International Journal of Biotechnology and Microbiology
www.biotechnologyjournals.com
Online ISSN: 2664-7680
Received: 26-01-2026, Accepted: 27-02-2026, Published: 13-03-2026
Volume 8, Issue 1, 2026, Page No. 64-74

# Advances in understanding bacterial and parasitic pathogens: From molecular mechanisms to clinical applications

**Luma abdullatef S N[1], Manal M Al Obaidi[2], Rahma Mozahim Al Attar[3]**
[1] College of Physical Education and Sports Science, Hamdaniya University, Mosul, Iraq
[2] Department of Biology, College of Education for Pure Sciences, Hamdaniya University, Mosul, Iraq
[3] Department of Medical Laboratories, Northern Technical University, Mosul, Iraq
**Corresponding Author:** Luma abdullatef salloum

**Abstract**
The novel technologies in the understanding of bacterial and parasitic pathogens has deepened out insight in molecular and clinical detail of these organisms and their pathogenic behavior. The goal of the current review is to analyze and present recent knowledge of the clinical and molecular intricacies of such pathogens and their hosts. The focus is on the genetics, biochemistry, and immunology of the infection and the subsequent survival of bacteria and parasitic organisms within the host and the defense mechanisms mounted against them. Also, we analyze the mechanisms developed by these pathogens toward the rational design of drugs, vaccines, and other diagnostics which target them. It is the intention of the article to present the latest available information on infection biology, molecular biology, genetics, and other branches of clinical research pertaining to pathogens for direct bedside use. We strongly emphasize the need for collaboration between clinical and basic researchers to address the rising problem of pathogens and other sophisticated infectious organisms in clinical practice.

**Keywords:** Bacterial pathogens, Parasitic pathogens, Infection biology, Molecular genetics, Drug and vaccine development

## Introduction

For the purpose of global health concerns, divisions of microbiology conduct studies on parasitic and bacterial pathogens. Novel and resurgent infections, the growing population of resistant pathogens, and the need to contain emerging threats all magnify the urgency to profile and assess these microorganisms [1]. As shown by the vitally important work carried out by molecular imaging, next-generation sequencing, and CRISPR biology, the biology of pathogens and their hosts utilizes concealed mechanisms of the host-pathogen relationship which, until now, remain unexplored [2]. This review seeks to disentangle such threads, molecularly articulate them, and offer pathways to reframe the clinically irrelevant and outdated concepts of the relationship in more clinically pertinent frames.

Disabling the immune response and successfully invading the host are the bacteria and parasites of highest public health concern. Beyond mere academic pursuit, it is the conceptually marvelous molecular design and construction necessary to define the different infectious pathologies, the science of new therapies, and rational vaccine development. Within the host-pathogen interface, there exists diabolical systems of the pathogen pathways which a pathogen has engineered for the sole purpose of survival and growth [3]. There has been a surge of interest in the uncontrolled systems of the indigenous organisms and the defeated pathogens [4].

The escalating danger from infections caused by bacteria and parasites is aggravated by the even faster-AMPLIFICATION rate at which these agents develop resistance to treatments [5]. Antimicrobial resistance (AMR) is now garnering the attention of world leaders because classic antibiotics and several regimes of antiparasitics have now made these treatments useless. Resistance at all levels of the clinical approach to treatment deepens the prevailing infection and mortality rates and at the same time increases the cost and toxicity of the treatment, and the agents which are used impose even more suffering [6]. The epidemiological surveillance which combines spine the pathways of infection and the resistance genomics is for that reason the only way of constructing the procedural and instrumental arsenal of which the world is left for its final and absolute defense [7].

**This review aims to fulfil a set of interrelated objectives.**

- Provide a synthesis of new findings resolving parts of molecular biology underpinning the virulence of bacteria and parasites.
- Analyse pathways of pathogenesis, focusing on the molecular crosstalk of the host–pathogen interface.
- Assess the emerging biological findings on earlier and more precise diagnosis, novel
- therapeutic frameworks, and more rationally designed vaccines.
- Also analyse some specific gaps in contemporary evidence and on that basis suggest a set of promising research directions to contain the unfolding resistance pandemic and protect the at-risk populations.

## Importance

The synthesis of the most recent findings concerning damaging bacteria and parasites make this review a crucial tool to researchers at the public health level, clinicians at the frontline, and science policymakers. The synthesis makes an explicit link of further molecular developments to clinical reality, allowing for a grasp of the concept ‘from bench to

bedside'. The main purpose is to relocate the peer-reviewed advancement on the control of pathogens and associated diseases to a context where it can greatly benefit from the lab-centric knowledge and, in turn, impact the real world.

**Methodology**

We will focus our literature review on articles published on PubMed, Scopus, and the Web of Science. To maintain contemporaneity, data published in the last five years will be considered. The chosen texts will also be organized in such a way as to create a coherent narrative.

**Scope of the Review**

**Molecular Mechanisms of Pathogenesis**

Certain parasites and some bacteria and their complex mechanisms for penetrating a host and optimizing their adhesive and invagination phases and control over signaling windows have been partially clarified using molecular biology techniques [8].

With regard to bacterial infections, the first step in the colonization of a host is the adhesion step which is accomplished due to surface located proteins termed 'adhesins' which bind to the receptors on the surface of a host cell. One example is the colonization of the uroepithelium and urinary tract infection (UTI) caused by *E. coli*. There are extremely sophisticated techniques developed by pathogens for invasion and control of a host cell [9]. The cells of certain bacteria, such as Salmonella, undergo an invasive phase during which a cytoplasmic to epithelial cell membrane Type III secretion system (T3SS) is activated, which aims to inject effector proteins into the cell while concurrently integrating a molecular system that restructures the cortical cytoskeleton [10]. In particular, some parasitic infections such as that of Plasmodium spp. target erythrocytes and evade host immunological defenses, and perforate host cell membranes through the action of specific proteins such as the circumsporozoite protein (CSP) that catalyzes membrane fusion and entry [11].

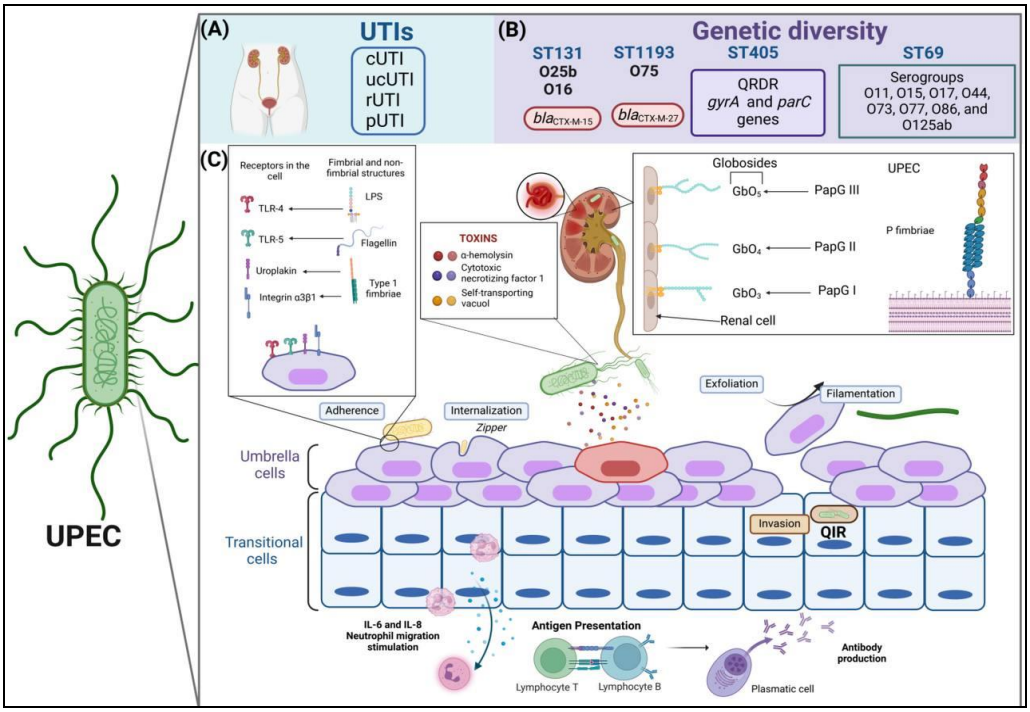


**Fig 1:** Molecular mechanism of pathogenesis of UTI caused by *E. coli*. [12].

As soon as an invasion happens, both bacterial and parasitic pathogens manipulate specific host cell signaling pathways to ensure conditions that are advantageous for their survival, reproduction, and replication [13]. For example, some bacteria can take control of host signaling cascades for immune suppression, such as the mitogen-activated protein kinase (MAPK) pathway [14]. Recent research has followed the way in which Listeria monocytogenes avoids host defenses, in particular, controlling the expression of some pro inflammatory cytokines via the activation of certain MAPK pathways. It, in turn, ensures that the bacteria escape the priming of immune response, and thus, ensures that the normal immune response is disrupted for the sake of sustained bacterial infection and survival [15].

