REVIEW ARTICLE

A Review on Analysis of Anti-Microbial Drugs in Biological Matrices Using Analytical Techniques

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Abstract

Antimicrobial resistance (AMR) is an increasing global health challenge that reduces the effectiveness of existing treatments against a broad spectrum of pathogens. The current review outlines about the classification and spread of AMR, with a specific focus on multidrug-resistant (MDR), extensively drug-resistant (EDR), and pan-drug-resistant (PDR) organisms. MDR infections account for a significant number of deaths annually, with drug-resistant tuberculosis (TB) being a major contributor. EDR TB cases have shown a marked rise in recent years, particularly in certain geographic regions. PDR Gram-negative bacterial infections are linked to high mortality rates, posing serious treatment challenges. The growing presence of resistant fungal species and critical bacterial strains further highlights the complexity of the issue. Addressing AMR requires better monitoring, improved diagnostic methods, and the development of new antimicrobial strategies. Our study mainly focuses on the development and applications of various analytical techniques for the detection and analysis of resistant microorganisms from biological matrices, offering essential support for research and clinical practices.

Key words: Analytical techniques, antimicrobial resistance, biological matrices, extensively drug-resistant, multidrug-resistant

INTRODUCTION

One of the major issues facing world health is antimicrobial resistance (AMR). A serious hazard to public health is the emergence of treatment-resistant pathogenic bacteria. The Centers for Disease Control and Prevention estimates that multidrug-resistant microorganisms cause fatalities annually throughout the world. According to World Health Organization predictions, 10 million individuals got tuberculosis (TB), with South East Asia accounting for 44% of cases. During the year, there were a startling 12,000 instances of extensively drug-resistant TB, which represents a 50% increase over 2015.[1]

Several processes, including as enzymatic drug inactivation, drug uptake inhibition, target alteration, and active efflux. These mechanisms might be extrinsic acquired by horizontal gene transfer or intrinsic, occurring spontaneously without previous exposure. For example, β-lactamases break down the β-lactam ring in antibiotics, such as cephalosporins and penicillins, making them ineffective shown in Figure 1. While mutations in ribosomal subunits prevent antibiotics that target protein synthesis from binding, changes in the bacterial cell wall can limit drug entrance.[2]

Including improper antibiotic use due to patient non-compliance or prescription errors, excessive prescribing by healthcare providers driven by high patient demand, and the extensive, which leads to improper environmental disposal.[3] In addition, global travel plays a key role in the transmission of AMR, as highlighted during, facilitating the resistant organisms, bites from animals or insects shown in Figure 2.

The continued use of conventional antimicrobial agents often results in increased resistance among pathogens and limits the availability of effective treatments for future infections. This challenge has driven extensive research into antimicrobial compounds and innovative delivery systems aimed at

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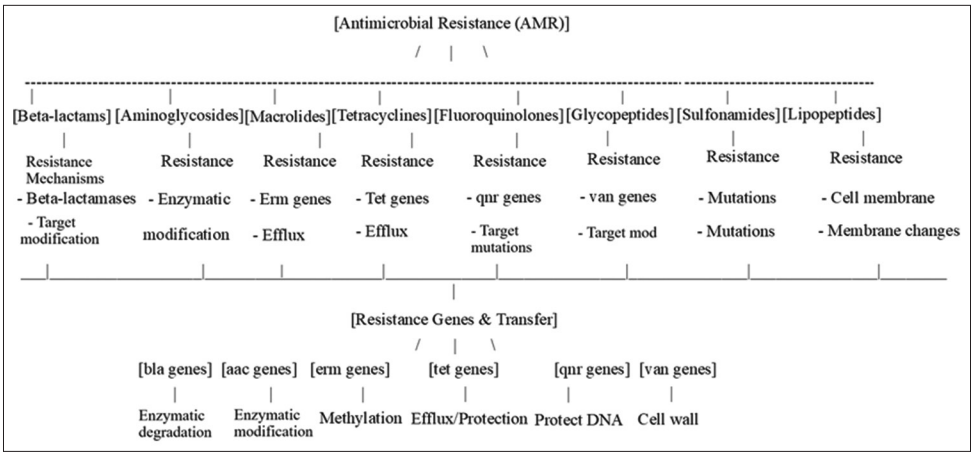

