The Research of Medical Science Review
ISSN: 3007-1208 & 3007-1216 Volume 4, Issue 6, 2026

THE GENOMIC REVOLUTION UNLOCKING THE PROMISE OF INDIVIDUALIZED PATIENT CARE

Sadia Zulfiqar [*1], Afnan Akram[2], H.Javeria Meraj[3], Tahreem Shahid[4], Wajeeha Shahid[5], Iqra Farooq[6], Hamza Rafeeq[7]

[*1,2,3,4,5,6,7]*Department of Biochemistry, Riphah International University Faisalabad, Punjab, Pakistan*

Corresponding email: [*1]sadiazak094@gmail.com

DOI: https://doi.org/10.5281/zenodo.21020266

Keywords
Artificial intelligence, Biomarker, Genomics, Multiomics, Pharmacogenomics, Precision medicine, Targeted therapy

Article History
Received: 22 April 2026
Accepted: 04 June 2026
Published: 21 June 2026

Corresponding Author: *
Sadia Zulfiqar

Abstract

Conventional therapeutic strategies that fit everyone are often unable to consider the remarkable inter-individual heterogeneity in disease manifestations and drug responsiveness. This variability results in suboptimal treatment efficacy, unpredictable adverse drug reactions and significantly higher healthcare costs in all medical fields. This review covers the development, status quo, and future outlook of precision therapeutics, from the genomic biomarkers, to multiomics strategies, to targeted delivery platforms. Next-generation sequencing has led to the discovery of druggable mutations across cancers and rare diseases, and long-read sequencing has proven powerful in resolving hitherto undruggable, complex pharmacogenes. The integration of multiomics such as genomics, proteomics, metabolomics, and artificial intelligence is ushering in a new era in diagnostic precision and therapeutic choice. New modalities such as antibody-drug conjugates, HIF-2α inhibitors and functional drug testing platforms are showing impressive clinical activity in a variety of therapeutic areas. Precision therapeutics is the process of transitioning medicine from a reactive to a pro-active, predictive and genuinely personalised field. But the barriers to implementation, such as reimbursement fragmentation, regulatory disharmony, and significant diversity of genomic reference datasets, are yet to be overcome to fully realize the promise of precision medicine for all patient populations around the world.

1. INTRODUCTION

1.1. The limitations of conventional therapeutics: efficacy and toxicity variability

For decades, the practice of medicine has largely followed a standard model in which the choice of therapeutics is made almost exclusively on the basis of disease diagnosis, without real regard for individual differences in their biology. This one-size-fits-all strategy has proved very successful in the treatment of infectious diseases and some acute diseases, but it often fails in the face of the complexity of human biology. The most obvious example of this limit is the large inter-individual differences in drug efficacy and toxicity. Patients with seemingly identical treatments can have widely different results, some may have a strong response to a treatment, while others may not benefit at all (Aarif, Hasan, Alam, Ali, & Pakruddin, 2025). Even worse, adverse drug reactions are unpredictable, and are one of the most common causes for morbidity, mortality and healthcare cost worldwide. The above unpredictable responses are a result of the combination of genetic variation, environmental exposures, epigenetic modifications, and underlying disease heterogeneity, which traditional therapeutic strategies cannot account for. The uncertainty and frustration of the

clinicians who have to make a lot of trial and error decisions with medications has been a major impetus towards more rational, biology-based approaches to therapeutic decisions (AbuAlrob, Itbaisha, & Mesraoua, 2025).

1.2. Defining precision medicine: from "personalized" to "precision" a paradigm shift

In the face of these ongoing hurdles, precision medicine has become a paradigm-changing approach to medicine, aiming to shift from a one-size-fits-all to a one-person-fits-all approach. It is crucial to understand the changes in meaning that have taken place in this area(Addissouky, Ali, El Sayed, & Wang, 2023). Although the term was used early on, there was some confusion of it being medicine tailored to the individual that would result in unique treatments for each patient, which is neither practical nor scientifically true. In the meantime, the field has been unified under the term precision medicine, which more aptly captures the key concept: stratifying patients into subpopulations based on molecular, environmental and lifestyle information, to identify those with similar biological features who are likely to respond to the same treatment (Adeghe, Okolo, & Ojeyinka, 2024). This stratification can help clinicians choose a therapy most appropriate for individual patients and help reduce the risk of adverse events. This transition from personalized to precision is much more than a semantic adjustment; it is a paradigm shift from the empirical trial-and-error of prescription to evidence-based, biomarker-guided prescription. This paradigm shift requires clinical trial study design and regulatory paradigms to evolve as well, and these are slowly changing to reflect the complexity of precision approaches, and healthcare delivery systems must change to reflect these changes as well (F. Ahmed, 2024).

Figure 1 shows a comparison between the traditional and precision medicine paradigms. As illustrated in the figure, the traditional medicine is that standard treatments are applied only according to the diagnosis of the disease, which means that the effects are not consistent on patients who are genetically different. Precision medicine, by contrast, incorporates genomic, proteomic, metabolomic and environmental information and uses them to find the best targeted treatments for each patient. This method is likely to make the treatment more effective and with fewer side effects, because the treatment is tailored to the molecular profile of the disease in each individual patient. The key point illustrated by the figure is that it is possible to achieve more predictable, favourable, clinical outcomes by replacing the one-size-fits-all paradigm with a stratification paradigm using biomarkers.

Traditional and Precision Medicine approach: comparative illustration. Traditional medicine usually uses the same medical practice in line with diagnosis of disease only, which yields more or less unpredictable results. Precision medicine combines information from a patient's genome, proteome, metabolome and environment to tailor the best targeted therapies for the patient to increase the efficacy and decrease the side effects of the drugs (M. S. Ahmed, Das, & Mandal).

