



Integrating artificial intelligence and One Health approaches for virtual screening and antimicrobial resistance prediction

Sarah Ahmed Hasan^{1,*}

¹ Kirkuk University. College of Nursing. Associate Professor in Microbiology, Kirkuk, Iraq.

*Corresponding author: Sarah Ahmed Hasan.

Kirkuk University. College of Nursing. Associate Professor in Microbiology, Kirkuk, Iraq.

E-mail: sarahahmed100@uokirkuk.edu.iq

DOI: <https://doi.org/10.54448/ijn26S306>

Received: 04-17-2026; Revised: 06-08-2026; Accepted: 06-09-2026; Published: 07-14-2026; IJN-id: e26S306

Editor: Dr. Luis Alberto Moreno Aznar, MD, Ph.D.

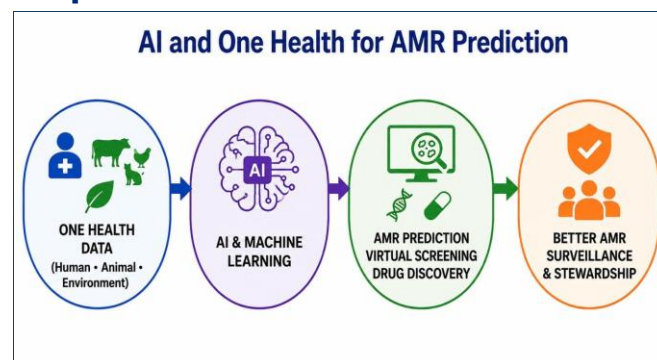
Abstract

Introduction: Antimicrobial resistance (AMR) has become a global health threat affecting human, animal, and environmental health. Artificial intelligence (AI) techniques, including machine learning (ML) and deep learning, have demonstrated significant potential in enhancing antimicrobial resistance prediction, antimicrobial discovery, and One Health surveillance systems. **Objective:** The purpose of this review was to evaluate the use of artificial intelligence and One Health approaches in virtual screening, antimicrobial resistance prediction, and antimicrobial stewardship, and to explore their potential applications in global antimicrobial resistance management. **Methods:** A narrative review was conducted on recent literature covering the application of AI in antimicrobial resistance prediction, drug discovery, machine learning algorithms, and One Health surveillance systems. Clinical, veterinary, environmental, and public health studies relevant to the topic were reviewed and synthesized. **Results:** The available evidence showed that AI can enhance resistance prediction, identify resistance-associated mutations, facilitate virtual screening of antimicrobial compounds, and support the discovery of novel therapeutic agents. AI models can also integrate clinical, veterinary, genomic, and environmental data, strengthening One Health surveillance and antimicrobial stewardship efforts. However, data quality, transparency, ethical considerations, and interoperability remain significant challenges. **Conclusion:** AI has the potential to be a powerful tool in combating antimicrobial resistance within a One Health framework. To fully realize the benefits of AI for antimicrobial

resistance prediction, antimicrobial discovery, and global surveillance programs, improved data integration, ethical governance, and interdisciplinary collaboration are essential.

Keywords: Artificial intelligence. Antimicrobial resistance. One Health. Virtual screening. Machine learning. Antimicrobial stewardship.

Graphical Abstract



Source: Own authorship.

Introduction

AMR has been regarded as a serious threat to global public health by the WHO [1-3]. According to the World Health Organization (2024), approximately 1.27 million people die annually from antimicrobial resistance and another 5 million deaths are associated with antimicrobial resistance. The Eastern Mediterranean Region reports that resistance rates for Gram-negative pathogens associated with hospital-acquired infections are above 60 percent [4-8]. Surveillance data in Iraq indicate that more than 50% of the clinical isolates are multidrug resistant [9].

Nowadays antimicrobial resistance is no longer limited to health care settings and human infections but is, indeed, considered a One Health issue, encompassing interconnected human, animal, food and environmental ecosystems. Livestock production and/or wastewater systems, contaminated environments and food chains can all provide a pathway for the spread of resistant pathogens and antimicrobial resistance genes, and hence help to spread AMR.