Figure 1: Classification and mechanism of antimicrobial resistance

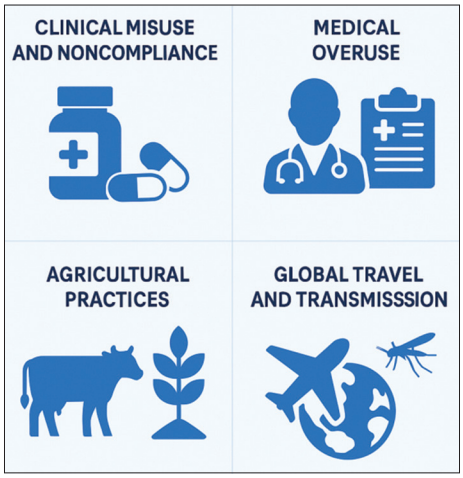

Figure 2: Graphical representation of resistance against antibiotics

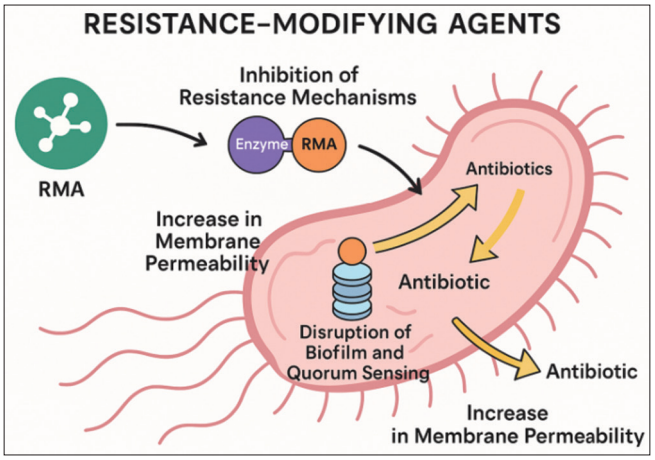

Figure 3: Inhibition of resistance mechanism

overcoming resistance.[4] To effectively resistance, there is now an urgent need to discover new antibiotic molecules and resistance-modifying agents that can restore or enhance existing therapies shown in Figure 3.

METHODOLOGY

The workflow for antimicrobial analysis begins with the collection of samples from clinical or preclinical studies and sending them to the laboratory. This is followed by sample clean-up or preparation, a critical step to remove interferences and improve analytical accuracy, requiring robust and standardized methods despite being time-consuming. Extraction from biological matrices can be performed through protein precipitation, liquid–liquid extraction, or solid-phase extraction, each chosen based on the sample's nature and analysis requirements. The final stage, sample analysis, ensures accurate identification and quality assessment of antimicrobial agents. Before routine use, these analytical methods must be validated in compliance with good manufacturing practice. Commonly used techniques include ultraviolet spectrophotometry [Figure 4],