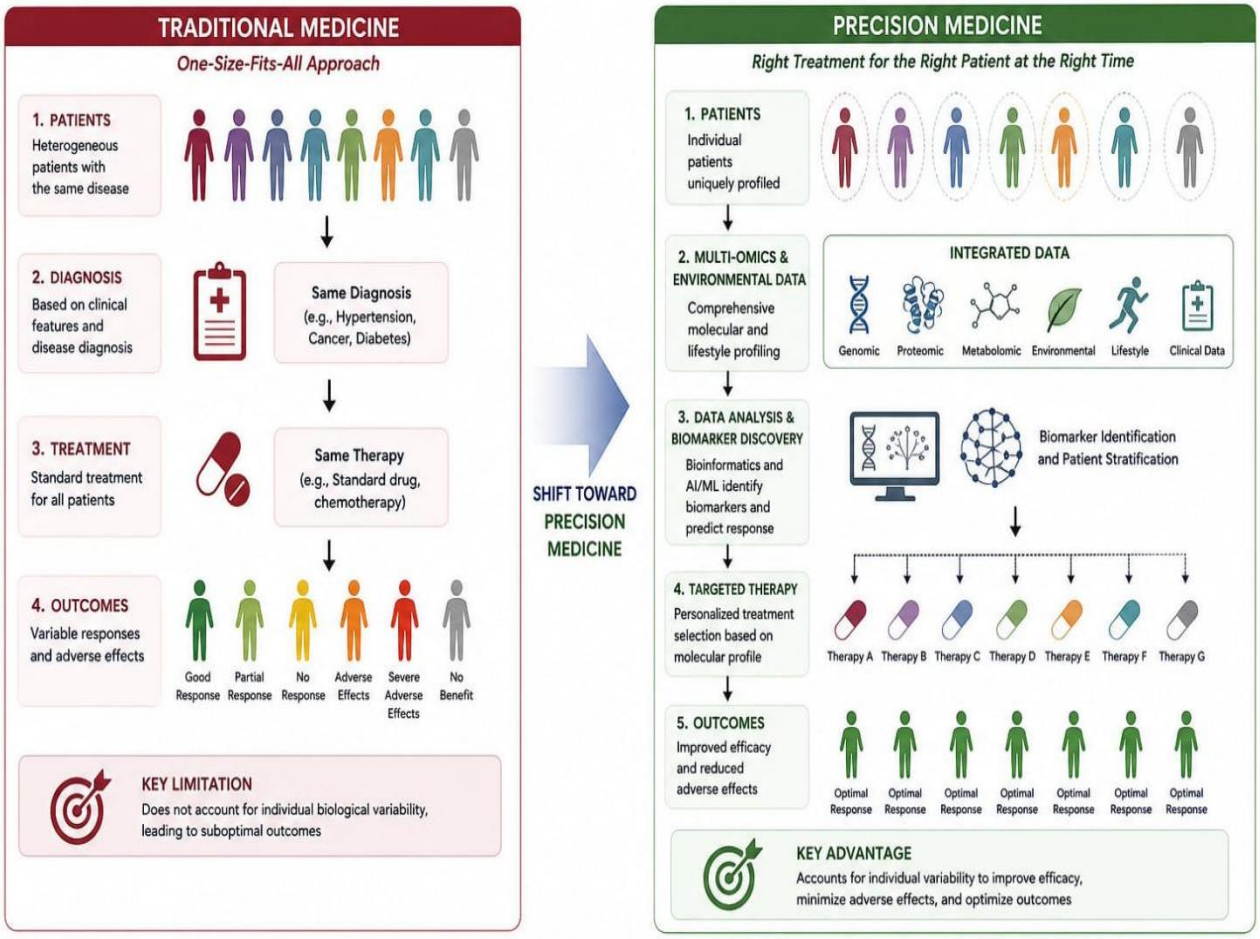

Figure 1. ***The Evolution from Traditional to Precision Medicine Paradigm***

1.3. The P4 healthcare framework: predictive, preventive, personalized, participatory

The promise of precision medicine does not just apply to matching drugs to patients through genomic profile. Those with foresight in the field have stated a comprehensive framework, based upon the four P's of medicine: predictive, preventive, personalized, and participatory healthcare (Alhajahjeh & Nazha, 2024). The use of molecular biomarkers can help predict susceptibility to disease, disease pathway trajectories, and therapeutic results prior to intervention, thus allowing for early intervention and risk reduction. Preventive medicine takes advantage of the rapid advances in early detection of disease risk factors through genomic and multiomic screening to move from dealing with disease to preventing it in the first place, fundamentally changing the focus of healthcare (A. Ali et al., 2023).

In the case of personalized medicine, as explained, intervention is designed according to the molecular profile of each patient, so each patient is treated with the optimal therapy for their molecular profile. Finally, participatory medicine views patients as not merely recipients of care, but partners in their own health, able to use their genomic and health data to make informed decisions with their health care provider (H. Ali, 2023). These four pillars form a holistic approach to a health care system that is proactive and not reactive, that maintains people's health and not just treats illness after it has taken hold. While not yet fully implemented, this framework has been widely adopted by both policymakers and patient

advocacy groups, as well as by healthcare systems (Allen, 2024).

1.4. Scope of the review: from molecular discovery to clinical implementation

The purpose of the review is to examine the past and present of precision therapeutics from the fundamental molecular discoveries to the clinical applications that have been realized. First, we set the stage for precision medicine, review how next generation and long-read sequencing technologies have allowed identification of actionable genetic variants across various diseases, and discuss the genomic underpinning of precision medicine (Arianpour, 2024). Next, we explore the world of pharmacogenomics, explaining how specific gene-drug relationships have been used to develop clinical guidelines that are now incorporated into drug prescribing practice for opioids, antiplatelet agents, chemotherapeutics and other drugs. Given this genomic foundation, we now turn to the new frontier of multiomics integration, where additional layers of transcriptomic, proteomic, metabolomic, epigenomic and microbiomic data are combined with artificial intelligence to create a comprehensive molecular profile of individual patients (ASLAM et al., 2024).

The review then addresses precision oncology, the most advanced field for clinical application, and introduces new modalities of therapeutic drugs such as antibody-drug conjugates, HIF-2α inhibitors, and functional drug testing platforms (Attaran & Attaran, 2024). We also discuss non-oncology uses, such as transplant medicine, neurology, and pediatrics, before turning to the ongoing implementation challenges that need to be addressed, including the absence of diversity in genomic reference data, regulatory fragmentation and reimbursement barriers. Finally, this review does not aim to exhaustively list scientific progress but to present a realistic picture of the current status of precision therapeutics and what still needs to be done to realize the significant promise of precision therapies for patients around the world (Ayoola, Oladele, & Faline, 2024).

1. The Genomic Foundation of Precision Therapeutics

2.1. The Human Genome Project and its legacy in precision medicine

A key milestone in the current state of precision therapeutics is something that would have been hard to believe even 10 years ago—the complete sequencing of the human genome. When the Human Genome Project was completed in 2003 after 13 years of international collaboration, it was much more than a technical achievement in molecular biology (Aziz et al., 2025). It revolutionized our understanding of human health and disease and created the first precision reference map of the instructions necessary for defining human biology. Before this accomplishment, the study of genetics in drug response was mostly limited to candidate gene studies, hypothesis-based research that allowed the study of only a few polymorphisms at a time. The Human Genome Project has freed scientists from these limitations and allowed for blind interrogation of the genome to study variants affecting therapeutic response (Bajjash Alhadi et al., 2023). This legacy is still living today in all precision medicine efforts, including pharmacogenomic implementation efforts, and multiomics profiling efforts.

The reference genome sequence has been improved over the years since the first draft, and serves as the universal coordinate system to which all patient genomes are mapped to identify clinically actionable variation (e.g. via the Telomere-to-Telomere Consortium). The identification of disease susceptibility alleles, tumor mutations, and pharmacogenetic variants without this resource would be only a theoretical possibility, and not a clinical reality (Balasubramanyam, Ramesh, Sudheer, & Honnavalli, 2024). Furthermore, the Project developed crucial ethical, legal and social implications research frameworks which continue to inform the responsible implementation of genomic medicine (Bhatia, Kumar, Kumar, & Jain, 2025).

2.2. Next-generation sequencing technologies: from Sanger to NovaSeq

Sequencing technology development has been a hothouse of innovation as they try to increase throughput and decrease the cost per base. The Sanger dideoxy chain termination method which allowed the original human genome project to proceed only gave read lengths of around 800-1000 base pairs, and required a lot of time and money to generate even a small amount of sequence data (Borawake, Shaikh, Shaikh, & Wadghule, 2025). Next generation sequencing technologies challenged this paradigm, allowing massively parallel sequencing reactions, with millions to billions of reads generated in a single run of a sequencing instrument. A number of different technological platforms developed during this revolution, each offering different advantages and disadvantages (Chacon et al., 2025). Sequencing by synthesis, most notably commercialized by Illumina, is still the method of choice for whole genome and whole exome applications with reversible terminator nucleotides providing highly accurate base calling over 150-300 bp read lengths (Channi, Sandhu, Kaur, & Ghai, 2025).