Frequent causes of antibiotic resistance include misuse of antibiotics, poor clinical decision making, incorrect antibiotic doses and noncompliance with treatment guidelines [10-14]. To fight the spread of antibiotic resistance, multi-disciplinary research and integrated intervention strategies are needed, as well as collaborative health policies. The One Health approach focuses on integrated monitoring and action plans in human, animal, veterinary and agricultural surveillance and intervention systems. AI offers a potential solution in this regard to integrate multidimensional AMR data into one unified predictive and surveillance platform.

AI has been used in various ways within the field of antimicrobial resistance (AMR) management, such as in discovery, prediction, monitoring, and analysis [15,16]. It can develop personalized therapeutic options according to genetic and clinical parameters. Recent research has demonstrated that AI can also be applied to the development of new drugs, specifically antibiotics and synergistic drug combinations [17]. Rational antibiotic use and predictive AMR modelling are now increasingly relevant in designing novel antimicrobials and finding useful synergistic combinations [18]. The interpretation of antibiotic consumption and resistance data can help guide evidence-based prescribing decisions by healthcare professionals and policymakers [19]. Structurally diverse antimicrobial compounds have also been discovered using deep learning techniques [20-22].

Additionally, AI-driven One Health surveillance systems can help detect emerging patterns of resistance in both humans and animals, and in the environment before they spread, resulting in more efficient global containment measures. Although there has been increased use of AI in the research of antimicrobial resistance, most studies have focused primarily on either clinical or computational aspects alone and have not fully adopted the One Health approach. Therefore, this review aimed to summarize the current application of AI in AMR prediction, drug discovery and One Health surveillance, and explore future challenges and opportunities in global antimicrobial stewardship.

AI roles in drug resistance management

The ability of AI to help quickly identify potential antimicrobial agents based on the recognition of specific compounds and predicting resistance patterns can be of great value. In the One Health approach, AI algorithms can be connected to data from human clinical practice, veterinary and environmental monitoring to make better predictions about resistance transmission pathways and to detect new multidrug-resistant organisms in the complex connected ecosystems. It also plays a role in the development of more powerful antibiotics via dynamic molecular modeling and target discovery [16].

AI can be used to forecast drug resistance and help health providers identify patients who may be at risk of developing resistance to specific drugs as shown in Figure 1. The figure underscores how AI-powered integration of genomic, phenotypic, and clinical data can help uncover potential resistance genes, assess the efficacy of drugs, and propose alternative treatment strategies.

The biggest benefit of AI is that it can analyze large volumes of data and uncover trends that a human wouldn't necessarily be able to see. AI can tailor treatment strategies to individual patients, which can improve the efficacy of the therapeutic process, taking into account genetic and clinical information.

In addition to identifying resistance genes, AI models can also forecast the likelihood of mutations and identify predictive biomarkers, allowing for early action on resistant infections [16,23] as illustrated in Figure1.

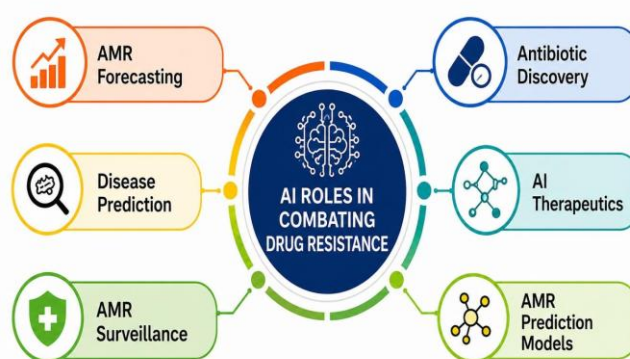


Figure 1. AI roles in combating drug resistance [15-23].