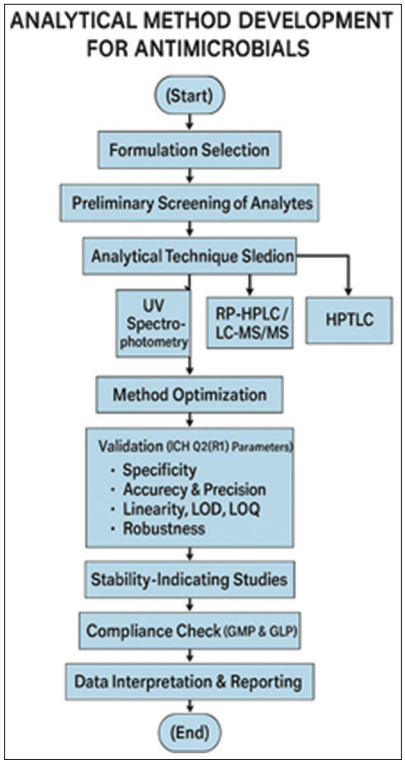

Figure 4: Work flow of analysis

S. No.	Authors	Year	Journal details	Title	Methodology
1.	Ningrum *et al*.	2024	Pharmacy Education, 24(3):197–203.	Vancomycin bioanalysis for TDM services using immunoassay and HPLC: A scoping review	This study reviews the validity and appropriateness of immunoassay and HPLC methods for therapeutic drug monitoring of vancomycin, concluding that immunoassay is suitable for fast results but not for patients with high immunoglobulin levels, while HPLC offers better selectivity and sensitivity.
2.	Borone *et al.*	2023	Biomedicine and Pharmacotherapy, 163:114790.	Fast and sensitive method for simultaneous quantification of meropenem and vaborbactam in Human plasma microsamples	Plasma microsamples, UHPLC- MS/MS Column: Agilent 6495cQ Linearity: 0.1–100 mg/L EMA validated Chromatographic runtime–4 min
3.	Riaezk *et al.*	2023	Anal Methods. 2023;15(6):746–751.	Triple quadrupole LCMS methods for the simultaneous quantitative measurement of cefiderocol and meropenem	Serum, Protein precipitation, Acetonitrile (standard), Triple quadrupole LCMS, injection volume – 2 µL, high accuracy and stability.
4.	Mulaa *et al.*	2023	Biomedicine and Pharmacotherapy 163(1):114790.	Analytical validation of a novel UHPLC-MS/MS method for 19 antibiotics quantification in plasma: Implementation in a LC-MS/MS Kit	Extraction method: Protein precipitation Extraction. Precipitation agent: Methanol and 10 % trichloroacetic acid concentration range: 0.1–600 ng/mL and 0.01 to 60 ng/mL Column: KIT Mobile phase: Mobile phase A consisting of 0.1% formic acid in water, and mobile phase B of 0.1% formic acid in acetonitrile. Retention time: 0.3–2.6 min Run time: 3 min
5.	Lufeng *et al.*	2022	Current Pharmaceutical Analysis. 18 (5) 449–454(6).	Comparison of HPLC-DAD and UPLC-MS/MS in monitoring serum concentration of lamotrigine	Concentration range: 0.59~22.20 mg/L by HPLC, and 0.28~23.97 mg/L by UPLC-MS/MS
6.	DelGuidice *et al.*	2022	Journal of Pharmaceutical and Biomedical Analysis. 5:217:114823.	Comparison of methods for quantitative analysis of ranibizumab and bevacizumab in human plasma using various bioanalytical techniques, including microfluidic immunoassay, triple quadrupole, and high-resolution liquid chromatography-tandem mass spectrometry approaches	Extraction method: Protein precipitation Extraction. Precipitation agent: Acetonitrile nano-liter microfluidic compact disc format for ligand binding assays
7.	Li *et al.*	2022	Anal Chem. 2022;92(15):10438–10446.	Hybridization liquid chromatography-tandem mass spectrometry: An alternative bioanalytical method for antisense oligonucleotide quantitation in plasma and tissue samples	Extraction method: Micro-solid phase extraction cartridges: C_{18}-SPE Concentration range: 0.009~0.071 µg/mL Column: Clarity 1.7 µm Oligo-XT 100 Å LC Column 50×2.1 mm