Pyrosequencing, pioneered by 454 Life Sciences, relies on measuring bioluminescence signals to determine nucleotide incorporation, but has not been widely used because of poor read accuracy and output (Chaudhary, Ali, Kumar, Sharma, & Jayakody, 2025). Ion semiconductor sequencing was commercialized by Thermo Fisher and involves measuring the pH change that occurs when a hydrogen ion is released as the polymerase is active, does not require optical detection and therefore lowers the cost of the instruments. These technological breakthroughs have led to an astounding drop in the cost of sequencing, from around one hundred million dollars to sequence one human genome in 2001, to under one thousand dollars today, making genome sequences available to anyone and allowing the large cohort studies which are the foundation of our present precision medicine research (Chauhan et al., 2024). The capacity to sequence thousands of genomes in a variety of different populations has transformed our understanding of human genetic variation and associated with disease (Chen, Hsiao, Lin, & Fann, 2025).

2.3. Long-read sequencing: resolving complex haplotypes and structural variants

Although the short-read sequencing technologies have achieved tremendous success, there have been critical challenges that are becoming more and more apparent with the development of precision medicine and the desire to comprehensive genomic profiling. The short-read platforms yield fragments ranging from one hundred fifty to three hundred base pairs and the fragments need to be computationally merged to yield contiguous sequences (Chigozie, Aniokete, Ogbonna, & Iroha, 2025). It works well for single nucleotide variants and small insertions or deletions, but it is problematic for regions of high homology, repetitive elements and complex structural rearrangements. One of the most challenging aspects for pharmacogenomic applications is the inability to phase variants over distances greater than the read length, and therefore to unable to reliably determine the cis-trans configuration of multiple polymorphisms (Chrysanthakopoulou & Koutsojannis, 2025). The highly polymorphic nature, presence of pseudogenes and complex structural variation of the pharmacogene CYP2D6 represents this challenge; the accurate genotyping of this gene has historically been extremely difficult with short-read technologies alone (Cioroboiu & Popescu, 2024).

The Oxford Nanopore and Pacific Biosciences long-read sequencing technologies have proven to be game-changers in overcoming these obstacles. Oxford Nanopore sequencing shoots strands of DNA through protein nanopores set in synthetic membranes, and records the drop in ionic current to determine the individual bases (Darwish, 2025). This yields reads regularly up to ten thousand base pairs with some reads as long as megabases. Pacific Biosciences uses single-molecule real-time sequencing, where reads are generated by observing the activity of polymerases in zero-mode waveguides and are of similar length. These long reads facilitate unambiguous phasing of distant variants, resolution of structural rearrangements

and accurate characterization of complex pharmacogenes. Studies have recently shown that the accuracy of phasing with long-read sequencing is >98% for CYP2D6, CYP2C9, and SLCO1B1, which allows for the identification of new star alleles and the resolution of ambiguous haplotypes that could not be resolved with short-read sequencing data alone (Das et al., 2025).

This capability has far reaching clinical implications, because genotype determination of diplotype configurations can directly impact phenotype predictions and therapeutic decisions. The advantages and disadvantages of the various technologies should be understood prior to choosing a sequencing platform for clinical pharmacogenomic applications (Desta & Aserese, 2024). Table 1 systematically compares short-read and long-read sequencing platforms based on important parameters pertinent to clinical decision making. Illumina short-read sequencing has the highest throughput and the lowest cost per gigabase, making it ideal for large-scale whole-genome sequencing projects in which the goal is to find all variants throughout the genome. But because it has a read length of 150-300 base pairs, it is not suitable to phase distant variants and resolve structurally complex regions (Dimple). Reads over ten thousand base pairs in length, with a high level of phasing accuracy >98%, and definitive resolution of complex pharmacogenes such as the CYP2D6, CYP2C9 and SLCO1B1 have been demonstrated using the Oxford Nanopore and PacBio long-read platforms (Domadiya, 2024).

They can detect systematic changes in DNA structure including gene duplications, deletions and rearrangements systematically missed by short-read approaches (Ehyaei Rad, 2025). The drawbacks are increased sample cost and decreased raw read accuracy, which can be remediated to a short-read level of accuracy with computational polishing. In some clinical use cases where accurate phasing and discovery of structural variants are critical to therapeutic decisions, the enhanced phasing accuracy and discovery of structural variants of the long-read platforms are beginning to make the investment worthwhile. Hybrid sequencing strategies that integrate together both the long-range information of long-read sequencing platforms and the high-depth, low-cost data of short-read platforms, are an emerging best practice for comprehensive pharmacogenomic profiling (Eskandar, 2023).

Table 1. ***Comparison of Short-Read and Long-Read Sequencing Technologies for Pharmacogenomic Applications***

Feature	Illumina (Short-Read)	Oxford Nanopore (Long-Read)	PacBio (Long-Read)
Read length	150–300 bp	10,000–1,000,000+ bp	10,000–50,000 bp
Phasing accuracy	<50% for distant variants	>98%	>98%
Structural variant detection	Poor	Excellent	Excellent
Complex pharmacogene resolution (CYP2D6)	Incomplete	Complete	Complete
Raw read accuracy	>99.9%	92–96%	87–95%
Cost per Gb	$5–10	$20–50	$50–100
Run time	1–3 days	Minutes to hours	Hours to days

Feature	Illumina (Short-Read)	Oxford Nanopore (Long-Read)	PacBio (Long-Read)
Best use case	Large cohort WGS, SNP detection	Targeted haplotyping, SV detection	De novo assembly, phasing

2. Pharmacogenomics: From Genotype to Drug Response Phenotype

3.1. Core pharmacogenes and their clinical relevance

Pharmacogenomics is an attempt to address a very simple, yet clinically important question: why do patients respond differently to the same drug? As has become increasingly apparent, the answer lies significantly in the variation in genes that regulates drug absorption, distribution, metabolism and elimination, and is inherited. The most well characterized pharmacogenes include the cytochrome P450 superfamily, including CYP2D6, CYP2C9, CYP2C19 and CYP3A4/CYP3A5 (Falkner). Together, these enzymes account for the metabolism of seventy to eighty percent of clinically prescribed medications, many of which are among the most widely prescribed drugs in cardiology, psychiatry, oncology, and pain management. CYP2D6, which only represents 2-4% of the total hepatic cytochrome P450 content, metabolizes nearly a quarter of all drugs such as codeine, tramadol, antidepressants and antipsychotics (Fatima, Siddiqui, & Parvez, 2024). This remarkable variability of the CYP2D6 gene gives rise to more than one hundred star alleles and to a spectrum of metabolic phenotypes ranging from poor to ultrarapid metabolizers. In addition to the cytochrome P450 family, drug transporters have proven to be important factors in therapeutic outcome (Fon et al., 2024).