AI Applications within the One Health Framework

One Health is an awareness that the health of humans, animals and the environment are interconnected. AI is playing an increasingly important role in tackling antimicrobial resistance challenges in

surveillance and prediction, which is made possible by the integration and enhancement of these multi-dimensional datasets [24-26]. The ability to predict a patient's susceptibility to multidrug resistant infections and optimize antimicrobial stewardship programs using data from human health care systems could be developed by AI models that analyze antimicrobial consumption in the hospital and genomic antibiotic resistance patterns, amongst other clinical data.

AI-powered surveillance can identify the misuse of antimicrobials, monitor the transmission pathways for zoonotic diseases and anticipate the risks of developing resistance associated with livestock and food production [14,24]. AI can also improve environmental monitoring systems in other areas such as wastewater surveillance, environmental genomic sequencing, and resistance gene tracking. These approaches can identify how antimicrobial resistance spreads before it can be clinically transmitted and help identify environmental reservoirs that are spreading antimicrobial resistance [14,24-26].

One Health AI platforms have the potential to provide real-time, global surveillance of clinical, veterinary and environmental data to support evidence-based public health action and antimicrobial use policies as mentioned in Figure 2.

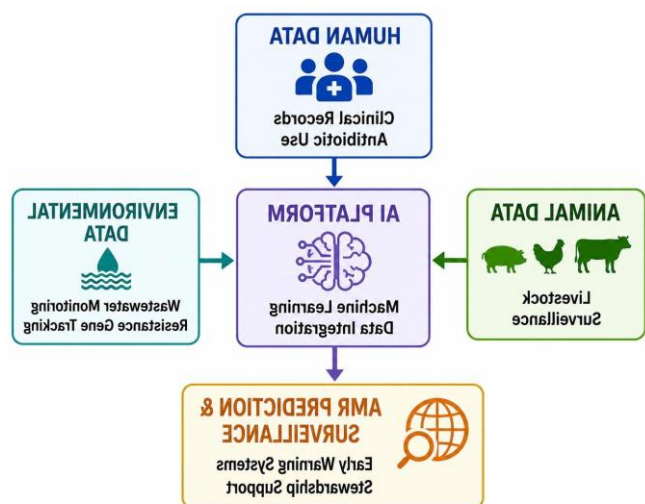


Figure 2. AI-driven One Health framework for AMR prediction and surveillance [14,24-26]

Machine learning algorithms in combating drug resistance

The AI algorithms can perform large-scale data processing and uncover more intricate patterns that human researcher tend to overlook. Machine learning algorithms of different types are employed in managing drug resistance [24-26]. The relative architecture and decision process of the major ML models used to predict AMR including Naive Bayes (NB), Support Vector Machine (SVM), Artificial Neural

Network (ANN), and Random Forest (RF) are shown in Figure 3. The figure shows that ensemble methods, such as RF, tend to be more accurate in their predictions than linear models, with prediction accuracy of around 90 percent in several clinical validation studies.

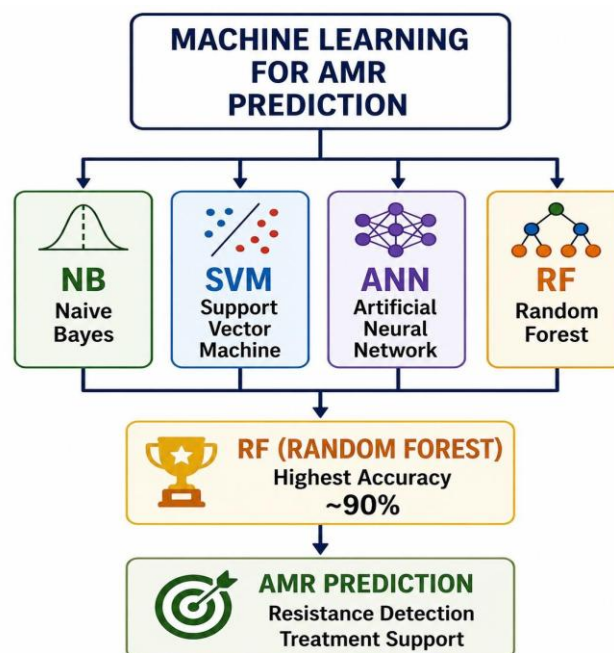


Figure 3. Machine learning algorithms used in predicting drug resistance. [14,24-26].