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S. No.	Authors	Year	Journal details	Title	Methodology
					Mobile phase: Mobile Phase A (100% Milli-Q water), Mobile Phase B (100% ACN), and Mobile Phase C (250 mM HFMIP and 150 mM 29DMCHA in 100% ACN) Run time: 4.5 min
8.	Fage *et al.*	2022	J Pharm Biomed Anal. 215:114776.	Development and Validation and clinical use of a LC-MS/MS for the simultaneous determination of the nine main antituberculosis human plasma	Sample preparation with protein precipitation; validated per FDA guidelines; applied in clinical TDM
9.	Abouzid *et al*.	2022	Molecules. 2024;29(2):337.	Development and validation of UPLC-MS/MS method for pharmacokinetic and stability studies of first-line antituberculosis drugs in urine	Urine sample prep via LLE; validated for TDM and pharmacokinetics
10.	Haiwei *et al.*	2022	Journal of Separation Science. 45(10):1683–1692.	A sensitive and selective HPLC-MS^3 method for meropenem and its validation by comparison with HPLC-MS methods	Extraction method: Protein precipitation Precipitation agent: Methanol Concentration range: 0.5–50 µg/mL Column: TELOS LU C18 (2) 5 µm, 100 × 4.6 mm Mobile phase: 20 mM Ammonium acetate (pH-3.0): Methanol:acetonitrile (20:20:60,%v/v) Run time: 7.0 min
11.	Haiwei *et al.*	2022	Journal of Separation Science.	A sensitive and selective HPLC-MS method for therapeutic drug monitoring of meropenem	Plasma samples Protein precipitation with methanol triple-stage MS with HPLC/MS study Recovery - >94% R^2->0.995 Precise and accurate
12.	Ganesh *et al.*	2021	Therapeutic Drug Monitoring. 1;43(3):335–345.	Microsampling assays for pharmacokinetic analysis and therapeutic drug monitoring of antimicrobial drugs in children: A critical review	Micro sampling techniques: DBS and VAMS - DBS: Collection of 30–50 µL blood on filter paper - VAMS: Accurate collection of 10–30 µL blood with micro sampling devices - Analytical method: Liquid chromatography with tandem mass spectrometry - Methodological aspects: Sample collection, extraction, validation outcomes (intra-assay and intra-assay accuracy and precision, recovery, stability, matrix effect)
13.	Karina *et al.*	2021	Animals (Basel). 14;11(5):1399.	Detection of antimicrobial residues in poultry litter: Monitoring a risk through a selective and sensitive HPLC-MS/MS method	Extraction method: SPE procedure cartridges: SPE Supel™ Select HLB Concentration range: 25~75.00 ng/mL

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S. No.	Authors	Year	Journal details	Title	Methodology
					Column: Sunfire™ C18 (3.5 µm and 150 × 2.1 mm) Mobile phase: 0.1% formic acid in water (Phase A) and 0.1% formic acid in methanol (Phase B) Run time: 25.423 min
14.	Luboš *et al.*	2021	Molecules. 7;26(8):2123.	Determination of antiviral drugs and their metabolites using micro-solid phase extraction and UHPLC-MS/MS in reversed-phase and hydrophilic interaction chromatography modes	Extraction method: Micro-solid phase extraction cartridges: C_{18}-SPE Concentration range: 0.009~0.071 µg/ml Column: 2.5 µm, 2.1 mm × 50 mm × Bridge™ Ethylene BEH Amid HILIC column Mobile phase: gradient elution ACN: Formic acid Run time: 6.0 min
15.	Catherine *et al.*	2021	Pharmaceuticals (Basel). 2021;14(12):1214.	Quantification of 15 antibiotics widely used in the critical care unit with a LC-MS/MS system: An easy method to perform a daily therapeutic drug monitoring	Extraction method: Protein precipitation extraction. Precipitation agent: Methanol Concentration range: 0.01~500 µg/mL Column: Acquity HSS T3 1.8 µm 2.1 mm × 50 mm Mobile phase: water and 0.1% formic acid (phase A) and acetonitrile and 0.1% formic acid (phase B) Run time: 4.0 min
16.	Julia *et al.*	2021	Antibiotics. 10(3):242.	HPLC-UV analytical method development, validation of cefiderocol	Extraction method: Protein precipitation extraction. Precipitation agent: acetonitrile/methanol (1:1) Concentration range: 4–160 mg/L Column: XR-ODS III 2.2 µm (150 mm × 2 mm) Mobile phase:0.1% formic acid+ 0.1%formic acid in acetonitrile Run time: 15.0 min
17.	Anjali *et al*.	2020	ACS Omega. 2020;5(51):31584–31597.	Rapid and simultaneous analysis of multiple classes of antimicrobial drugs by liquid chromatography-tandem mass spectrometry and its application to routine biomedical, food, and soil analyses	Extraction method: SPE procedure Cartridges: Discovery DSC-18 cartridges (H. plasma) SPE using Oasis HLB (1 cc, 30 mg) (Animal tissues) Concentration range: 0.25~50.00 ng/mL Column: Waters Symmetry Shield C18 (150 × 4.6 mm 2, 5 µm) Mobile phase: Methanol (MeOH)-0.5% FA (80:20, v/v) Run time: 3.0min