The uptake transporter SLCO1B1 is encoded by SLCO1B1, and specific variants in this gene significantly boost the risk of myopathy caused by statin therapy, including simvastatin, leading to genetic testing of this gene before initiation of statin therapy. ABCB1 encodes P-glycoprotein, which is an efflux transporter that helps to reduce the access of drugs to the brain and other protected compartments: variants impact everything from response to antidepressants to chemoresistance. Completing the picture of pharmacogenetics are the conjugation enzymes, of which the reduction of glucuronidation of irinotecan caused by polymorphisms in the UGT1A1 gene is known to lead to a dramatic increase in the risk of severe neutropenia, and polymorphisms in the TPMT gene are the classic example of clinically actionable pharmacogenetics in thiopurine therapy for inflammatory diseases and childhood leukemia (Frascarelli et al., 2023). Together these core pharmacogenes make up the most clinically actionable targets for preemptive genotyping for which there are evidence-based guidelines for therapeutic adjustment according to genotype results (Fu, Tang, Tan, & Srivastava, 2024).

3.2. Star alleles, haplotypes, and phenotype prediction

To transform the translation of genomic variation to clinically relevant inferences of drug response, a standardized nomenclature and systematic framework are needed to help infer phenotype from genotype (Geanta, Boata, Cucos, Cioroboiu, & Popescu, 2024). This important infrastructure is provided by the star allele system, which is maintained by the Pharmacogene Variation Consortium, which provides functional annotations for specific combinations of variants along a single chromosome, known as haplotypes (Ghebrehiwet, Zaki, Damseh, & Mohamad, 2024). A star allele is a defined haplotype with one or more variants whose combined effect is a predictable effect on the function of the protein. The most frequent null allele in European populations is the so-called CYP2D6 star allele 4 which is caused by a splicing defect that leads to a non-functional enzyme. Star allele 10 is a decreased function enzyme, with the reference (fully functional) allele being labeled as star allele 1 (Goswami & Sharma, 2024).

Two star alleles, one from each parent, are combined into a "diplotype", which determines the predicted metabolic phenotype of a person. The activity score system associated with CYP2D6 diplotype is a way to convert diplotype to a continuous scale ranging from zero (poor metabolizer) to three or more (ultrarapid metabolizer) (Gouripur, 2024). A poor metabolizer (usually with 2 null alleles) cannot activate prodrugs such as codeine and hence has an excess buildup of the active drug metabolized by CYP2D6, which makes toxicity more likely. An ultrarapid metabolizer is someone who, due to having gene duplications, breaks down codeine into morphine very quickly and thus uses normal doses of codeine can lead to dangerous respiratory depression (Gupta, 2024). Although for major pharmacogenes this genotype-to-phenotype conversion is well known, it is still in a constant flux of change as new haplotypes and structural variants are discovered through long-read sequencing, and not through conventional genotyping methods. The situation becomes more complicated, because there is a high degree of ethnic variation in the frequency of alleles of many pharmacogenes and hence population-specific issues in test interpretation and clinical decision making (Gupta, 2024). But notwithstanding these intricacies, the basic message is still sound: knowledge of a patient's diplotype can help better predict drug response than does a purely empirical approach to drug prescribing.

3.3. Clinical implementation examples

Advances in the theory of pharmacogenomics now have turned into real-world applications for prescribing for millions of patients around the world. The most compelling example might be the use of CYP2D6 to guide opioids use for post-operative pain management. The analgesics codeine and tramadol are prodrugs that need to be metabolized by CYP2D6 to be active (Han et al., 2024). In poor metabolizers, these medications offer little benefit for pain control and other pain relief measures like nonsteroidal anti-inflammatory drugs or different opioids like hydromorphone should be used. On the other hand, ultrarapid metabolizers will metabolize morphine very quickly and a standard dose may cause fatal respiratory depression which is why regulatory bodies have black box warnings against the use of codeine in children after tonsillectomy and by breastfeeding mothers (Harrison, 2024). Perioperative medication safety has progressed to preemptive genotyping to help identify the right opioids or other non-opioid options to use before adverse events can take place. For example, DPYD and UGT1A1 testing are now standard of care for patients receiving fluoropyrimidines and irinotecan, respectively, in oncology (Heesen et al., 2024).

DPYD encodes the protein dihydropyrimidine dehydrogenase, which is the rate-limiting enzyme that breaks down fluorouracil and capecitabine. In a small number of patients (about 3-5% of the population) DPYD deficiency results in excessive and potentially life-threatening toxicity such as neutropenia, diarrhea and neurotoxicity at normal doses. Preemptive DPYD genotyping with prospective dose reduction decreases severe toxicity by more than 70% over standard dosing, and some health care systems are now requiring preemptive DPYD testing prior to initiation of fluoropyrimidine therapy. In the same way, UGT1A1 genotyping is used to detect patients who are susceptible to neutropenia that can result from irinotecan treatment, thus allowing dose adjustments or the use of different chemotherapies. Cardiovascular medicine provides a good example of a pharmacogenetic interaction that is of great public health significance:

The case of CYP2C19 and clopidogrel. CYP2C19 is required for the activation of the prodrug antiplatelet agent, clopidogrel. Patients with loss-of-function alleles of CYP2C19 (which are present in about thirty percent of the entire population worldwide and vary significantly across different ethnic groups) have a lower active metabolite level, lower platelet inhibition and higher risk of major adverse cardiovascular events such as stent thrombosis and myocardial infarction. Current clinical practice guidelines suggest that other antiplatelet drugs like prasugrel or ticagrelor be used instead of clopidogrel in patients with intermediate and poor metabolizers who are

undergoing percutaneous coronary intervention (PCI). Together, these examples illustrate that the field of pharmacogenomics has matured as a discovery science to a clinical implementation (Husnain, Rasool, Saeed, & Hussain, 2023).

Professional consortia to create evidence-based guidelines for genotype-directed prescribing have made a significant contribution to the translation of pharmacogenomic findings to the clinic. Table 2 provides a subset of pharmacogene-drug combinations that have known clinical guidelines that have been published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and other reputable sources. CYP2C19 and clopidogrel: carriers of loss of function alleles are intermediate or poor metabolizers and alternative antiplatelet therapy is strongly recommended in patients receiving PCI. In the case of SLCO1B1 and simvastatin, the c.521T>C variant is used to identify poor functioner and simulation of simvastatin dose or use of other statins to avoid myopathy is strongly recommended. For DPYD and fluoropyrimidines, the recommendation for dose reduction or alternative therapy in intermediate and poor metabolizers is considered strong and there are several healthcare systems that have instituted mandatory prospective testing (Husnain et al., 2023).

The advice is also strong not to use codeine with CYP2D6 ultrarapid metabolizers because they are at risk of life-threatening respiratory depression. Of note, the strength of recommendations differs for each gene-drug pair, depending on the quality and quantity of the evidence available; in some cases, it is a moderate recommendation, rather than strong, because of the limitations of prospective validation or in estimating the effect size (Hussain, 2024). These guidelines are continually revised as new information is gained and are increasingly integrated into clinical decision support systems in electronic health records to facilitate real-time genotype-guided prescribing at the point of care (Ikwelle et al., 2025).