Naive Bayes (NB)

Naive Bayes can be used for prediction of drug resistance patterns by using conditional probability and assuming that features are independent. NB is known to be simple, fast and computationally efficient.

Applications: NB can be used to predict drug resistance, effective drug combinations and can also be used when evaluating treatment outcomes.

Examples: With multidrug data, improved NB algorithms can predict successful drug combinations with approximately 85 percent classification accuracy. NB is very effective for high-dimensional data and can calculate the probability of an ineffective treatment due to AMR [27, 28].

Decision Tree (DT)

Decision Trees predict and inform the prescription of antibiotics for drug resistance. They are based on feature selection, construction of trees and pruning, and they employ unique modeling techniques which improve predictive accuracy. **Applications:** Prediction of drug resistance, choice of appropriate antibiotics, prediction of mutations. **Examples:** Decision Trees have the capability of allocating medical resources according to the estimated AMR burden. Procalcitonin-based Decision Trees can be used to reduce treatment duration and Treesist-TB can predict resistance to TB

drugs. In hospital AMR studies, DTs yield a predictive accuracy of around 80-88 percent [29, 30].

Support Vector Machine (SVM)

SVM provides binary classification models for AMR prediction, and its accuracy is very high, particularly for the prediction of antibiotic resistance in *E. coli*. **Applications:** AMR phenotype and drug resistance prediction. **Examples:** SVM has been used to predict drug resistance in *E. coli*, and to study the correlation between miRNA and drug resistance. It also helps to enhance the outcomes of TB treatment [31, 32].

Artificial Neural Network (ANN)

ANNs are used for evaluation of drug repurposing and prediction of antibiotic resistance. They gain knowledge from patterns and examples, and are useful in finding new antibiotics. **Applications:** Evaluation and prediction of antibiotic resistance, drug repurposing.

Examples: ANNs have been used to discover new antibiotics, to forecast resistance profiles, and to provide information that could help in combating AMR [33, 34].

Random Forest (RF)

RF is an ensemble algorithm which consists of several decision trees for predicting drug resistance. It is based on random sampling and sub-feature selection with high predictive capability. **Applications:** Drug resistance prediction, estimation of the burden of AMR, and optimization of antibiotic combinations. **Examples:** RF models can accurately predict effective antibiotic combinations and are more efficient than other models in predicting MDR-TB with high accuracy [35].

Table 1. Comparative overview of machine learning algorithms used in antimicrobial resistance prediction [27-35].

Algorithm	Main Application	Advantages	Limitations	Reported Accuracy
Naive Bayes	Drug resistance prediction and treatment outcome evaluation	Simple, fast, and suitable for highdimensional data	Assumes feature independence	Approximately 85%
Decision Tree	Antibiotic selection, mutation prediction, and AMR burden estimation	Easy to interpret and clinically understandable	May overfit without pruning	Approximately 80-88%
Support Vector Machine	AMR phenotype prediction and resistance classification	High accuracy in binary classification tasks	Less interpretable and sensitive to parameter selection	High accuracy in selected studies

Artificial Neural Network	Drug repurposing and resistance profile prediction	Learns complex nonlinear patterns	Requires large datasets and may lack transparency	Variable depending on dataset
Random Forest	MDR prediction and antibiotic combination optimization	High predictive performance and robust ensemble learning	Less transparent than single decision trees	Around or above 90%

Source: Own authorship.

AI in Drug Resistance Management in Real-Time

There are many drug resistance management software tools and each of them has specific capabilities. Figure 4 illustrates a real-time AI tool for analysing antimicrobial resistance data that traces the evolution of the process from data entry through decision making, prediction and model refinement. It shows how AI can be dynamically updated to changing bacterial resistance profiles to assist clinicians in making timely and informed decisions.