There are also parasites. They, too, have developed their specific methods of manipulating host cell signaling. The Tier–1–Trypanosoma brucei complex–which causes African sleeping sickness, shifts signaling equilibrium in the host's immune system by modulating certain responses to the phosphoinositidase 3 kinase (PI3K) immune pathway. In so doing, there is a reduction in the activation of immune effector cells. It is another method by which the parasite escapes detection and destruction by immune cells [16]. Moreover, recent studies have shown some parasites can induce apoptosis of the host immune system, therefore, acting to diminish the overall immune competence of the host [17].

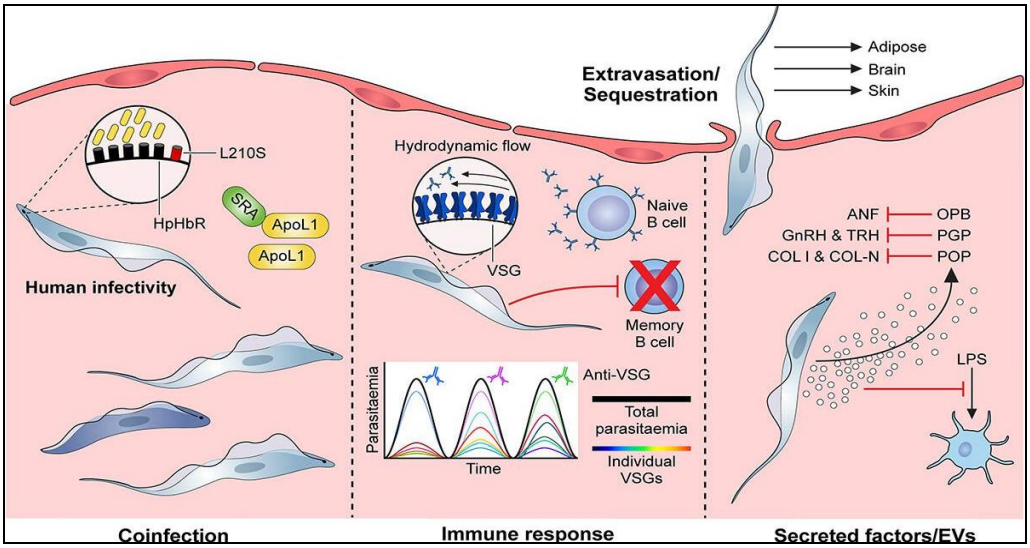


**Fig 2:** Overview of pathogenesis of African sleeping sickness by *T. bruceii* [18].

A host with immune cells can simultaneously possess exosomes—membranous structures which along with proteins, RNA, and small vesicles, are released by both cells. The relationship of pathogens with exosomes is an intricate one. Exosomes from infected cells can change the behavior of surrounding uninfected cells which is an indirect form of transmitting an infection that can influence its impact even in the absence of direct contact with pathogens [19]. Recent research indicates that exosomes containing pathogen–derived molecules from infected macrophages can modulate immune responses in the surrounding tissues [20].

Considering various mechanisms, the role of microbiota in host-pathogen interactions has been analyzed. Microbiota in the intestines can modify the risk of infection by changing immune responses, changing immune modulating pathogen, changing pathogen nourishments, and suppressing immune responses pathogenically. Studying interactions is critical for the development of new treatment strategies that improve host defense, or selectively target the pathogen interaction pathways [21].

**Immune Evasion Strategies**

Antigens for several species of bacteria and unrefined organisms as discussed in some of works focuses on secretsystem along on modulatory factors and antigenic variation as complex strategies of immune evasion [22]. In antigenic variation, there has been evidence for antigenic 'cloak'' mechanism allowing some surface antigen to be expressed and evaded by the immune defences of the host. For instance, the malaria causing protozoa *Plasmodium falciparum* exhibits wide spread complex antigenic variation on the surface of the acrassin PfEMP1 due to the expansion of many member in the var gene subsystems. Such escape mechanism enables the parasite to change surface proteins and attach to the neutralizing antibodies, leading to persistent infection which is very difficult to manage [23]. In much the same way, Neisseria gonorrhoeae has been shown to sustain infection of host under immune pressure by the alteration of its pili and outer membrane proteins [24].

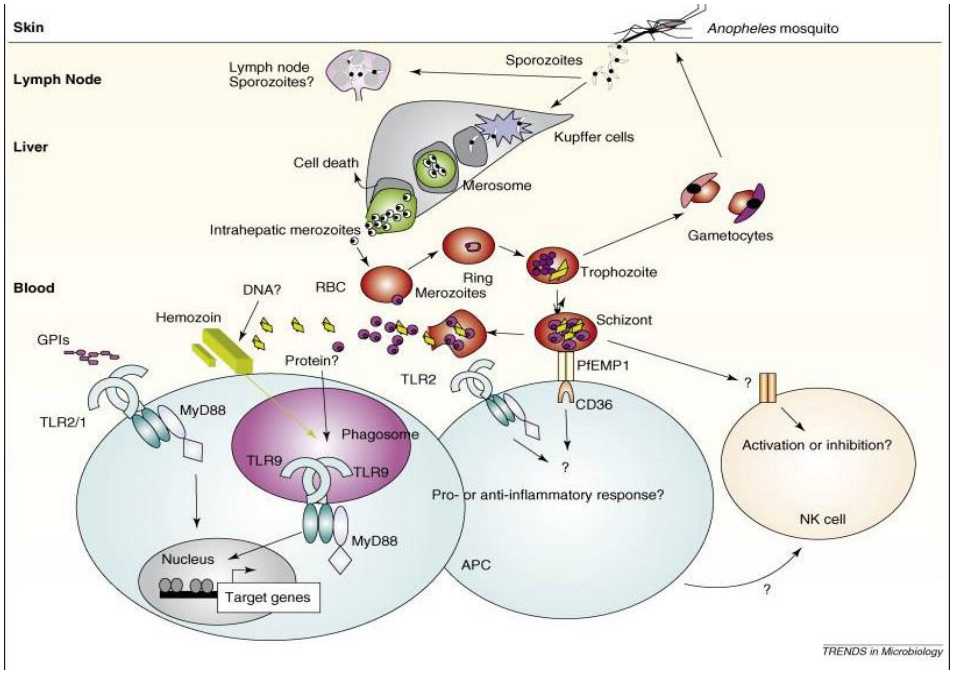


**Fig 3:** Invasion and manipulation of host innate immune responses by the *P. Falciparum* [25].

Novel findings in genetics have solved the mysteries of how these changes occur through genetic recombination and subsequent epigenetic alterations due to the immune pressure of the host [26]. Apart from antigenic variation, numerous pathogens possess specialized secretion systems that enable the direct dislocation of effector molecules to host cells, modulating their immune systems for their benefit [27]. A prototypical case is the type III secretion system, a nanomachine found in Salmonella, Shigella, and a handful of other pathogens-lineage that successfully siphons and injects a battery of virulence factors, each engineered to hijack specific host molecular circuits.

