerous compounds, and enhances the comprehension of the underlying mechanisms associated with toxicity. Bioinformatics will continue to play a crucial role in safeguarding the integrity of products, medications, and the environment as the science progresses.

5. Conclusion

The present chapter has explored the crucial function of bioinformatics in the field of drug metabolism and pharmacology, emphasizing its importance in multiple facets of drug discovery and development. The discipline of bioinformatics has become an essential instrument that has brought about significant changes by expediting the process of identifying targets, assisting in the design of drugs based on logical principles, easing the screening of large volumes of data, and supporting the development of biomarkers for personalized medicine. Nevertheless, this process has encountered many difficulties. In order to effectively use the promise of the discipline of bioinformatics, several challenges need to be addressed, including data quality and integration, computational resources, ethical considerations, and the translation of findings into clinical applications. Notwithstanding these hurdles, the prospects for bioinformatics in the fields of drug metabolism and pharmacology appear to be auspicious. In summary, the prospects of bioinformatics in the domains of drug metabolism and pharmacology are characterized by a notable emphasis on novel advancements and cooperative efforts. As the comprehension of biological systems and computational approaches progresses, bioinformatics will persist as a pivotal catalyst in the transformation of drug development, enhancement of patient outcomes, and introduction of groundbreaking medicines to the market. Through the acknowledgment and resolution of obstacles, as well as the adoption of emerging technology, the area is positioned to experience additional significant advancements in the foreseeable future.

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References

[1] Yildirim O, Gottwald M, Schüler P, Michel MC. Opportunities and challenges for drug development: Public– private partnerships, adaptive designs and big data. Frontiers in Pharmacology [Internet]. 2016;7:761. Available from: http://journal.frontiersin.org/ article/10.3389/fphar.2016.00461/full

[2] Villoutreix BO. Post-pandemic drug discovery and development: Facing present and future challenges. Frontiers in Drug Discovery. 2021;**1**:728469

[3] Schenone M, Dančík V, Wagner BK, Clemons PA. Target identification and mechanism of action in chemical biology and drug discovery. Nature Chemical Biology. 2013;**9**(4):232-240

[4] Ma H, Zhao H. Drug target inference through pathway analysis of genomics data. Advanced Drug Delivery Reviews. 2013;**65**(7):966-972

[5] Emmerich CH, Gamboa LM, Hofmann MCJ, Bonin-Andresen M, Arbach O, Schendel P, et al. Improving target assessment in biomedical research: The GOT-IT recommendations. Nature Reviews. Drug Discovery. 2021;**20**(1):64-81

[6] Cava C, Bertoli G, Castiglioni I. In silico identification of drug target pathways in breast cancer subtypes using pathway cross-talk inhibition. Journal of Translational Medicine. 2018;**16**(1):154

[7] Steinmetz KL, Spack EG. The basics of preclinical drug development for neurodegenerative disease indications. BMC Neurology. 2009;**9**(Suppl 1):S2

[8] Singh N, Vayer P, Tanwar S, Poyet JL, Tsaioun K, Villoutreix BO. Drug discovery and development: Introduction to the general public and patient groups. Frontiers in Drug Discovery. 2023;**3**:1201419

[9] Mohs RC, Greig NH. Drug discovery and development: Role of basic biological research. Alzheimer's & Dementia: Translational Research & Clinical Interventions. 2017;**3**(4):651-657

[10] Singh S, Loke YK. Drug safety assessment in clinical trials: Methodological challenges and opportunities. Trials. 2012;**13**(1):138

[11] Weaver RJ, Valentin JP. Today's challenges to de-risk and predict drug safety in human "mindthe-gap". Toxicological Sciences. 2019;**167**(2):307-321

[12] Bioinformatics XX, Discovery D.Current Topics in Medicinal Chemistry.2017;17(15):1709-1726

[13] Wishart DS. Bioinformatics in drug development and assessment.Drug Metabolism Reviews.2005;37(2):279-310

[14] Sankar A, Ranu S, Raman K.Predicting novel metabolic pathways through subgraph mining.Bioinformatics. 2017;33(24):3955-3963

[15] Baranwal M, Magner A, Elvati P, Saldinger J, Violi A, Hero AO. A deep learning architecture for metabolic pathway prediction. Bioinformatics. 2020;**36**(8):2547-2553

[16] Shah HA, Liu J, Yang Z, Feng J. Review of machine learning methods for the prediction and reconstruction of metabolic pathways. Frontiers in Molecular Biosciences. 2021;**8**:634141