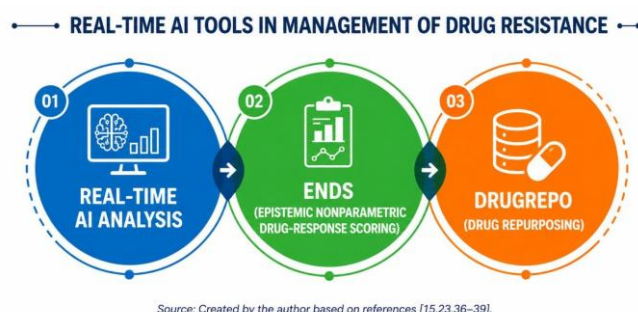


Figure 4. Real-time AI tools in management of drug resistance.

DrugRepo

DrugRepo is a computer platform designed to repurpose drugs already approved for use to other indications, such as kidney disease, cancer and cardiovascular disease. The DrugRepo workflow involves different activities including compound-target data analysis, structural analysis, gene-disease correlations and pathway analysis. It has a pipeline that can utilize about 0.8 million compounds in 606 diseases [36]. Although DrugRepo is not a specific tool for drug-resistance management, it can be used to identify drugs that can be repurposed, such as those that could be used in the treatment of drug-resistant infections and/or to improve existing treatments. However, solving the specific drug resistance problem would demand other machine learning algorithms and analysis methods which can assess, predict and control the patterns of drug resistance [34,37,38].

Epistemic Nonparametric Drug-response Scoring (ENDS)

ENDS is a computer program designed to fit and score drug dose-response curves in a nonparametric

fashion, as a web-based program. Unlike linear models, ENDS does not require any parametric assumptions and parallel indexing such as half-maximal inhibitory concentration (IC₅₀) and area under the curve (AUC) is permitted. The tool provides models (spline (npS), monotonic), as well as Bayesian approaches and indices (maximum effective dose, drug-response gradient). Although ENDS was not designed specifically for the management of drug resistance, it is helpful to assess responses to drugs to understand and manage resistance. These drug-pathogen interactions and mechanisms of drug resistance can be clarified by ENDS, and therefore more accurate analyses can be made by providing more objective and unbiased evaluation [34,39].

There are five problems that need to be addressed to implement AI in drug resistance management. Implementing AI in drug resistance management presents several important challenges. While AI has demonstrated impressive results in combating drug resistance, there are still some obstacles that need to be addressed [16,23]: 1- Data limitations: Lack of or missing information on antimicrobial use and antimicrobial resistance to train an AI model often makes the model inaccurate; 2- Complexity and transparency: Artificial intelligence models might not be easily understood and this will reduce decision making transparency; 3- Generalizability: Most AI models are difficult to use in novel clinical or geographical contexts; 4- Regulatory and ethical considerations: Issues of informed consent and data privacy need to be taken into account; 5- Infrastructure and adaptability: The inability to apply AI solutions more broadly and the rigidity of systems could limit the use of AI in the management of drug resistance; 6- Despite the potential, the integration of One Health data, such as clinical, veterinary, agricultural, and environmental information, is still technically and logistically difficult because of disparities in data quality, regulatory frameworks, and surveillance systems.

Future Perspectives

In future, the development of AI-driven antimicrobial resistance management will emphasize the development of more transparent and explainable AI systems that will enhance clinician trust and decision-making. New technologies like federated learning could enable the sharing of antimicrobial resistance data in a secure manner between institutions, without compromising data privacy. Furthermore, integrated One Health real-time AMR surveillance systems have the potential to improve detection of resistant pathogens in the human, animal,

and environmental sectors. The implementation of ethical AI, interoperability of surveillance platforms and the creation of global One Health collaborative networks will be important future steps towards improved antimicrobial stewardship and resistance control strategies [23,24,40].

Limitations

This review has a number of limitations. First, it was based primarily on published literature, and no quantitative analysis was performed. Second, the findings may have limited long-term applicability due to the rapidly evolving nature of AI technologies. Third, the availability and quality of One Health data vary considerably across settings, which may affect the generalizability of AI-based AMR prediction models. Lastly, many reported AI applications remain in the early developmental or experimental stage, and further clinical validation is required before widespread implementation.