Within Salmonella, the effector protein SopE selectively pries open the Rho GTPases of the host cell, causing pro-cytoskeletal rearrangements that practically roll out the red carpet for the invader, while simultaneously muffling pro-inflammatory signals. This choreography not only secures a foothold for the virulent strain but lights the fuse for chronic infection, as confirmed in the literature [28].

Independent studies have uncovered a svelte yet clever novel strategy adopted by some pathogens which now encase multiple virulence factors within exosomes—tiny packets of host cell material captured and excreted by pathogens themselves—essentially "sending out" a preemptive memo to neighboring, uninfected target cells, teaching them how to evade immune detection long before the pathogens arrive on the scene [29]. The Fc region of antibodies is bound by protein A excreted by S. aureus, thereby preventing subsequent phagocytosis by immunocytes. Such an example of immunomodulation does not only target the host's immune system. Take the case of M. tuberculosis, which illustrates the point. It uses the intricate signaling pathways of macrophages to gain immune evasion in order to survive and replicate within those immune cells for extensive periods of time. Such examples demonstrate the complex nature of these problems that can suggest the formulation of new approaches for potentiating immunotherapy [30].

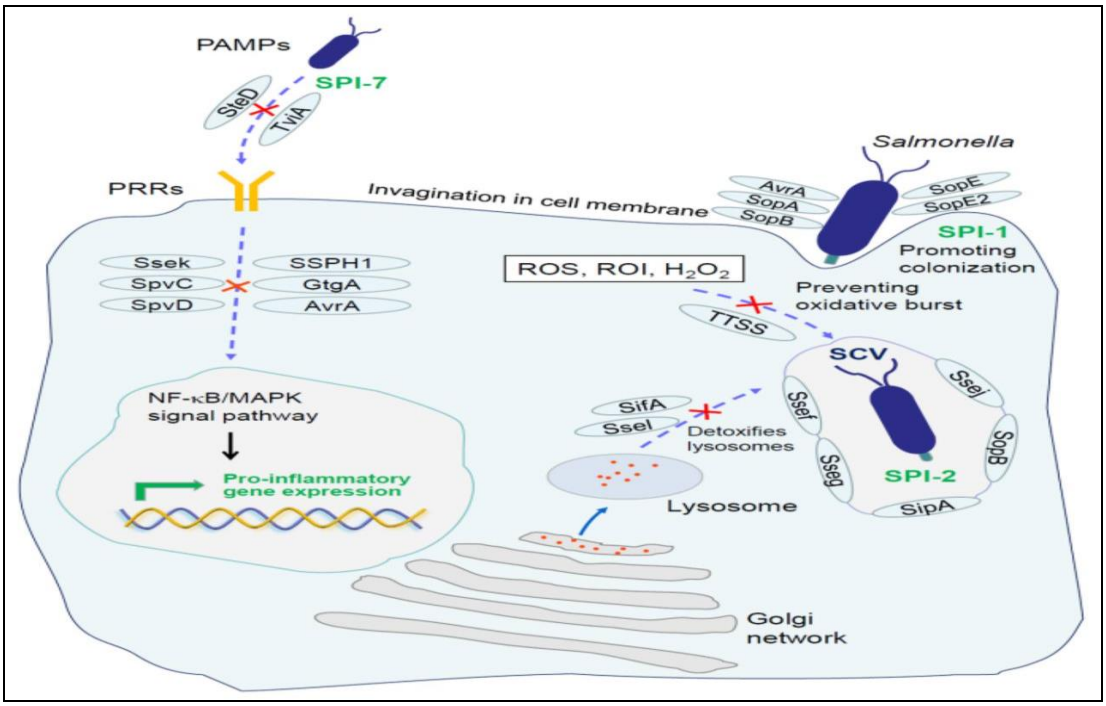


**Fig 4:** Host Immunity Escape by Salmonella Spp. [31].

The host and pathogen relationship and the various ways by which an organism survives exploit its host is easily understandable and is common knowledge. This, however, is the inspiration for the efforts made to improve the range of a vaccine and therapeutic efficacy aimed at augmenting host defenses to prevent if not entirely avoid infections. Prophylactic evolution and adaptations are still the main focus on the less investigated aspects of the relationship between host pathogen cross. This is an active field of research that highlights the necessity for interdisciplinary collaboration spanning the fields of biology, immunology and genomics, to address the critical issues concerning immune evasion by a multitude of pathogens [32, 33].

**Resistance Mechanisms**

The last few years have brought an understanding to very sophisticated approaches taken by parasites and bacteria in pathogen resistance to antibiotics and antiparasitic agents in terms of the molecular basis of resistance and the necessary environmental factors for the development of resistance [1]. The resistance of bacteria is most of the time the consequences of spontaneous mutations, horizontal gene transfer, and the geneic and environmental selective pressures driving the use of antibiotics. For instance, the lateral transfer of resistance plasmids is recorded within and between bacteria and facilitates the very rapid dissemination of beta-lactamase production, the ability to resist penicillins and penicillin derivatives [34]. Research Gate published a paper in which they explained how the capture of mobile genetic elements permits pathogenic strains of *E. coli* to respond to selective antibiotic pressures characteristic of many clinical environments very quickly [35]. Furthermore, subtherapeutic and over a long time antibiotic use in farming, and other environmental restrictions, are even more important as they form reservoirs of resistant bacteria to enter the human population [36].

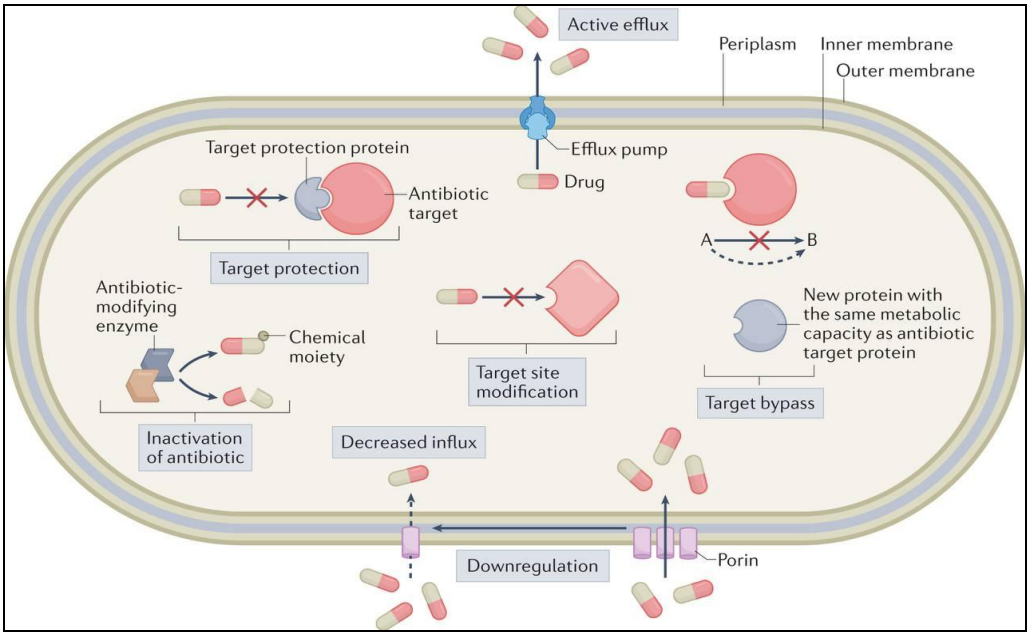


**Fig 5:** Mechanisms of Antibiotis Resistance by Bacteria. [37].

In parasitology, the recent investigations done on the mechanisms of resistance of the parasites of the genus *Plasmodium falciparum* and species of Leishmania to antiparasitic agents have been very intensive. Resistance to antifolates has been attributed to the mutations in some crucial bioreductases like dihydrofolate reductase in Plasmodium [38, 39]. In addition to these, the availability of these compounds and restricted movement of the vectors of these parasites are also very important in resistance. A deeper analysis was published in the Lancet Infectious Diseases which suggested that temperature shifts and changes in population dynamics of specific vectors can induce stress response among parasites which may help them persist and develop resistance [40].