Table 2. ***Clinically Actionable Pharmacogene-Drug Pairs with Evidence Levels***

Gene	Affected Drug(s)	Variant(s)	Phenotype Consequence	Recommendation	Evidence Level
CYP2C19	Clopidogrel	Loss-of-function alleles (2,3)	Intermediate/ poor metabolizer	Alternative antiplatelet (prasugrel, ticagrelor)	Strong
SLCO1B1	Simvastatin	c.521T>C (p.Val174Ala)	Poor function	Lower dose or alternative statin	Strong
DPYD	Fluorouracil, capecitabine	2A, 13, c.2846A>T, c.1236G>A	Intermediate/ poor metabolizer	Dose reduction or alternative therapy	Strong
UGT1A1	Irinotecan	28, 37	Poor metabolizer	Dose reduction	Moderate
CYP2D6	Codeine, tramadol	Gene duplications	Ultrarapid metabolizer	Avoid codeine, alternative analgesic	Strong

CYP2D6	Tamoxifen	Loss-of-function alleles (4, 5)	Poor metabolizer	Consider alternative endocrine therapy	Moderate

4. Multiomics Integration: Beyond Genomics

4.1. The multiomics landscape: transcriptomics, proteomics, epigenomics, metabolomics, microbiomics

Genomic variation is the basic blueprint for inherited drug response phenotypes, but it is just the first layer of biological complexity that is of relevance to precision medicine. Central Dogma of molecular biology: Direction of information flow from DNA to RNA to protein is under regulatory control and is modulated by environment. Transcriptomics provides a snapshot of the dynamic state of gene expression, to see which genes are being transcribed in a given tissue under a given condition (Jabbar Basha et al., 2024). This layer can provide valuable information in addition to the static genomic data: two people with the same genotype may show very different expression patterns because of epigenetic changes or environmental influences. Proteomics takes this analysis one step further, to quantify the amount of the protein, post-translational modifications, and protein-protein interactions that are the functional effector molecules of the cell that ultimately dictate cellular behavior.

Epigenomics is the study of heritable changes in gene expression that do not involve changes in the DNA sequence, such as the DNA methylation state, the accessibility of chromatin, and the modification of the structure of proteins that bind to DNA. Metabolomics is used to capture the small molecule complement of the biological sample which includes the substrates, the intermediates and the products of cellular metabolism and is a reflection of the integrated output of the genome, transcriptome and proteome as well as environmental influences (Jain). Last, microbiomics describes the intricate microbial communities that inhabit the human body and affect drug metabolism, immune system function, and disease susceptibility to a great extent in ways that are becoming better understood, especially in the case of the gut microbiome. These multiomics layers provide a highly complex data space with the potential of providing a full characterization of patients' biology. But these data are numerous and complex, making their integration and interpretation challenging and requiring advanced computational methods (Khan, Danishuddin, Khan, Guarnera, & Akhtar, 2025).

4.2. Integrative multiomics: why layered data surpasses single-omics approaches

The underlying principle of multiomics integration is based on the fact that biological systems have emergent properties that cannot be predicted by looking at any one data layer alone. Metabolic flux may not be well correlated with protein abundance because of allosteric regulation or substrate availability, and compensatory transcriptional regulation may explain why genomic variants are not functional. These nonlinear relationships make single-omics approaches useful but limited in capturing all aspects of the biological complexity that influences clinical phenotypes (Khare & Khare, 2024). Integrative multiomics explicitly models relationships across data layers, which allows to uncover associations and biomarkers and therapeutic targets that would be hidden in any one of the individual omics technologies. A patient with a pathogenic genomic variant, for instance, may exhibit no disease phenotype as the mutant allele is epigenomically silenced that information is only available in a combination of genomic and epigenomic profiling (Khondakar, Tripathi, Mazumdar, Ahuja, & Kaushik, 2024).

Likewise, a patient with cancer may have an actionable mutation at the DNA level in its tumor, but its proteomic profile might show that the protein is not produced due to post-transcriptional regulation, and therefore, the use of targeted therapy would have been of no benefit. By contrast, metabolic imbalances can contribute to pathogenesis even without any known genetic

defects, such as in some of the complex metabolic disorders and neurodegenerative diseases (Kolanu, 2024). The strength of multiomics integration is that it can help overcome such ambiguities: the multiple lines of evidence converge to a coherent molecular diagnosis. Moreover, cross-disciplinary integration of omics layers can uncover new biological mechanisms that would not be visible from individual data layers alone, such as metabolite-mediated modulation of gene expression or modulation of drug metabolism by the microbiome. The price of multiomics profiling continues to drop and a complete molecular characterization of individual patients is becoming more feasible, but the analytical challenges of integrating the various types of data still are significant (LB et al., 2024).

Figure 2 depicts the schematic view of integrative multiomics approach to precision medicine. The genomic, transcriptomic, proteomic, epigenomic, metabolomic and microbiomic data layers are acquired from patient samples and integrated through bioinformatics pipelines and the use of artificial intelligence algorithms as shown in the figure. This integration generates a comprehensive molecular profile for each patient, allowing for accurate diagnosis, prognosis prediction, and treatment selection. The figure highlights that no one single layer of omics alone can capture all information, but the intersections and interactions between the layers can provide information that are not captured by a single omics approach. The integrated analysis leads to a comprehensive view of disease processes and personalized treatment approaches that consider the entire patient biology.