Conclusion

AI can be used to customize treatment options and understand how resistance might develop. These technologies have the potential to turn genomic, clinical, veterinary, and environmental data into actionable information that can contribute to prevention and therapeutic intervention. In some pilot cases, AI has proven to be very predictive when combined with statistical models and real-time analytics. But there is ethical transparency, data quality, interoperability and reproducibility issues. Thus, future antimicrobial resistance strategies must go beyond the current prediction models that rely on hospital-based data and move towards integrated One Health surveillance systems that encompass human, veterinary, food-chain and environmental antimicrobial resistance. AI's incorporation into the One Health approach is a promising solution for tackling the worldwide challenge of AMR by combining evidence-based and interdisciplinary methods. AI-driven One Health approaches can also help achieve Sustainable Development Goals (SDGs) including SDG 3 (Good Health and Well-being), SDG 6 (Clean Water and Sanitation), and SDG 12 (Responsible Consumption and Production).

CrediT

Author contributions: Conceptualization; Data curation; Formal Analysis; Investigation; Methodology; Project administration; Writing - original draft; Writing-review & editing- Sarah Ahmed Hasan.

Acknowledgment

Not applicable.

Ethical Approval

Not applicable.

Informed Consent

Not applicable.

Funding

Not applicable.

Data Sharing Statement

No additional data are available.

Conflict of Interest

The authors declare no conflict of interest.

Similarity Check

It was applied by Ithenticate®.

Application of Artificial Intelligence (AI)

Not applicable.

Peer Review Process

It was performed.

About The License©

The author(s) 2026. The text of this article is open access and licensed under a Creative Commons Attribution 4.0 International License.

References

1. Ahmed Hasan S. Evaluation of trimethoprim nanoemulsion for combating antibiotic resistant *Proteus mirabilis* in urinary tract infections. *Iran J Med Microbiol.* 2025;19(3):182-190. DOI:10.30699/ijmm.19.3.182
2. Hasan SA. Drug resistant bacteria and antimicrobial activity of medicinal plants. *Int. J. Nutrology.* 2025 Aug. 5:18(3). Available from: <https://ijn.zotarellifilhoscientificworks.com/index.php/ijn/article/view/470>
3. Ahmed Hasan S, Mohammed Bakr M. Bacteriological and Molecular Detection of *Klebsiella oxytoca* and its Resistance to Antibiotics among Clinical Specimens from Kirkuk, Iraq. *Arch Razi Inst.* 2022 Oct 31;77(5):1521-1525. doi: 10.22092/ARI.2022.357753.2095. PMID: 37123151; PMCID: PMC10133605.
4. Hasan SA, Raoof WM, Rachid SK. The current status of carbapenem resistance in Iraq: A systematic review. *World Bull Public Health.* 2022;13:88–94.
5. Hasan SA, Abass KS. Prevalence of Gram Negative Bacteria Isolated from Patients with Burn Infection and their Antimicrobial Susceptibility Patterns in Kirkuk City, Iraq. *Indian Journal of Public Health Research & Development.* 2019 Aug 1;10(8). DOI:10.5958/0976-5506.2019.02184.3
6. Hasan, S.A.; Mohamed, A.H.; Karim, G.F. Extensively Drug-Resistant (XDR) and Pandrug-Resistant (PDR) *Acinetobacter baumannii* as Sentinel Indicators of Cumulative System-Level Antimicrobial Pressure in Iraqi Burn and High-Risk Hospital Units. *Microorganisms* **2026**, *14*, 996. <https://doi.org/10.3390/microorganisms14050996>
7. Ahmed Hasan S, Fakhraddin Raheem T, Mohammed Abdulla H. Phenotypic, Antibiotyping, and Molecular Detection of *Klebsiella Pneumoniae* Isolates from Clinical Specimens in Kirkuk, Iraq. *Arch Razi Inst.* 2021 Oct 31;76(4):1061-1067. doi: 10.22092/ari.2021.355770.1721. PMID: 35096342; PMCID: PMC8790972
8. Ahmed Hasan S, Hasan Mohamed A and F. Karim G. Clinical Risk Factors and Antimicrobial Resistance Patterns of Multidrug Resistant Enterobacter cloacae Isolates from Hospitalized Patients. *F1000Research* 2025, 14:1427 (<https://doi.org/10.12688/f1000research.173842.1>)
9. Hasan S, Raoof W, Ahmed K. FIRST REPORT OF CO-HARBORING BLEOMYCIN RESISTANCE GENE (bleMBL) AND CARBAPENEMASE RESISTANCE GENE (blaNDM-1) KLEBSIELLA PNEUMONIAE IN IRAQ WITH COMPARISON STUDY AMONG THE SENSITIVITY TEST, THE BD PHOENIX CPO DETECT TEST, AND THE RAPIDEC® CARBA NP TEST. *SJLSA*;16(4):208-37. Available from: <https://discover-journal.ru/jour/index.php/sjlsa/article/view/1249>
10. Hasan SA, Raoof WM, Ahmed KK. Antibacterial activity of deer musk and Ziziphus spina-christi against carbapenem resistant gram negative bacteria isolated from patients with burns and wounds. *Regul. Mech. Biosyst.* [Internet]. 2024 Apr;17;15(2):267-78. Available from: <https://medicine.dp.ua/index.php/med/article/view/988>
11. Hasan SA. *Pseudomonas aeruginosa* and the