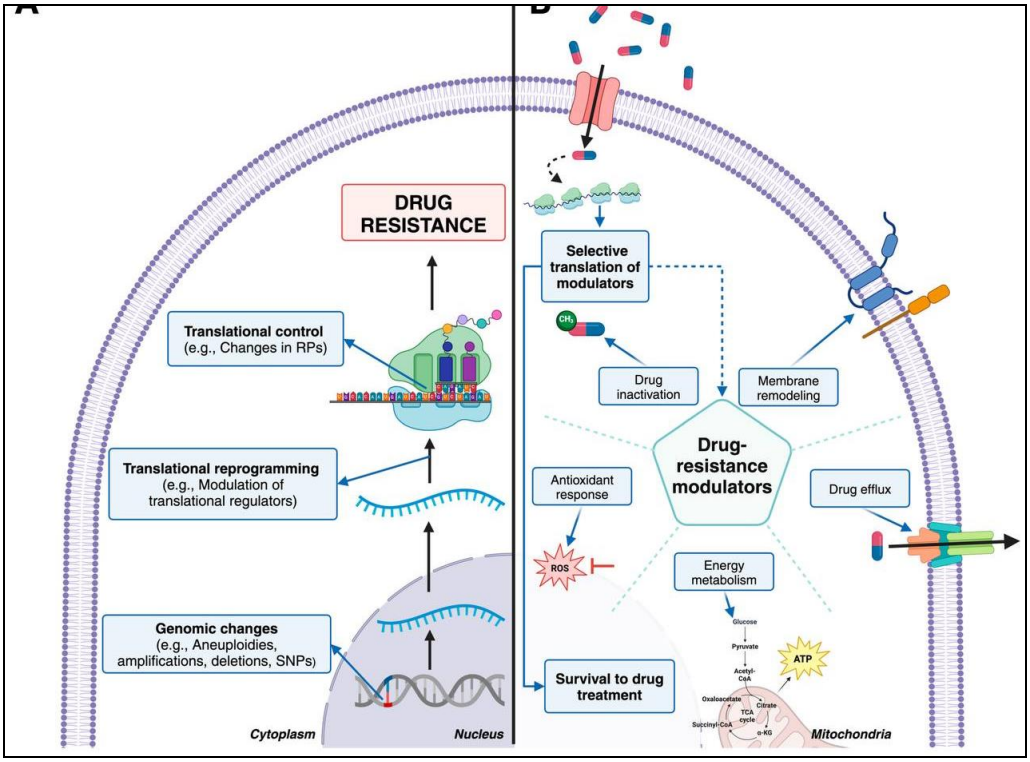


**Fig 6:** Molecular Mechanisms of Drug Resistance in Leishmania Spp. [41]

Bacteria biofilms can protect biofilm populations from immune responses and defensive host focused therapy, which is why biofilms and biofouling are being researched [42]. Advances in genomic science enable tracking of certain genes and regulatory circuits dealing with muster-up anticipation response to Earth\u2019s perpetual changes. Targeting GIs of resistant subcultures indicates extrinsic forms of resistance, needing further study. The genetically and ecologically distributed are subordinate- resistance components can formulate the scaffold of intervention which integrates new microsystems, redirectioned compounds, and opt systems that manage to reduce the

steering pressure on resistant populations. Bacteria resistance is syndrome with societal plights that necessitate a converging response from public health, microbiology, and epidemiology. Interdisciplinary collaboration allows tracking of resistance mechanisms and their epidemiology regarding the new and old interventions. Maintaining resistance, a moving target, highlights the importance and urgency with which cross-disciplinary, joint collaboration is pursued. Synthesis of theory and practice on the same framework, combine organized, laboratory approaches and complex, field tactics. The further development of resistance and the effectiveness of future, long-term interventions will be ensured with this integrative approach [43, 44].

## Clinical Applications

### Diagnostics

The integration of molecular diagnostics has revolutionized the identification of specific bacteria and parasites [45]. Conventional microbiology, relying heavily on culture, not only consumes several days but also inefficiently represents the full microbial spectrum of clinical specimens [46]. Modern approaches—polymerase chain reaction (PCR), next-generation sequencing (NGS), and loop-mediated isothermal amplification (LAMP)—offer superior sensitivity and specificity, with considerably shorter turnaround times [47]. A pertinent illustration can be found in a recent Nature Microbiology report, which employed multiplex PCR assays that enable simultaneous detection of multiple pathogens from a single specimen. This allows faster turnaround times at clinical sites, enabling speedier intervention. Onsets of sepsis illustrate the impact best, when rapid identification of the causative organism can markedly improve clinical outcomes [48]. Recent advances give laboratories the ability to perform comprehensive metagenomic studies on clinical samples through NGS, thereby enabling untargeted retrieval of both bacterial and parasitic DNA [49]. A notable demonstration published in The Lancet Infectious Diseases shows NGS unveiling hidden pathogens in cases where conventional methods usually fail, broadening the range of diagnostics and guiding therapy in complex infections [50]. Beyond the laboratory, the development of portable, molecular diagnostics allows molecular assays to move to the bedside, or even to remote or under-resourced settings, thus accelerating the overall diagnostic cascade [51].

For parasitic diseases—particularly malaria and schistosomiasis—rapid diagnosis is essential for guiding effective treatment. Recent trailing evidence shows that LAMP-based tests are now able to detect Plasmodium species with the speed and specificity needed to enable prompt therapy [52]. Molecular diagnostics are also crucial for monitoring antimicrobial resistance (AMR). Studies employing whole genome sequencing (WGS) have successfully traced resistance determinants in key bacterial pathogens, allowing for tailored therapeutic and public health responses [53]. The utility of genomic surveillance is reinforced in a review from Clinical Microbiology, which indicates that longitudinal sequencing provides a time-resolved view of AMR dynamics, thereby informing targeted control strategies [54]. Parallel advancements in bioinformatics, where sequencing data are processed and interpreted with efficient pipelines, have accelerated turnaround time for clinicians. The latest enhancements stem from integrating artificial intelligence and machine learning, which harness predictive algorithms to extract diagnostic signals from genomic profiles, thereby further increasing accuracy and speed in identifying infectious agents. As these technologies are advancing, they have the potential to change clinical diagnostics with personalized medicine approaches, adjusting treatment according to the pathogens found in the individual patient [55]. In general, the studies support the steam of a rapid and comprehensive change, innovative diagnostic approaches that improve patient care and support public health efforts by managing the rapid and effective treatment of bacterial and parasite infections. The increasing use of molecular diagnostics means more research to overcome these barriers, including the standardization of the protocols, minimizing the costs, and increasing the availability of the methods to secure a foothold in clinical use [56].