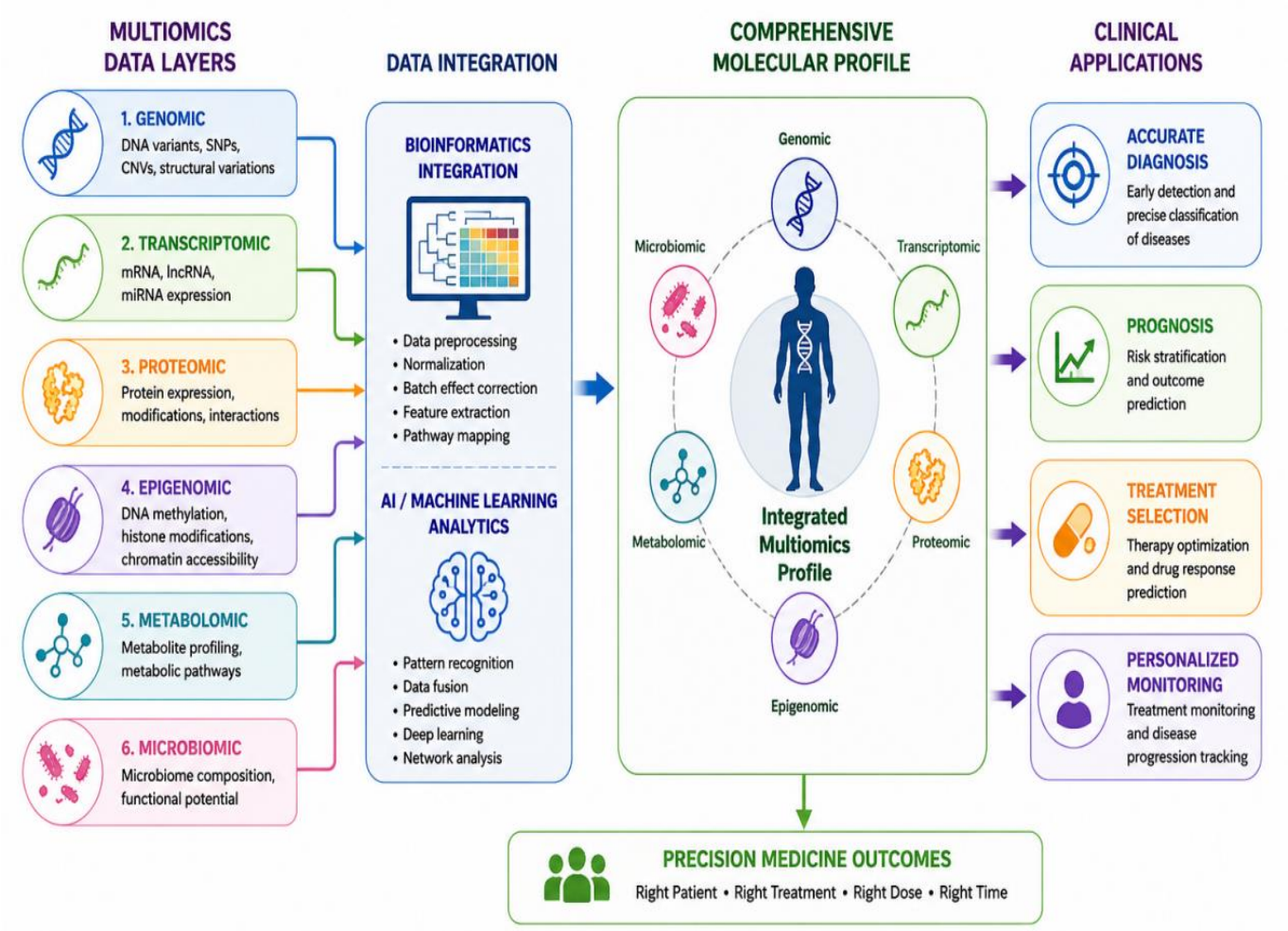

Figure 2. ***Integrative Multiomics Framework for Precision Medicine***

4.3. Bioinformatics and AI for multiomics data integration

However, effective utilization of multiomics data requires sophisticated computational techniques that can process large volumes of data from diverse sources and deal with the intricacies of complex data. The bioinformatics pipelines need to tackle issues from raw data processing to quality control, normalization, and batch effect correction of the various omics platforms (Maleki Varnosfaderani & Forouzanfar, 2024). Machine learning methods have been especially useful for integrating multiomics data because it is capable of discovering patterns and relationships that are relevant without needing to be explicitly programmed with biological rules. Variants are classified using machine learning tools such as CADD, REVEL and DeepVariant, which use various machine learning architectures to predict the impact of genomic variants based on conservation, evolutionary constraint, and molecular features to estimate the probability of harmfulness (Maleki Varnosfaderani & Forouzanfar, 2024).

These methods significantly outperform rule-based approaches for prioritizing VUS, but experimental validation is still necessary for clinical use. Specifically, for multiomics integration, a variety of methods have been developed that range from sparse CCA to deep neural networks, aiming to identify common signals across the layers and that also deal with

layer-specific noises and technical artifacts (Maleki Varnosfaderani & Forouzanfar, 2024). Population allele frequencies, clinical assertions, and expert-curated knowledge, all important components of variant interpretation, can be aggregated in public data repositories such as gnomAD, ClinVar, and ClinGen to assist with clinical decision-making. The Genome Aggregation Database (GnomAD) has collected sequencing data from more than one hundred forty thousand people from various populations around the world and can provide a good estimate of the rarity of a variant as an indicator of likely pathogenicity (Mandala, Reddy, Nishanth, Yasmeen, & Maguluri, 2023).

ClinVar is a resource for a curated archive of relationships between human variants and observed health status contributed by clinical testing laboratories, research groups, and expert panels. ClinGen Clinical Genome Resource (NLMK) builds standard interpretation frameworks and gene-disease validity curation to ensure uniformity in clinical laboratories. Still, there are major current limitations, such as the necessity for better ways to incorporate non-coding variants, more effective ways of representing non-European ancestry populations in reference data sets, and better ways to account for structural variants (Mazumdar, Khondakar, Das, Halder, & Kaushik, 2025).

5. Precision Oncology: The Leading Frontier

5.1. Tumor biomarkers and precision targeting systems

Oncology is a mainstay of precision medicine, in part because cancer is a basic genomic disease where acquired mutations promote uncontrolled growth, immune evasion, and metastasis. Precision targeting systems have been developed that target molecular characteristics that are unique to the tumor, but not to normal tissues, because of tumor biomarker identification (Mohammadi, Amini, et al., 2024). These targeting systems encompass the simple single-biomarker targeting, including tyrosine kinase inhibitors targeting of specific driver mutations, as well as more sophisticated dual-biomarker and triple-biomarker targeting strategies that involve the simultaneous targeting of multiple targets to achieve therapeutic effect (Mohammadi, Far, Amini, et al., 2024). The shift to multi-biomarker targeting conveys an understanding of the heterogeneity of tumors, both between patients with the same histologic diagnosis and within a tumor over time and space. Although single-biomarker approaches have shown efficacy in certain settings, they are susceptible to the emergence of resistance by outgrowth of biomarker-negative subclones or by out-growth of bypass signaling pathways (Mohammadi, Far, Fathi, et al., 2024).

To overcome this limitation, dual-biomarker and triple-biomarker strategies have been developed, which means that more than one feature of therapeutic susceptibility is needed for the tumor cells, decreasing the likelihood of pre-existing or acquired resistance. In targeting strategies, important to distinguish between sequential targeting – therapeutic agents that sequentially bind to biomarkers, and co-binding – therapeutic agents that require multiple targeting moieties to bind simultaneously for therapeutic effect (Molla & Bitew, 2024). In theory, co-binding strategies would provide more specific specificity in that the normal cells that express one but not all the necessary biomarkers would be spared, but they will require more stringent targeting system design and manufacture. The selection of the optimal strategy will depend on the type of tumor and the availability of a high quality targeting ligand as well as the therapeutic window needed to achieve clinical success (Molla & Bitew, 2025).

The sophistication of precision targeting systems is paralleled by an expanding appreciation of the complexity of the tumor biomarker landscape, and now includes conditionally activatable binding sites, prodrug strategies that rely on tumor-specific activation of prodrugs, and immunomodulatory domains that activate and recruit endogenous tumor-killing immune responses (Muminov et al., 2025). Precision targeting strategies based on single, dual or triple tumor biomarkers are shown in figure 3. Sequential targeting strategies include stepwise binding to various tumor associated markers, but therapeutic effect is only achieved if markers are bound in a certain sequence, as illustrated in the figure. Co-binding strategies use

multiple ligands at the same time — where all the targeted biomarkers must exist in the same cell for therapeutic effect (Naithani, Tiwari, Chauhan, & Wadawadagi, 2025). This multi-ligand strategy increases specificity by minimising off tumour toxicity as normal cells are unlikely to express all the tumour associated markers. The figure illustrates that using a single biomarker to target a tumor with a homogeneous biomarker expression is effective; however, the use of multiple biomarkers is more appropriate for the treatment of a heterogeneous tumor in which antigen loss variants could potentially be resistant.