- multifactorial antibiotic resistance. *Eurasian Med Res Periodical*. 2022;11:85–94.
12. Majeed ZH, Hasan SA, Ismail RM. Evaluate the beneficial effects of *Dodonaea viscosa* in kidneys of infected rats with *Staphylococcus aureus*. *J Pharm Negat Results*. 2022;13(3):291-297. DOI:10.47750/pnr.2022.13.03.046
 13. Raheem TF, Hasan SA. Prevalence and multidrug resistance patterns of uropathogenic *Escherichia coli* isolated from female patients in Kirkuk City, Iraq. *Iran J Med Microbiol*. 2022;16(6):609-614. DOI:10.30699/ijmm.16.6.609
 14. Hasan SA. Converging frontiers in bioethics: Navigating the ethical nexus of CRISPR, artificial intelligence, and environmental responsibility. *CME*. 2025;30:1.
 15. Elalouf A, Elalouf H, Rosenfeld A, Maoz H. Artificial intelligence in drug resistance management. *3 Biotech*. 2025;15(5):126. doi:10.1007/s13205-025-04282-w.
 16. Ali T, Ahmed S, Aslam M. Artificial intelligence for antimicrobial resistance prediction: Challenges and opportunities toward practical implementation. *Antibiotics*. 2023;12:523.
 17. Stokes JM, Yang K, Swanson K, et al. A deep learning approach to antibiotic discovery. *Cell*. 2020;180(4):688–702.e13. doi:10.1016/j.cell.2020.01.021.
 18. Trafton A. Using AI, MIT researchers identify a new class of antibiotic candidates. *MIT News*. Published December 2023. Accessed January 28, 2024.
 19. Wong F, Zheng EJ, Valeri JA, et al. Discovery of a structural class of antibiotics with explainable deep learning. *Nature*. 2023;624:145–152. doi:10.1038/s41586-023-06887-8.
 20. Nicholson M. Revolutionising antibiotic discovery: How AI is transforming the search for new antibiotics. *NES Fircroft Blog*. 2023. Available from: <https://www.nesfircroft.com/resources/blog/revolutionising-antibiotic-discovery>. Accessed January 2024.
 21. Trafton A. Artificial intelligence yields new antibiotic. *MIT News*. 2020. Available from: <https://news.mit.edu/2020/artificial-intelligence-identifies-new-antibiotic-0220>.
 22. Marchant J. Powerful antibiotics discovered using AI. *Nature*. 2020;578(7795):353–354. doi:10.1038/d41586-020-00018-3.
 23. Liu GY, Yu D, Fan MM, et al. Antimicrobial resistance crisis: Could artificial intelligence be the solution? *Mil Med Res*. 2024;11(7):1–10.
 24. Farhat F, Athar MT, Ahmad S, et al. Antimicrobial resistance and machine learning: Past, present, and future. *Front Microbiol*. 2023;14:1179312. doi:10.3389/fmicb.2023.1179312.
 25. Sakagianni A, Koufopoulou C, Feretzakis G, et al. Using machine learning to predict antimicrobial resistance: A literature review. *Antibiotics*. 2023;12(4):452.
 26. Quoc VT, Ngoc DNT, Hoang TN, et al. Predicting antibiotic resistance in ICU patients by applying machine learning in Vietnam. *Infect Drug Resist*. 2023;16:5535–5546. doi:10.2147/IDR.S415885.