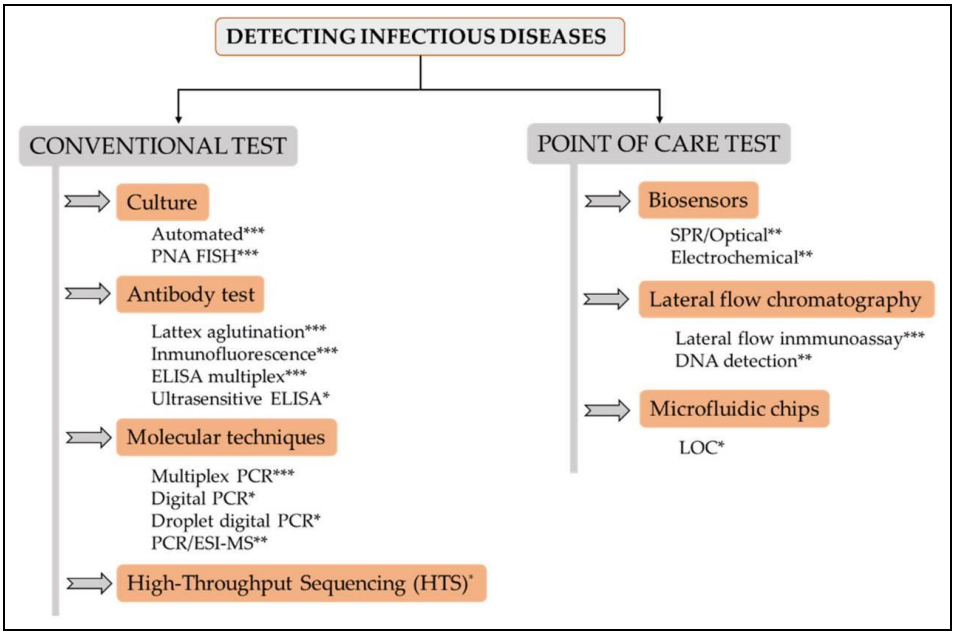


**Fig 7:** Conventional and Developed Diagnostic Approaches of Infectious Diseases [57].

**Therapeutics**

The latest advancement in vaccine development focuses on the molecular biology of the pathogen in developed more precise and effective approaches to immunization. A case in point, published in Nature, highlights the significance of structural biology in finding and characterizing immunodominant epitopes on the surfaces of selected bacteria. In one example, cryo-electron microscopy was used to determine the 3D structures of the outer membrane proteins of Neisseria meningitidis and vaccine candidates that could drive protective immunity to be targeted. The development of subunit vaccines on these cross-reacting antigens has been shown to improve the immunogenicity of the vaccines [58]. Furthermore, reverse vaccinology is revolutionizing how researchers mine pathogen genomes for promising vaccine targets. A pivotal research article in Frontiers in Immunology [59] illustrates this clearly. By analyzing the complete genomic dataset of Streptococcus pneumoniae, the team uncovered previously uncharacterized surface proteins. These candidate antigens possess the potential to enhance the immunogenicity of existing pneumonia vaccines and to guide the design of entirely new formulation strategies.

Single infections caused by parasites are now known to benefit clearly from molecular biology tools in vaccine design. A recent illustrated analysis from the Journal of Infectious Diseases centred on combating the protozoan *Plasmodium falciparum*, the visual perpetrator of malaria. Inspecting the complete proteome of the parasite, the authors focused on select antigens that drive critical transitions in the parasite stage while also guiding immune evasion. The Addressing Immune Responses multilayered vaccine design incorporates several parasite stages and increases immune signals to promote a broader, deeper, and longer lasting protective response as shown through a proteomic approach [60]. Adjuvants, a class of microscopic diversifying immune response steering modulators, significantly impacted the design's overall effectiveness. Confirming this evidence, a recent publication in Nature Communications describes how certain novel adjuvants actively target and prime specific TLRs to markedly augment the cellular immune response to parasites [61].

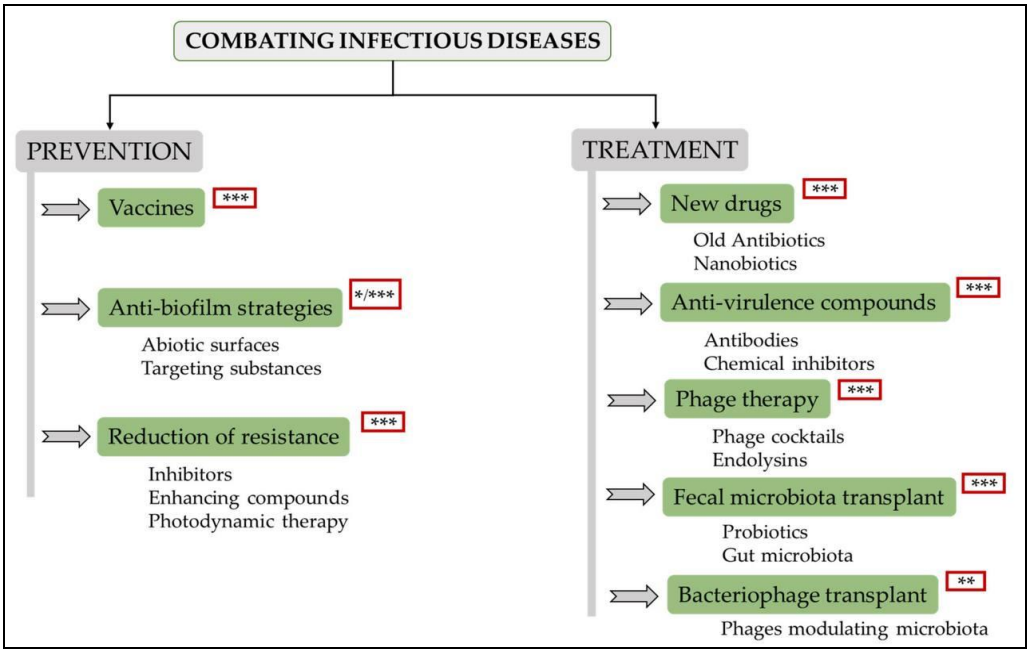


**Fig 8:** Novel Strategies for Combating Infectious Diseases [57].

Likewise, novel approaches to vaccine development using nanoparticle formulations have been introduced to address bacterial and parasitic infections. For example, a recent publication in Nature Nanotechnology describes the enhanced immunogenicity and immune response to the subcutaneous implantation of biodegradable leptin-releasing peptide nanoparticles conjugated to Leishmania antigens [62]. Rather. More precisely, my intent is to augment immune response by improving the stabilization, retention, and targeted delivery of the antigen to the presenting cells. The construction of the pathogen like nanoparticles greatly increases the stimulation of strong and sustained humoral and cellular responses critical for effective immunization against complex, persistent pathogens such as those in bacterial and parasitic infections [63].

The interest in personalized vaccine strategies is also on the rise. This is particularly true in the case for vaccine strategies that seek to subdue the heterogeneity of bacterial and parasitic infections. New research has proved that vaccines that incorporate specific antigens to particular strains of mycobacterium tuberculosis have proved to be more effective in a disease that poses a major challenge due to the presence of varying genetic mycobacterial strains [64]. In a research published in Cell Reports, it was demonstrated that diverse immunogenic components in a vaccine that targets bacterial infections provide more effective control over a bacterial infection [65].

**Vaccine Development**

Innovative ways of dealing with bacterial infections involves determining particular molecules that could be useful in developing therapeutics. One of the many bacterial infections is Pseudomonas aeruginosa, this particular pathogen is well-known for being extremely multi-drug resistant. In one of the latest studies published in Nature, it was found that there are inhibitors that target the

mechanisms that are used for the bacteria to Quorum Sensing [66]. The researchers were able to lower bioflim formation and increase the effectiveness of the antibiotic by improving the systems that moderated the bacterial systems that produced factors for the virulence biofilms. This shifts the paradigm of how antibiotic resistance can be countered, and lays the foundation for new Antiobiotic Combination Therapy (ACT) approaches that maximize clinical outcomes [67]. The malaria-causing parasite, *Plasmodium falciparum*, is able to thrive and multiply due to the inhibition of the glycolistic stage. In one of the recent studies the researchers used high-throughput screening methods to analyze ways of targeting the metabolic web of the *Plasmodium falciparum*. Combating complex eukaryotic pathogens through direct metabolic targeting therapy is a promising strategy [68]. A recent report in Cell Host & Microbe illustrates the paradigm shift toward harnessing the host immune system for infection control, rather than relying solely on external agents. Employing targeted immunomodulation, the team observed that activating specific immune pathways markedly improved survival in S. aureus-infected mice. By steering the immune response rather than delivering outright cytotoxic compounds, the intervention promotes a durable host defence without outright permitting pathogens direct exposure to damaging agents. This durable enhancement aligns with the emerging vision of infection management wherein the host immune system itself becomes the lead protagonist [69]. Parallel advances arrive from CRISPR technology, which has proven capable of precise gene editing in intracellular pathogens. A paper in Science documents the first effective deployment of the CRISPR-Cas9 platform against the Mycobacterium tuberculosis genome in the host cell. By disrupting critical genes, the system reduced bacterial replication in infected macrophages, underscoring the potential of genome editing to curate pathogen biology from within the host without widespread tissue damage. Collectively, these approaches point toward a future where sophisticated, self-resustained host defences—modulated, educated, and even sculpted through genetic precision—serve as the frontline against infection, auguring a new era of clinical intervention in which the anticipated reliance on conventional antibiotics is either limited or entirely circumvented and the hist tissue remains the primary focus of protective intervention [70].