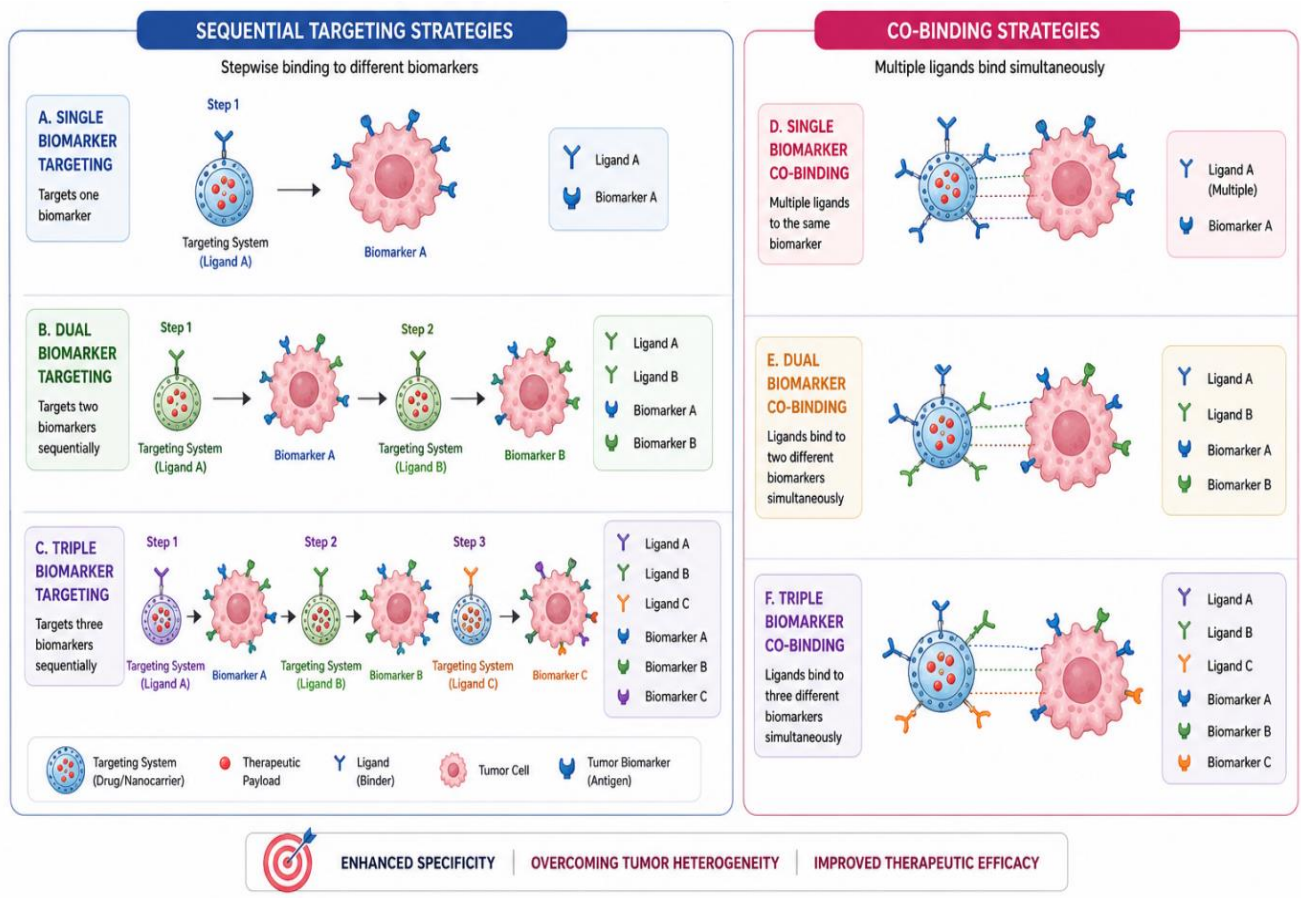

Figure 3. Precision Targeting Strategies Based on Tumor Biomarkers

5.2. Antibody-drug conjugates: expanding beyond breast cancer

Antibody-drug conjugates are one of the most successful and fast-growing categories of precision therapeutics that brings together the targeting power of monoclonal antibodies with the lethal power of chemical payloads. The general structure of an antibody-drug conjugate consists of three parts: a tumor-targeting antibody that binds to a cell surface antigen, a cytotoxic drug that is toxic to cells after internalization and released from the antibody, and a chemical linker that links the antibody to the drug, provides stability in circulation and allows drug release inside target cells (Nguyen, Rivera, & Gualtieri, 2023). The remarkable clinical potential of this class is exemplified by trastuzumab deruxtecan. This antibody-drug conjugate was developed originally for breast cancer that is HER2-positive, but has shown interesting activity in an expanding spectrum of HER2-positive malignancies. DESTINY-CRC02 investigated trastuzumab deruxtecan in patients with metastatic CRC with previously treated with other therapies in an

overall poor prognosis patient population with limited therapies (Nori et al., 2025).

The results were impressive, with objective response rates of 37-40% and progression-free survival of 5-6 months in a heavily pretreated population. These responses were sustained; some patients had long-term disease control for more than a year. The shift from breast cancer to colorectal, gastric, lung and other tumor types for indications of antibody-drug conjugates is an example of the concept of precision medicine defining therapeutic eligibility, as opposed to the path of histologic diagnosis. Regulatory frameworks that allow approval of drugs on the basis of biomarker-defined populations regardless of the tumor type have paved the way for this paradigm shift for drug development (Normanno et al., 2022). There are some issues however, such as the handling of different toxicity profiles as interstitial lung disease, the development of resistance mechanisms such as antigen loss and altered intracellular traffic and the high costs which limit access in many health care systems (Normanno et al., 2022).

5.3. HIF-2α inhibition: targeting tumor metabolism

HIF-2α is becoming a druggable target in tumors that exhibit a deregulated hypoxic signaling pathway. HIF-2α is hydroxylated under normal oxygen conditions, which makes it susceptible to proteasomal degradation and precludes accumulation and transcription activity. In tumors containing mutations in the von Hippel-Lindau tumor suppressor gene or in hypoxic microenvironments, HIF-2α becomes stabilized, moves to the nucleus, and activates transcription of pro-angiogenic, pro-metabolic, and pro-survival genes (Molla & Bitew, 2025). Belzutifan is a first in class HIF-2α inhibitor that has been seen to have outstanding clinical activity in von Hippel-Lindau disease associated tumors, such as renal cell carcinomas, hemangioblastomas, and pancreatic neuroendocrine tumors. The LITESPARK-015 trial tested the use of belzutifan in patients with metastatic pheochromocytoma (PHEO) and paraganglioma (PGL) (metastatic disease is often due to the presence of abnormalities in the hypoxia signaling pathways), and it was found to be effective in patients with disease that was progressive.

With few patients having effective treatment options, the trial demonstrated objective response rates of around forty percent and median progression-free survival of greater than fourteen months, which is a significant improvement. HIF-2α inhibition works through a different mechanism of action compared to traditional cytotoxic chemotherapy or targeting of VEGF, with the potential to develop rational combination therapy and sequential therapy to overcome resistance. Moreover, HIF-2α is not essential under normoxic conditions for normal adult physiology and thus the therapeutic window of targeting it is favorable, with manageable toxicities of anemia and fatigue. Today belzutifan success demonstrates the value of targeting metabolic vulnerabilities unique to a tumor and has spurred the discovery of other agents targeting other hypoxia-driven pathways (Onciul et al., 2025).