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S. No.	Authors	Year	Journal details	Title	Methodology
18.	Sebastiano *et al*.	2020	J Pharm Biomed Anal. 15;186:113273.	A liquid chromatography-tandem mass spectrometry platform for the routine therapeutic drug monitoring of 14 antibiotics: Application to critically ill pediatric patients	Extraction method: Protein precipitation Extraction. Precipitation agent: Methanol and 10 % trichloroacetic acid concentration range: 0.1–600 ng/mL and 0.01–60 ng/mL Column: Polar Premium column (50 mm × 2.1 mm, i.d. 2.6 mm, Thermo Fisher Scientific Mobile phase: Mobile phase A consisting of 0.1% formic acid in water, and mobile phase B of 0.1% formic acid in acetonitrile. Retention time: 0.3–2.6 min Run time: 3 min
19.	Caro *et al*.	2020	Talanta. Apr 1;210:120619.	A review of bioanalytical methods for the therapeutic drug monitoring of β-lactam antibiotics in critically ill patients: Evaluation of the approaches used to develop and validate quality attributes.	This review evaluates the development and validation of analytical methods for β-lactam antibiotics in critically ill patients, highlighting the need for reliable methods, complexities in pretreatment procedures, and inconsistencies in analytical ranges and calibration strategies.
20.	Decosterd *et al*.	2020	J Chromatogr B Analyt Technol Biomed Life Sci. 10:1157:122160.	Validation and clinical application of a multiplex high performance liquid chromatography - tandem mass spectrometry assay for the monitoring of plasma concentrations of 12 antibiotics in patients with severe bacterial infections	Extraction method: Protein precipitation Extraction. Precipitation agent: Methanol Concentration range: 0.1–600 ng/mL and 0.01–60 ng/mL Column:Acquity UPLC HSS-T3 2.1 × 50 mm, 1.8 µm (Waters®) Mobile phase: Mobile phase A consisting of 0.1 % formic acid in water, and mobile phase B of 0.1% formic acid in acetonitrile. Retention time: 0.3–2.6 min Run time: 9 min
21.	Ramadon *et al*.	2020	J Pharm Biomed Anal. 10:189:113429.	A sensitive HPLC-UV method for quantifying vancomycin in biological matrices: Application to pharmacokinetic and biodistribution studies in rat plasma, skin, and lymph nodes	Extraction method: Protein precipitation Extraction. Precipitation agent: Methanol Concentration range: 0.05–50 µg/mL Column:Cortecs® C18 column (4.6 × 150 mm, 2.7 µm particle size) Mobile phase: 20 mM phosphate buffer containing 0.5% v/v of triethylamine and a mixture of methanol - acetonitrile (70:30, v/v) Run time: 12 min
22.	Ferrari *et al*.	2020	Journal of Chromatography. B, Analytical Technologies in the Biomedical and Life Sciences. 11:1148:122151.	Validation of a simple and economic HPLC-UV method for the simultaneous determination of vancomycin, meropenem, piperacillin, and tazobactam in plasma samples	Extraction method: Protein precipitation Extraction. Precipitation agent: Acetonitrile Concentration range: 1 and 100 µg/mL Column: Kinetex C18 column Mobile phase: phosphate buffer 0.1 M pH 3.15, and methanol in gradient, Run time: 25 min