The Massachusetts Institute of Technology researchers used synthetic phage therapeutics to resolve antibiotic resistant *E. coli* infections by resolving antibiotic insensitive infections in preclinical models while re-establishing sensitivity. Phage therapy might be an answer to the waning efficacy of antibiotics. The evidence supports paradigm shifts seeking an antibiotic of specific therapeutic and molecular action abstracted to the studied bacteria and parasitic organisms [71]. Batched epitheliotropic small molecular weight antimicrobial agents, manipulators of metabolic cascades, immunotherapy agents, gene therapy, and antibiotics to phage sensitive bacteria therapeutics represent paradigm shifts in infection control practices. Phage therapeutics and bacteria control offers the most pressing solutions to infection. These modified approaches can amplify treatment efficacy, overcome antimicrobial treatment failures, conserve antimicrobial agents shielding therapeutic potentials, and combat rising resistance to newly emerging antimicrobial resistant infections [5].

**Perspectives**

Step by step analysis is revealing substantial holes in the biology, the one-handed mechanistic interaction, and the crystal interfaces of known pathogenic organisms and their systems of resistance [59]. Probably the most exciting nudges to the bench is the microbe-held universe in the gut and the skin: there are new reports which aim to tighten the threads to the technicolor ways the microbiota orient and sometimes reorient the human immune and other physiological surrenders to bacterial, fungal, and protozoal invasions. Nature Reviews Microbiology published that the gut microbiota could be one of the factors to one's susceptibility to infections which suggests there are therapeutic targets to enhance resistance to diseases managed by the microbiome [72]. However, there are insufficient studies on the specific microbial communities and their metabolites that are protective against bacterial and parasitic infections [73]. Furthermore, new developments in single-cell sequencing technologies are transforming the understanding of the diversity of microbial communities and the immune response to the host, and vice versa. A recent publication in Cell that used single-cell RNA sequencing found novel immune cell subsets to Mycobacterium tuberculosis, illustrating the potential of targeting them for new therapeutic approaches. This technology could be used in parallel to understand the dynamics of interactions between a host and pathogen in multiple infections, delineating critical areas for future work [74]. Another exciting area is the use of CRISPR-based technologies for accurate gene targeting in pathogens and host cells [2].

Newer studies reported in Science have explored how CRISPR-Cas9 can induce lethality by targeting critical genes in *Plasmodium falciparum* and thus shutting down parasite life cycles [75]. Furthermore, building efficient platforms for quickly uncovering novel antimicrobial classes has become a pressing global need [76]. One promising approach, outlined in Nature Biotechnology, combines programmable robotics with software-guided high-throughput screening to probe resistant bacterial collections against a wide array of small molecules. While such automation can accelerate the acceleration of promising compounds, the remaining hurdle is bridging the gap to clinical relevance [77]. To complement this, a detailed mapping of the molecular circuitry underlying resistance remains essential, because rationally engineered inhibitors will only succeed if they match the specific mechanism being interrogated [78]. Yet even state-of-the-art molecular analysis can be eclipsed without the systematic application of advanced computation within microbiology. Algorithms are being developed to predict, several steps ahead, the microbial fate after exposure to a therapeutic, thereby illuminating the window for optimal intervention and informing decisions about future stewardship [79].

AI's capability to parse vast genomic datasets has proven instrumental in pinpointing both virulence determinant and resistance-conferring sequences, thereby reinforcing the argument that cutting-edge computational tools can supplement existing pipeline methodologies in infectious disease research [80]. Equally pressing, however, is the persistent shortage of advanced *in vivo* systems that mimic human infections in a credible manner. The majority of presently deployed experimental models fail to capture the nuances of human immunobiology or the multilayered pathogenesis associated with bacterial and parasitic

organisms. Hence the creation of refined systems—such as micro-engineered organ-on-chip platforms alongside genetically tailored animal models—promises to clarify host–pathogen interactions and furnish a rigorous testing ground for emerging therapeutics [81]. To recapitulate, identified shortcomings in the sphere of bacterial and parasitic infections stand to gain from sustained exposure to contemporary and forthcoming technologies. A cohesive superstructure that melds microbiomic interrogation, single-cell transcriptomics, CRISPR-based editing, high-throughput phenotyping, computational data science, and next-generation *in vivo* models portends the emergence of innovative treatment paradigms. Deliberate and sustained allocation of resources to these domains is requisite, as it would deepen mechanistic understanding while delivering a validated scaffold for bespoke interventions capable of ameliorating the global threat of antibiotic resistance and enhancing patient recovery globally.