[17] Wang P, Schumacher AM, Shiu SH. Computational prediction of plant metabolic pathways. Current Opinion in Plant Biology. 2022;**66**:102171

[18] Hamdalla MA, Rajasekaran S, Grant DF, Măndoiu II. Metabolic pathway predictions for metabolomics: A molecular structure matching approach. Journal of Chemical Information and Modeling. 2015;55(3):709-718

[19] Wooller SK, Benstead-Hume G, Chen X, Ali Y, Pearl FMG. Bioinformatics in translational drug discovery. Bioscience Reports. 2017;**37**(4):BSR20160180

[20] Huang LC, Wu X, Chen JY. Predicting adverse side effects of drugs. BMC Genomics. 2011;**12**(S5):S11

[21] Liang X, Fu Y, Qu L, Zhang P, Chen Y. Prediction of drug side effects with transductive matrix co-completion. Bioinformatics. 2023;**39**(1):btad006

[22] Yamanishi Y, Pauwels E, Kotera M. Drug side-effect prediction based on the integration of chemical and biological spaces. Journal of Chemical Information and Modeling. 2012;**52**(12):3284-3292

[23] Chen Y, Juan L, Lv X, Shi L. Bioinformatics research on drug sensitivity prediction. Frontiers in Pharmacology. 2021;**12**:799712

[24] Wu Z, Peng Y, Yu Z, Li W, Liu G, Tang Y. NetInfer: A web server for prediction of targets and therapeutic and adverse effects via networkbased inference methods. Journal of Chemical Information and Modeling. 2020;**60**(8):3687-3691

[25] Katara P. Role of bioinformatics and pharmacogenomics in drug discovery and development process. Network Modeling Analysis in Health Informatics and Bioinformatics. 2013;2(4):225-230 [26] Saberian N, Peyvandipour A, Donato M, Ansari S, Draghici S. A new computational drug repurposing method using established disease–drug pair knowledge. Bioinformatics. 2019;**35**(19):3672-3678

[27] Tanoli Z, Seemab U, Scherer A, Wennerberg K, Tang J, Vähä-Koskela M. Exploration of databases and methods supporting drug repurposing: A comprehensive survey. Briefings in Bioinformatics. 2021;**22**(2):1656-1678

[28] Amiri Souri E, Chenoweth A, Karagiannis SN, Tsoka S. Drug repurposing and prediction of multiple interaction types via graph embedding. BMC Bioinformatics. 2023;**24**(1):202

[29] Duarte Y, Márquez-Miranda V, Miossec MJ, González-Nilo F. Integration of target discovery, drug discovery and drug delivery: A review on computational strategies. WIREs Nanomedicine Nanobiotechnology. 2019;11(4):e1554

[30] Ma R. Bioinformatics-key to drug discovery and development. Journal of Pharmaceutical Research. 2017;1(5):000126

[31] Berger SI, Iyengar R. Network analyses in systems pharmacology. Bioinformatics. 2009;**25**(19):2466-2472

[32] Leung EL, Cao ZW, Jiang ZH, Zhou H, Liu L. Network-based drug discovery by integrating systems biology and computational technologies. Briefings in Bioinformatics. 2013;**14**(4):491-505

[33] Alam MS, Sultana A, MDS R, Amanullah M, Kabir SR, MDNH M. Integrated bioinformatics and statistical approaches to explore molecular biomarkers for breast cancer diagnosis, prognosis and therapies. PLoS One. 2022;**17**(5):e0268967

[34] Hermawan A, Putri H. Bioinformatics analysis reveals the potential target of rosiglitazone as an antiangiogenic agent for breast cancer therapy. BMC Genomic Data. 2022;**23**(1):72

[35] Elbasyouni A, Wilson Kpordze S, Suliman Hussein H, Soro O, Mulondo S, Nshimirimana J, et al. The crosstalk between phytotherapy and bioinformatics in the management of cancer. In: Recent Advances in Alternative Medicine [Working Title] [Internet]. London, UK: IntechOpen; 2023. Available from: https://www. intechopen.com/online-first/1141766

[36] Ren Y, Deng R, Zhang Q, Li J, Han B, Ye P. Bioinformatics analysis of key genes in triple negative breast cancer and validation of oncogene PLK1. Annals of Translational Medicine. 2020;**8**(24):1637-1637