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S. No.	Authors	Year	Journal details	Title	Methodology
23.	Qi *et al*.	2020	Drug Testing and Analysis. 12 (8).	Colistin A/B and colistin methanesulfonate in biological matrix	Extraction method: SPE procedure cartridges: HLB-SPE Concentration range: 0.009~0.071 µg/ml Column: 2.5 µm, 2.1 mm × 50 mm XBridge™ Ethylene BEH Amid HILIC column Mobile phase: 0solvent A (acetonitrile containing 0.1% formic acid) and solvent B (water with 0.1% formic acid). Run time: 5.4 min
24.	Kuhli *et al*.	2020	Int J Antimicrob Agents. 2020;56(5):107523.	Development of LC–MS/MS method for simultaneous quantification of five TB drugs	Solid-phase extraction; method validation per FDA
25.	Lei	2020	Biomedical Chromatography.	Simultaneous quantification of β-lactam antibiotics in plasma	Protein precipitation; validated as per FDA
26.	Sutherland and Nicolau	2020	Journal of Chromatographic Science. Volume 58, Issue 8, 726–730.	Development of an HPLC Method for the determination of meropenem/vaborbactam in biological and aqueous matrices	Extraction method: Liquid-liquid extraction. Amicon Ultra 0.5 mL Concentration range: 0.01~500 µg/mL Column: a 5-µm BDS Phenyl-Hypersil C18 Mobile phase: methanol and 25-mM sodium phosphate buffer Run time: 16.0 min
27.	Prasad *et al*.	2019	Pharm Methods. 10(2):47–52.	Estimation of eravacycline dihydrochloride in biological matrices by LC-MS/MS	Extraction method: Protein precipitation extraction. Precipitation agent: 1.0 mL of Acetonitrile:Methanol (50:50%,v/v) Concentration range: 15.00–120.00 pg/mL Column: TELOS LU C18 (2) 5 µm, 100 × 4.6 mm Mobile phase: 20mM Ammonium acetate (pH-3.0): Methanol:Acetonitrile (20:20:60%v/v) Run time: 4.0 min

TDM: Therapeutic drug monitoring, HPLC-UV: High-performance liquid chromatography ultraviolet, FDA: Food and Drug Administration, LC-MS/MS, Liquid chromatography-tandem mass spectrometry, UHPLC-MS/MS: Ultra-high performance liquid chromatography-tandem mass spectrometry, BEH: Bridged hybrid, TB: Tuberculosis, DBS: Dried blood spotting, VAMS: Volumetric absorptive micro sampling, LLE: Liquid-Liquid extraction, EMA: European medicines agency, SPE: Solid phase extraction, BDS: Base deactivated silica, ACN: Acetonitrile

high-performance liquid chromatography, high-performance thin-layer chromatography, and stability-indicating methods, which collectively ensure reliable monitoring and quality control during drug development and manufacturing.[5-30]

CONCLUSION

The comprehensive evaluation of analytical techniques for the detection and quantification of antimicrobial drugs in biological matrices highlights significant advancements in accuracy, sensitivity, and applicability for therapeutic drug monitoring, pharmacokinetic profiling, and residue analysis. The evolution from conventional chromatographic methods to advanced platforms such as liquid chromatography-tandem mass spectrometry, ultra-high performance liquid chromatography-tandem mass spectrometry, and high-resolution mass spectrometry has enabled rapid, selective, and reliable detection of multiple drug classes, even at trace concentrations. These improvements are further supported

by optimized sample preparation approaches including protein precipitation, liquid–liquid extraction, solid-phase extraction, micro-solid phase extraction, and microsampling that enhance method robustness while accommodating complex and low-volume samples.

Despite this progress, the review underscores persistent challenges, including variability in method validation standards, differences in pre-analytical handling procedures, and limited harmonization across laboratories. Furthermore, the adaptability of these methods to diverse biological matrices and varied patient populations remains an area requiring greater standardization. The integration of emerging analytical technologies with automation, miniaturization, and green chemistry principles offers promising avenues for addressing these gaps.

Ultimately, the effective monitoring and quantification of antimicrobial agents, particularly in the face of growing AMR, will depend on the continued development of validated, reproducible, and globally accepted analytical protocols. Such advancements will not only improve patient-specific dosing and treatment outcomes but also support antimicrobial stewardship programs, contribute to public health surveillance, and guide policy-making in combating the global threat of AMR.