**References**


1. Ahmed SK, Hussein S, Qurbani K, Ibrahim RH, Fareeq A, Mahmood KA, *et al*. Antimicrobial resistance: Impacts, challenges, and future prospects. Journal of Medicine, Surgery, and Public Health.,2024:2:100081.
2. Xu Y, Le H, Wu Q, Wang N, Gong C. Advancements in CRISPR/Cas systems for disease treatment. Acta Pharmaceutica Sinica B., 2025.
3. Hitzler SU, Fernández-Fernández C, Montaño DE, Dietschmann A, Gresnigt MS. Microbial adaptive pathogenicity strategies to the host inflammatory environment. FEMS Microbiology Reviews.,2025:49:fuae032.
4. Tripathi D, Garg R. Host-pathogen crosstalk: implications in host cellular processes by intracellular pathogens. Frontiers in Microbiology.,2024:15:1508345.
5. Oliveira M, Antunes W, Mota S, Madureira-Carvalho Á, Dinis-Oliveira RJ, *et al*. An overview of the recent advances in antimicrobial resistance. Microorganisms.,2024:12(9):1920.
6. Muteeb G, Rehman MT, Shahwan M, Aatif M. Origin of antibiotics and antibiotic resistance, and their impacts on drug development: A narrative review. Pharmaceuticals.,2023:16(11):1615.
7. Muteeb G, Rehman MT, Shahwan M, Aatif M. Origin of antibiotics and antibiotic resistance, and their impacts on drug development: A narrative review. Pharmaceuticals.,2023:16(11):1615.
8. Murphy KN, Brinkworth AJ. Manipulation of focal adhesion signaling by pathogenic microbes. International journal of molecular sciences.,2021:22(3):1358.
9. Govindarajan DK, Eskeziyaw BM, Kandaswamy K, Mengistu DY. Diagnosis of extraintestinal pathogenic *Escherichia coli* pathogenesis in urinary tract infection. Current Research in Microbial Sciences.,2024:7:100296.
10. Worley MJ. *Salmonella* type III secretion system effectors. International Journal of Molecular Sciences.,2025:26(6):2611.
11. Sanyaolu A, Marinkovic A, Prakash S, Balendra V, Shazley O, Gardellini T, *et al*. Emerging Molecular Mechanisms in Malaria Pathogenesis and Novel Therapeutic Approaches: A Focus on *P. falciparum* Malaria. Biomolecules.,2025:15(7):1038.
12. García-García JD, Contreras-Alvarado LM, Cruz-Córdova A, Hernández-Castro R, Flores-Encarnacion M, Rivera-Gutiérrez S, *et al*. Pathogenesis and Immunomodulation of Urinary Tract Infections Caused by Uropathogenic *Escherichia coli*. Microorganisms.,2025:13(4):745.
13. Guillen N. Signals and signal transduction pathways in *Entamoeba histolytica* during the life cycle and when interacting with bacteria or human cells. Molecular microbiology.,2021:115(5):901-15.
14. Nandi I, Aroeti B. Mitogen-activated protein kinases (MAPKs) and enteric bacterial pathogens: a complex interplay. International Journal of Molecular Sciences.,2023:24(15):11905.
15. Shang L, Xiang W, Lun M, Qu S, Yin Y, Xu Y, *et al*. Recent Advances in Host Immune Mechanisms Against *Listeria monocytogenes* Infection. Journal of Inflammation Research., 2025, 10821-33.
16. Rashidi S, Mansouri R, Ali-Hassanzadeh M, Mojtahedi Z, Shafiei R, Savardashtaki A, *et al*. The host mTOR pathway and parasitic diseases pathogenesis. Parasitology Research.,2021:120(4):1151-66.
17. Sadr S, Sharifi I, Morovati S, Sepahvand H, Nazemian S, Bamorovat M, *et al*. An inclusive assessment of apoptosis mechanisms in *Leishmania* species: a narrative literature review. Current Research in Parasitology & Vector-Borne Diseases., 2025, 100260.
18. Morrison LJ, Steketee PC, Tettey MD, Matthews KR. Pathogenicity and virulence of African trypanosomes: From laboratory models to clinically relevant hosts. Virulence.,2023:14(1):2150445.
19. Cruz CG, Sodawalla HM, Mohanakumar T, Bansal S. Extracellular vesicles as biomarkers in infectious diseases. Biology.,2025:14(2):182.
20. Wang W, Qiao S, Kong X, Zhang G, Cai Z. The role of exosomes in immunopathology and potential therapeutic implications. Cellular & Molecular Immunology., 2025, 1-21.
21. Zeng J, He Z, Wang G, Ma Y, Zhang F. Interaction Between Microbiota and Immunity: Molecular Mechanisms, Biological Functions, Diseases, and New Therapeutic Opportunities. MedComm.,2025:6(7):e70265.
22. Turki H, Shamseddin J, Pournasrolla N, Kahrizi S, Kahrizi S, Kazemi E. Molecular and cellular aspects of medical parasitology: Insights into pathogenesis and host interactions. Cellular, Molecular and Biomedical Reports., 2025, 253-76.
23. Hadjimichael E, Deitsch KW. Variable surface antigen expression, virulence, and persistent infection by *Plasmodium falciparum* malaria parasites. Microbiology and Molecular Biology Reviews.,2025:89(1):e00114-23.
24. Walker E, Van Niekerk S, Hanning K, Kelton W, Hicks J. Mechanisms of host manipulation by *Neisseria gonorrhoeae*. Frontiers in microbiology., 2023, 14.
25. Coban C, Ishii KJ, Horii T, Akira S. Manipulation of host innate immune responses by the malaria parasite. Trends in microbiology.,2007:15(6):271-8.
26. Brennan RS, deMayo JA, Finiguerra M, Baumann H, Dam HG, Pespeni MH. Complementary genetic and epigenetic changes facilitate rapid adaptation to

multiple global change stressors. Proceedings of the National Academy of Sciences.,2025:122(29):e2422782122.
27. Zhou G, Zhao Y, Ma Q, Li Q, Wang S, Shi H. Manipulation of host immune defenses by effector proteins delivered from multiple secretion systems of *Salmonella* and its application in vaccine research. Frontiers in Immunology., 2023, 14.
28. Worley MJ. *Salmonella* type III secretion system effectors. International Journal of Molecular Sciences.,2025:26(6):2611.
29. Xiong J, Ashraf U, Ye J, Cao S. Extracellular vesicles in pathogenic infection, transmission, and immunity. Engineering.,2024:43:228-40.
30. Bear A, Locke T, Rowland-Jones S, Pecetta S, Bagnoli F, Darton TC. The immune evasion roles of *Staphylococcus aureus* protein A and impact on vaccine development. Frontiers in Cellular and Infection Microbiology., 2023, 13.
31. Wang M, Qazi IH, Wang L, Zhou G, Han H. *Salmonella* virulence and immune escape. Microorganisms.,2020:8(3):407.
32. Zhuang L, Yang L, Li L, Ye Z, Gong W. *Mycobacterium tuberculosis*: immune response, biomarkers, and therapeutic intervention. MedComm.,2024:5(1):e419.
33. Arevalo-Romero JA, Chingaté-López SM, Camacho BA, Alméciga-Díaz CJ, Ramirez-Segura CA. Next-generation treatments: immunotherapy and advanced therapies for COVID-19. Heliyon.,2024:10(5):e26423.
34. Galgano M, Pellegrini F, Catalano E, Capozzi L, Del Sambro L, Sposato A, *et al*. Acquired bacterial resistance to antibiotics and resistance genes: from past to future. Antibiotics.,2025:14(3):222.
35. Andryukov BG, Besednova NN, Zaporozhets TS. Mobile genetic elements of prokaryotes and their role in the formation of antibiotic resistance in pathogenic bacteria. Antibiot Khimioter= Antibiotics and Chemotherapy.,2022:67(1-2):62-74.
36. Trinchera M, De Gaetano S, Sole E, Midiri A, Silvestro S, Mancuso G, *et al*. Antimicrobials in Livestock Farming and Resistance: Public Health Implications. Antibiotics.,2025:14(6):606.
37. Darby EM, Trampari E, Siasat P, Gaya MS, Alav I, Webber MA, *et al*. Molecular mechanisms of antibiotic resistance revisited. Nature Reviews Microbiology.,2023:21(5):280-95.
38. Wicht KJ, Mok S, Fidock DA. Molecular mechanisms of drug resistance in *Plasmodium falciparum* malaria. Annual review of microbiology.,2020:74(1):431-54.
39. Bharadava K, Upadhyay TK, Kaushal RS, Ahmad I, Alraey Y, Siddiqui S, *et al*. Genomic insight of *leishmania* parasite: In-depth review of drug resistance mechanisms and genetic mutations. ACS omega.,2024:9(11):12500-14.
40. Ratcliffe NA, Mello CB, Castro HC, Dyson P, Figueiredo M. Immune reactions of vector insects to parasites and pathogens. Microorganisms.,2024:12(3):568.
41. Moncada-Diaz MJ, Rodríguez-Almonacid CC, Quiceno-Giraldo E, Khuong FT, Muskus C, Karamysheva ZN. Molecular Mechanisms of Drug Resistance in *Leishmania* spp. Pathogens.,2024:13(10):835.
42. Sharma S, Mohler J, Mahajan SD, Schwartz SA, Bruggemann L, Aalinkeel R. Microbial biofilm: a review on formation, infection, antibiotic resistance, control measures, and innovative treatment. Microorganisms.,2023:11(6):1614.
43. Zou Z, Tang F, Qiao L, Wang S, Zhang H. Integrating sequencing methods with machine learning for antimicrobial susceptibility testing in pediatric infections: current advances and future insights. Frontiers in Microbiology., 2025, 16.
44. Elshobary ME, Badawy NK, Ashraf Y, Zatioun AA, Masriya HH, Ammar MM, *et al*. Combating antibiotic resistance: Mechanisms, multidrug-resistant pathogens, and novel therapeutic approaches: An updated review. Pharmaceuticals.,2025:18(3):402.
45. Alsharksi AN, Sirekbasan S, Gürkök-Tan T, Mustapha A. From tradition to innovation: Diverse molecular techniques in the fight against infectious diseases. Diagnostics.,2024:14(24):2876.
46. Yakobi SH, Nwodo UU. Microbiological methodologies: Comparative evaluation of microbial community and enhanced antibiotic susceptibility testing. Electronic Journal of Biotechnology., 2025.
47. Xu J, Akhtar M, Meng W, Bai J, Prince S, Huang R. Advances in Pathogen Detection: From Traditional Methods to Nanotechnology, Biosensing and AI Integration. Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology.,2025:17(4):e70022.
48. Serapide F, Pallone R, Quirino A, Marascio N, Barreca GS, Davoli C, *et al*. Impact of Multiplex PCR on Diagnosis of Bacterial and Fungal Infections and Choice of Appropriate Antimicrobial Therapy. Diagnostics.,2025:15(8):1044.
49. Zhao Y, Zhang W, Zhang X. Application of metagenomic next-generation sequencing in the diagnosis of infectious diseases. Frontiers in Cellular and Infection Microbiology., 2024, 14.
50. Elbehiry A, Abalkhail A. Metagenomic Next-Generation Sequencing in Infectious Diseases: Clinical Applications, Translational Challenges, and Future Directions. Diagnostics.,2025:15(16):1991.
51. Aborode AT, Adesola RO, Scott GY, Arthur-Hayford E, Otorkpa OJ, Kwaku SD, *et al*. Bringing Lab to the Field: Exploring Innovations in Point-of-Care Diagnostics for the Rapid Detection and Management of Tropical Diseases in Resource-Limited Settings. Advances in Biomarker Sciences and Technology., 2025.
52. Jang WS, Choi MK, Choe YL, Lim CS. Development of a rapid malaria LAMP-MS assay for diagnosis of malaria infections. Scientific reports.,2025:15(1):8547.
53. Sherry NL, Lee JY, Giulieri SG, Connor CH, Horan K, Lacey JA, *et al*. Genomics for antimicrobial resistance progress and future directions. Antimicrobial agents and chemotherapy.,2025:69(5):e01082-24.
54. Kajumbula HM, Amoako DG, Tessema SK, Aworh MK, Chikuse F, Okeke IN, *et al*. Enhancing clinical microbiology for genomic surveillance of antimicrobial resistance implementation in Africa. Antimicrobial Resistance & Infection Control.,2024:13(1):135.
55. Hudu SA, Alshrari AS, Abu-Shoura EA, Osman A, Jimoh AO. A Critical Review of the Prospect of Integrating Artificial Intelligence in Infectious Disease