[37] Santos LHS, Ferreira RS, Caffarena ER. Integrating molecular docking and molecular dynamics simulations. In: De Azevedo WF, editor. Docking Screens for Drug Discovery [Internet]. New York, NY: Springer New York; 2019. pp. 13-34. (Methods in Molecular Biology; vol. 2053). Available from: http://link.springer. com/10.1007/978-1-4939-9752-7_2

[38] Subhaswaraj P, Siddhardha B. Molecular docking and molecular dynamic simulation approaches for drug development and repurposing of drugs for severe acute respiratory syndrome-Coronavirus-2. In: Computational Approaches for Novel Therapeutic and Diagnostic Designing to Mitigate SARS-CoV-2 Infection [Internet]. Elsevier; 2022. pp. 207-246. Available from: https:// linkinghub.elsevier.com/retrieve/pii/ B9780323911726000078

[39] Vidal-Limon A, Aguilar-Toalá JE, Liceaga AM. Integration of molecular docking analysis and molecular dynamics simulations for studying food proteins and bioactive peptides. Journal of Agricultural and Food Chemistry. 2022;**70**(4):934-943

[40] Fernald GH, Capriotti E, Daneshjou R, Karczewski KJ, Altman RB. Bioinformatics challenges for personalized medicine. Bioinformatics. 2011;**27**(13):1741-1748

[41] Li YY, Jones SJ. Drug repositioning for personalized medicine. Genome Medicine. 2012;**4**(3):27

[42] Hartl D, De Luca V, Kostikova A, Laramie J, Kennedy S, Ferrero E, et al. Translational precision medicine: An industry perspective. Journal of Translational Medicine. 2021;**19**(1):245

[43] Stern AM, Schurdak ME, Bahar I, Berg JM, Taylor DL. A perspective on implementing a quantitative systems pharmacology platform for drug discovery and the advancement of personalized medicine. SLAS Discovery. 2016;**21**(6):521-534

[44] Mak KK, Pichika MR. Artificial intelligence in drug development: Present status and future prospects. Drug Discovery Today. 2019;**24**(3):773-780

[45] Batool S, Javed MR, Aslam S, Noor F, Javed HMF, Seemab R, et al. Network pharmacology and bioinformatics approach reveals the multi-target pharmacological mechanism of Fumaria indica in the treatment of liver cancer. Pharmaceuticals. 2022;**15**(6):654

[46] Li L, Wang X, Guo X, Li Y, Song Q, Li A. Network pharmacology and

computer-aided drug design to explored potential targets of Lianhua Qingwen and Qingfei Paidu decoction for COVID-19. Frontiers in Pharmacology. 2022;**13**:1013428

[47] Jin J, Chen B, Zhan X, Zhou Z, Liu H, Dong Y. Network pharmacology and molecular docking study on the mechanism of colorectal cancer treatment using Xiao-chai-Hu-Tang. PLoS One. 2021;**16**(6):e0252508

[48] Afshari CA, Hamadeh HK, Bushel PR. The evolution of bioinformatics in toxicology: Advancing toxicogenomics. Toxicological Sciences. 2011;**120**(Suppl 1):S225-S237

[49] Pognan F. The evolving role of investigative toxicology in the pharmaceutical industry. Nature Reviews. Drug Discovery. 2023;**22**:317-335

[50] Singh AV. Integrative toxicogenomics: Advancing precision medicine and toxicology through artificial intelligence and OMICs technology. Biomedicine & Pharmacotherapy. 2023;**163**:114784

[51] Yamagata Y, Yamada H, Horii I. Current status and future perspective of computational toxicology in drug safety assessment under ontological intellection. Journal of Toxicological Sciences. 2019;44(11):721-735. DOI: 10.2131/jts.44.721. PMID: 31708530

[52] Palermo A. Metabolomics- and systems-biology-guided discovery of metabolite lead compounds and druggable targets. Drug Discovery Today. 2023;**28**(2):103460

[53] Barupal DK, Fan S, Fiehn O. Integrating bioinformatics approaches for a comprehensive interpretation of metabolomics datasets. Current Opinion in Biotechnology. 2019;**54**:1-9 [54] Alarcon-Barrera JC. Recent advances in metabolomics analysis for early drug development. Drug Discovery Today. 2022;**27**(6):1763-1773

[55] Paananen J, Fortino V. An omics perspective on drug target discovery platforms. Briefings in Bioinformatics.2020;21(6):1937-1953

[56] Phapale P. Pharmaco-metabolomics opportunities in drug development and clinical research. Analytical Science Advances. 2021;**2**:611-616