 27. Lv J, Deng S, Zhang L. A review of artificial intelligence applications for antimicrobial resistance. *Biosaf Health*. 2021;3(1):22–31.
 28. Abd El-Hafeez T, Shams MY, Elshaier YAMM, et al. Harnessing machine learning to find synergistic combinations for FDA-approved cancer drugs. *Sci Rep*. 2024;14:1–23. doi:10.1038/s41598-024-52814-w.
 29. Yasir M, Karim AM, Malik SK, et al. Application of decision tree-based machine learning algorithms for prediction of antimicrobial resistance. *Antibiotics*. 2022;11(11):1593. doi:10.3390/antibiotics11111593.
 30. Yurtseven A, Buyanova S, Agrawal AAA, et al. Machine learning and phylogenetic analysis allow for predicting antibiotic resistance in *Mycobacterium tuberculosis*. *BMC Microbiol*. 2023;23(1):1–12. doi:10.1186/s12866-023-03147-7.
 31. Kanesamoorthy K, Dissanayake M. Prediction of treatment failure of tuberculosis using support vector machine with genetic algorithm. *Int J Mycobacteriol*. 2021;10(3):279–284. doi:10.4103/ijmy.ijmy_130_21.
 32. Duan T, Kuang Z, Deng L. SVMMDR: Prediction of miRNAs-drug resistance using support vector machines based on heterogeneous networks. *Front Oncol*. 2022;12:987609. doi:10.3389/fonc.2022.987609.
 33. Popa SL, Pop C, Dita MO, et al. Deep learning and antibiotic resistance. *Antibiotics*. 2022;11(11):1674.
 34. Deelder W, Napier G, Campino S, et al. A modified decision tree approach to improve prediction and mutation discovery for drug resistance in *Mycobacterium tuberculosis*. *BMC Genomics*. 2022;23(46):1–12. doi:10.1186/s12864-022-08291-4.
 35. Wang CC, Hung YT, Chou CY, et al. Using random forest to predict antimicrobial minimum inhibitory concentrations of non-typhoidal

- Salmonella* in Taiwan. Vet Res. 2023;54(1):1–10. doi:10.1186/s13567-023-01141-5.
36. Wang Y, Aldahdooh J, Hu Y, et al. DrugRepo: A novel approach to repurposing drugs based on chemical and genomic features. Sci Rep. 2022;12(1):1–13. doi:10.1038/s41598022-24980-2.
 37. Liu Y, Tong Z, Shi J, et al. Drug repurposing for next-generation combination therapies against multidrug-resistant bacteria. Theranostics. 2021;11(11):4910–4928.
 38. Drózd W, Wiciński M, Szota AM, et al. Augmentation therapies as treatments for coexisting somatic problems in schizophrenia: A systematic review. J Clin Med. 2023;12(12):4012.
 39. Amiryousefi A, Williams B, Jafari M, Tang J. The ENDS of assumptions: An online tool for epistemic non-parametric drug-response scoring. Bioinformatics. 2022;38(13):3132–3133. doi:10.1093/bioinformatics/btac217.
 40. World Health Organization. One Health Joint Plan of Action (2022–2026). Geneva: WHO; 2022.