Diagnosis and Prognosis. Interdisciplinary Perspectives on Infectious Diseases., 2025, 2025(1).
56. Ryu H, Abdul Azim A, Bhatt PJ, Uprety P, Mohayya S, Dixit D, *et al*. Rapid diagnostics to enhance therapy selection for the treatment of bacterial infections. Current pharmacology reports.,2023:9(4):198-216.
57. Fernández L, Cima-Cabal MD, Duarte AC, Rodriguez A, García P, García-Suárez MD. Developing diagnostic and therapeutic approaches to bacterial infections for a new era: implications of globalization. Antibiotics.,2020:9(12):916.
58. Eslami M, Fadaee Dowlat B, Yaghmayee S, Habibian A, Keshavarzi S, Oksenych V, *et al*. Next-Generation Vaccine Platforms: Integrating Synthetic Biology, Nanotechnology, and Systems Immunology for Improved Immunogenicity. Vaccines.,2025:13(6):588.
59. Eslami M, Fadaee Dowlat B, Yaghmayee S, Habibian A, Keshavarzi S, Oksenych V, *et al*. Next-Generation Vaccine Platforms: Integrating Synthetic Biology, Nanotechnology, and Systems Immunology for Improved Immunogenicity. Vaccines.,2025:13(6):588.
60. Hashim O, Dimier-Poisson I. Computational vaccine development against protozoa. Computational and Structural Biotechnology Journal., 2025.
61. Zhao T, Cai Y, Jiang Y, He X, Wei Y, Yu Y, *et al*. Vaccine adjuvants: mechanisms and platforms. Signal transduction and targeted therapy.,2023:8(1):283.
62. Saleh M, El-Moghazy A, Elgohary AH, Saber WI, Helmy YA. Revolutionizing nanovaccines: A new era of immunization. Vaccines.,2025:13(2):126.
63. Márquez PG, Wolman FJ, Glisoni RJ. Nanotechnology platforms for antigen and immunostimulant delivery in vaccine formulations. Nano Trends., 2024, 8.
64. Barazani O, Erdos T, Chowdhury R, Kaur G, Venketaraman V. New Advances in the Development and Design of *Mycobacterium tuberculosis* Vaccines: Construction and Validation of Multi-Epitope Vaccines for Tuberculosis Prevention. Biology.,2025:14(4):417.
65. Lloren KK, Senevirathne A, Lee JH. Advancing vaccine technology through the manipulation of pathogenic and commensal bacteria. Materials Today Bio., 2024, 29.
66. Sathe N, Beech P, Croft L, Suphioglu C, Kapat A, *et al*. *Pseudomonas aeruginosa*: Infections and novel approaches to treatment “Knowing the enemy” the threat of *Pseudomonas aeruginosa* and exploring novel approaches to treatment. Infectious medicine.,2023:2(3):178-94.
67. Azeem K, Fatima S, Ali A, Ubaid A, Husain FM, Abid M. Biochemistry of bacterial biofilm: insights into antibiotic resistance mechanisms and therapeutic intervention. Life.,2025:15(1):49.
68. van Niekerk DD, du Toit F, Green K, Palm D, Snoep JL. A detailed kinetic model of glycolysis in *Plasmodium falciparum*-infected red blood cells for antimalarial drug target identification. Journal of Biological Chemistry.,2023:299(9).
69. Kashyap R, Tiwari S, Bhattacharya S. Innovative strategies in the fight against bacterial infections: Phage therapy, nanotechnology, and new antimicrobial agents for multidrug-resistant pathogens. Results in Chemistry., 2025, 102304.
70. Akter F, Kumar S. CRISPR-Cas9: A Cutting-edge Genome-editing Technology with Many Potential Applications. Journal of Advances in Biology & Biotechnology.,2024:27(11):59-73.
71. Faruk O, Jewel ZA, Bairagi S, Rasheduzzaman M, Bagchi H, Tuha AS, *et al*. Phage treatment of multidrug-resistant bacterial infections in humans, animals, and plants: The current status and future prospects. Infectious Medicine., 2025.
72. Kamel M, Aleya S, Alsubih M, Aleya L. Microbiome dynamics: a paradigm shift in combatting infectious diseases. Journal of personalized medicine.,2024:14(2):217.
73. Al-Rashidi HS, El-Wakil ES. Parasites and microbiota: dual interactions and therapeutic perspectives. Microorganisms.,2024:12(10):2076.
74. Lyu M, Xu G, Zhou J, Reboud J, Wang Y, Lai H, *et al*. Single-Cell Sequencing Reveals Functional Alterations in Tuberculosis. Advanced Science.,2024:11(11):2305592.
75. Lu J, Tong Y, Dong R, Yang Y, Hu W, Zhang M, *et al*. Large DNA fragment knock-in and sequential gene editing in *Plasmodium falciparum*: a preliminary study using suicide-rescue-based CRISPR/Cas9 system. Molecular and Cellular Biochemistry.,2024:479(1):99-107.
76. Kumar S, Mahato RP, Ch S, Kumbham S. Current strategies against multidrug-resistant *Staphylococcus aureus* and advances toward future therapy. The Microbe., 2025.
77. Pydipalli R. High-Throughput Screening in Microbiology Using Robotics: Accelerating Biotech Discovery. Robotics Xplore: USA Tech Digest.,2024:1(1):15-28.
78. Vivekanandan KE, Kumar PV, Jaysree RC, Rajeshwari T. Exploring molecular mechanisms of drug resistance in bacteria and progressions in CRISPR/Cas9-based genome expurgation solutions. Global Medical Genetics., 2025.
79. Mohseni P, Ghorbani A. Exploring the synergy of artificial intelligence in microbiology: Advancements, challenges, and future prospects. Computational and Structural Biotechnology Reports., 2024, 1.
80. Zhang X, Zhang D, Zhang X, Zhang X. Artificial intelligence applications in the diagnosis and treatment of bacterial infections. Frontiers in Microbiology., 2024, 15.
81. Rong N, Liu J. Development of animal models for emerging infectious diseases by breaking the barrier of species susceptibility to human pathogens. Emerging Microbes & Infections.,2023:12(1):2178242.