REFERENCES

1. Simal-Gandara J, Nainu F, Permana AD, Djide NJ, Anjani QK, Utami RN, *et al*. Pharmaceutical approaches on antimicrobial resistance: Prospects and challenges. Antibiotics (Basel) 2021;10:981.
2. Pauter K, Szultka-Młyńska M, Buszewski B. Determination and identification of antibiotic drugs and bacterial strains in biological samples. Molecules 2020;25:2556.
3. Tyagi A, Dave H. Analytical method development and validation of antimicrobial formulations - A review. Int J Pharm Sci Res 2023;14:4344-57.
4. Ningrum VD, Amalia SP, Wibowo A. Vancomycin bioanalysis for TDM services by using immunoassay and HPLC: A scoping review. Pharm Educ 2024;24:197-203.
5. Mishra A, Chhonker YS, Bisen AC, Prasad YD, Tulsankar SL, Chandasana H, *et al*. Rapid and simultaneous analysis of multiple classes of antimicrobial drugs by liquid chromatography-tandem mass spectrometry and its application to routine biomedical, food, and soil analyses. ACS Omega 2020;5:31584-97.
6. Barco S, Mesini A, Barbagallo L, Maffia A, Tripodi G, Pea F, *et al*. A liquid chromatography-tandem mass spectrometry platform for the routine therapeutic drug monitoring of 14 antibiotics: Application to critically ill pediatric patients. J Pharm Biomed Anal 2020;186:113273.
7. Caro YS, Cámara MS, De Zan MM. A review of bioanalytical methods for the therapeutic drug monitoring of β-lactam antibiotics in critically ill patients: Evaluation of the approaches used to develop and validate quality attributes. Talanta 2020;210:120619.
8. Mula J, Chiara F, Manca A, Palermiti A, Maiese D, Cusato J, *et al*. Analytical validation of a novel UHPLC-MS/MS method for 19 antibiotics quantification in plasma: Implementation in a LC-MS/MS kit. Biomed Pharmacother 2023;163:114790.
9. Moorthy GS, Vedar C, Downes KJ, Fitzgerald JC, Scheetz MH, Zuppa AF. Microsampling assays for pharmacokinetic analysis and therapeutic drug monitoring of antimicrobial drugs in children: A critical review. Ther Drug Monit 2021;43:335-45.
10. Decosterd LA, Mercier T, Ternon B, Cruchon S, Guignard N, Lahrichi S, *et al*. Validation and clinical application of a multiplex high performance liquid chromatography - tandem mass spectrometry assay for the monitoring of plasma concentrations of 12 antibiotics in patients with severe bacterial infections. J Chromatogr B Analyt Technol Biomed Life Sci 2020;1157:122160.
11. Ramadon D, Courtenay AJ, Permana AD, Tekko IA, McAlister E, McCrudden MT, *et al*. A sensitive HPLC-UV method for quantifying vancomycin in biological matrices: Application to pharmacokinetic and biodistribution studies in rat plasma, skin and lymph nodes. J Pharm Biomed Anal 2020;189:113429.
12. Milla P, Ferrari F, Muntoni E, Sartori M, Ronco C, Arpicco S. Validation of a simple and economic HPLC-UV method for the simultaneous determination of vancomycin, meropenem, piperacillin and tazobactam in plasma samples. J Chromatography B Analyt Technol Biomed Life Sci 2020;1148:122151.
13. Yévenes K, Pokrant E, Trincado L, Lapierre L, Galarce N, Martín BS, *et al*. Detection of antimicrobial residues in poultry litter: Monitoring a risk through a selective and sensitive HPLC-MS/MS method. Animals (Basel) 2021;11:1399.
14. DelGuidice CE, Ismaiel OA, Mylott WR Jr., Halquist MS. Comparison of methods for quantitative analysis of ranibizumab and bevacizumab in human plasma using various bioanalytical techniques, including microfluidic immunoassay, triple quadrupole, and high-resolution liquid chromatography-tandem mass spectrometry approaches. J Pharm Biomed Anal 2022;217:114823.
15. Qi B, Gijsen M, Van Brantegem P, De Vocht T, Deferm N, Abza GB, *et al*. Quantitative determination of colistin A/B and colistin methanesulfonate in biological samples using hydrophilic interaction chromatography tandem mass spectrometry. Drug Test Anal 2020;12:1183-95.
16. Wang X, Chen Z, Ke X, Wang Y, Hu L, Tang C. Comparison of HPLC-DAD and UPLC-MS/MS in monitoring serum concentration of lamotrigine. Curr Pharm Anal 2022;18:449-54.
17. Khalikova M, Kočová Vlčková H, Lhotská I, Hadysová Z, Vokřál I, Červený L, *et al*. Determination of antiviral drugs and their metabolites using micro-solid

phase extraction and UHPLC-MS/MS in reversed-phase and hydrophilic interaction chromatography modes. Molecules 2021;26:2123.
18. Li P, Gong Y, Kim J, Liu X, Gilbert J, Kerns HM, *et al*. Hybridization liquid chromatography-tandem mass spectrometry: An alternative bioanalytical method for antisense oligonucleotide quantitation in plasma and tissue samples. Anal Chem 2020;92:10548-59.
19. Feliu C, Konecki C, Candau T, Vautier D, Haudecoeur C, Gozalo C, *et al*. Quantification of 15 antibiotics widely used in the critical care unit with a LC-MS/MS system: An easy method to perform a daily therapeutic drug monitoring. Pharmaceuticals 2021;14:1214.
20. Fage D, Brilleman R, Deprez G, Payen MC, Cotton F. Development, validation and clinical use of a LC-MS/MS method for the simultaneous determination of the nine main antituberculosis drugs in human plasma. J Pharm Biomed Anal 2022;215:114776.
21. Zheng X, Jongedijk EM, Hu Y, Kuhlin J, Zheng R, Niward K, *et al*. Development and validation of a simple LC-MS/MS method for simultaneous determination of moxifloxacin, levofloxacin, prothionamide, pyrazinamide and ethambutol in human plasma. J Chromatogr B Analyt Technol Biomed Life Sci 2020;1158:122397.
22. Abouzid M, Kosicka-Noworzyń K, Karaźniewicz-Łada M, Rao P, Modi N, Xie YL, *et al*. Development and validation of a UPLC-MS/MS method for therapeutic drug monitoring, pharmacokinetic and stability studies of first-line antituberculosis drugs in urine. Molecules 2024;29:337.
23. Pandey S, Dhanani J, Lipman J, Roberts JA, Wallis SC, Parker SL. Development and validation of LC-MS/MS methods to measure tobramycin and lincomycin in plasma, microdialysis fluid and urine: Application to a pilot pharmacokinetic research study. Clin Chem Lab Med 2020;58:274-84.
24. Ramirez S, Scapaticci M, Barbella F, Panico MM, Fecca IA, Cocchini B, *et al*. Development of a rapid LC-MS/MS method for simultaneous quantification of ten commonly used antibiotic drugs in human serum. J Pharm Biomed Anal 2024;244:116119.
25. Alam P, Ezzeldin E, Iqbal M, Mostafa GA, Anwer MK, Alqarni MH, *et al*. Determination of delafloxacin in pharmaceutical formulations using a green RP-HPTLC and NP-HPTLC methods: A comparative study. Antibiotics (Basel) 2020;9:359.
26. Zhu X, Li L, Dai B, Liu Z, Wang Z, Cui L, *et al*. A simple and rapid LC-MS/MS method for the quantification of nirmatrelvir/ritonavir in plasma of patients with COVID-19. Int J Anal Chem 2024;2024:6139928.
27. Roenfanz HF, Nicolau DP, Kuti JL. Quantification of sulbactam and durlobactam in saline and human plasma via ultra-performance liquid chromatography tandem mass spectrometry. J Chromatogr B Analyt Technol Biomed Life Sci 2025;1261:124654.
28. Abouelhassan Y, Shen Y, Chen A, Ye X, Nicolau DP, Kuti JL. *Ex vivo* assessment of sulbactam-durlobactam clearance during continuous renal replacement therapy to guide dosing recommendations. Antimicrob Agents Chemother 2025;69:e0167423.
29. Li WZ, Wu HL, Chen YC, Guo BN, Liu XF, Wang Y, *et al*. Pharmacokinetics, pharmacodynamics, and safety of single- and multiple-dose intravenous ceftobiprole in healthy Chinese participants. Ann Transl Med 2021;9:936.
30. Llopis B, Bleibtreu A, Schlemmer D, Robidou P, Paccoud O, Tissot N, *et al*. Simple and accurate quantitative analysis of cefiderocol and ceftobiprole in human plasma using liquid chromatography-isotope dilution tandem mass spectrometry: Interest for their therapeutic drug monitoring and pharmacokinetic studies. Clin Chem Lab Med 2021;59:1800-10.

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