5.4. YAP-TEAD inhibitors: targeting the undruggable

The Hippo signaling pathway is a conserved pathway that controls the size of organs and tissue homeostasis and has become an important pathway in the generation of tumors in several types of cancer. YAP and TAZ (transcriptional co-activators) are at the center of this pathway; these proteins, when translocated into the nucleus, bind TEAD family transcription factors, leading to activation of genes that promote proliferation, survival and stem cell maintenance. YAP activation is aberrant across a variety of mechanisms such as mutations in the upstream pathway, mechanical signaling via tissue architecture, and oncogenic pathway crosstalk. Although genetic evidence highlights the role of the YAP-TEAD pathway in cancer, the pathway has long been regarded as undruggable because there is no enzymatic activity that could be targeted by traditional small molecule inhibitors (Ozcelik et al., 2024). The YAP/TEAD interaction is protein-protein interaction, which is difficult to target using traditional drug discovery strategies. These barriers are starting to be addressed in

recent advances with several parallel approaches. High throughput screening and structure-based optimization have led to the identification of direct inhibitors of the YAP-TEAD interaction, but properties such as potency and pharmacokinetics are still not optimal for clinical development.

In preclinical models, more drug-like palmitoylation inhibitors have been demonstrated that inhibit autopalmitoylation of TEAD, a post-translational modification necessary for the transcriptional activity of TEAD. In addition, upstream kinases such as MST1 and LATS1 and LATS2 inhibitors are being studied for indirect modulation of YAP activity. Several YAP-TEAD inhibitors have been taken into the early period clinical trials and preliminary results can be anticipated in the coming years. The clinically successful development of this class would be a major advance for tumors that depend on Hippo pathway alteration for their growth, such as mesothelioma, meningioma, and subsets of lung, pancreatic and colorectal cancers.

5.5. Functional precision medicine: ex vivo drug testing platforms

Although genomic profiling of tumors has led to great progress in precision oncology, there is a basic problem: there is no perfect correlation between tumor genotype and therapeutic response. Epigenetic differences, microenvironmental effects or unrepresented genetic interactions may account for the fact that different tumors showing the same genomic alterations may react differently to the same targeted therapy. Functional precision medicine fills this void by directly assessing tumor response to drugs ex vivo and offering a phenotypic readout that incorporates all molecular determinants of drug response without necessitating complete understanding of the underlying mechanisms. The quantitative pathology of oncogenic protein perturbations (QPOP) platform is an example of this approach applied to soft tissue sarcomas (STS), which are a diverse group of mesenchymal tumors with complex genomics and limited treatment options. The platform is capable of culturing patient-derived tumor cells in the microfluidic device and exposing them to panels of approved and investigational drugs and measuring their viability using automated microscopy and image analysis (Ozcelik et al., 2024).

In prospective studies, QPOP demonstrated accuracy of more than seventy percent in predicting patient response to treatment which is significantly better than the accuracy of genomic biomarker approaches for this type of tumor. Testing dozens of drugs at once allows for discovery of effective drugs, even when there is no indication for a genomically targeted drug, including repurposed drugs from other disease areas. Technical limitations of setting up short term cultures from tumour biopsies, turn around time requirements to match clinical decisions and demonstration of prospective clinical efficacy in RCTs are challenges for functional precision medicine. However, functional methods are becoming popular as adjuncts to genomics, especially for tumors with complex molecular pathology or with a poorly defined molecular pathology (Pamulaparthyv, 2022).

5.6. The evolving landscape of precision oncology

All of these combined progressions in the precision oncology space reflect a rapidly evolving landscape that not only is becoming more sophisticated with regard to targeting strategies, but is also diversifying the range of tumors that can be targeted and combining precision oncology with other complementary methods such as genomics, functional testing and immune profiling. Implications from this landscape are moving beyond the single agent approach to combination therapies to combat resistance, using precision medicine approaches to other disease settings, such as adjuvant and neoadjuvant therapy, and the development of adaptive trial designs that match patients to therapies based on real time molecular profiling (Pan, 2024). Liquid biopsy methods for serial analysis of tumor evolution are now being increasingly adopted as tools to detect the emergence of resistance mutations and tailor treatment before the onset of clinical progression, without the need for invasive tissue biopsies. The regulatory landscape has now adapted to precision

oncology, with tissue-agnostic approvals, biomarker-defined indications, and accelerated approvals for less common molecular subsets. However, significant challenges still exist, such as equitable access to genomic testing and targeted treatments across the health care system, financial toxicity of high-cost precision treatments, and the need for ongoing investment in discovery science to establish effective targeted treatments for tumor types and molecular subsets that are not yet treatable (Panahi, 2025).

6. Precision Medicine Beyond Oncology

6.1. Transplant precision medicine

One area where precision medicine has tremendous potential is in the field of solid organ transplantation, with the promise of personalized immunosuppression and rejection monitoring. The basic problem in transplantation is that of providing enough immunosuppression to prevent graft rejection and at the same time not providing too much to enhance the risks of infection, malignancy and drug toxicity. Genomic variants in drug metabolizing enzymes and transporters have a significant impact on drug metabolism of immunosuppressants, particularly for the drug-metabolizing enzyme, CYP3A5 (Parisi et al., 2025). Patients with at least one functional CYP3A5 allele (CYP3A5 expressors) metabolise tacrolimus about 50% faster than non-expressors who need higher weight-based doses to obtain therapeutic concentrations. Preemptive CYP3A5 genotype testing helps to improve initial dosing and the time to therapeutic range while potentially optimizing graft outcomes (Parvin, Joo, Jung, & Mandal, 2025). In addition to pharmacogenetics, molecular testing has revolutionized the field of monitoring for biomarkers of rejection, as detection of donor-derived cell-free DNA is a sensitive and noninvasive biomarker that is currently available to detect graft injury before loss of graft function (Paulson & Johnson, 2025).

An increase in the peripheral blood levels of donor-derived cell-free DNA is associated with acute rejection episodes, allowing for earlier interventions and the potential reduction of invasive graft biopsies. Algorithms that integrate genomic, pharmacokinetic, biomarker and clinical data and incorporate artificial intelligence are starting to be used to manage immunosuppression in a personalized way, and some of these systems predict the occurrence of rejection events better than conventional algorithms. All of these principles are applicable beyond oncology, and can be seen in the field of transplantation, where precision medicine is being applied (Rajuroy).

6.2. Neurology: plasma-based assays for neurodegenerative disease detection

The challenge of precision medicine has been slow to be accepted in the field of neurology, perhaps in part because it is difficult to access diseased tissue and the central nervous system pathophysiology is complex. However, the plasma-based biomarker assays are undergoing changes in recent years which are now changing the landscape for neurodegenerative disease detection and management. These include phosphorylated tau species, amyloid beta peptides, neurofilament light chain, and glial fibrillary acidic protein, which can all be detected in peripheral blood by highly sensitive immunoassay and mass spectrometry methods during neurodegeneration. These markers allow for precise identification of Alzheimer disease pathology without death, and with performance almost equivalent to PET imaging or CSF analysis (which are very expensive and quite invasive) (Saeed, 2024).

Plasma phosphorylated tau at threonine 181 and threonine 217 discriminates between Alzheimer disease and other dementias with area under the curve scores > ninety percent, which will improve diagnosis and patient selection for clinical trials. In addition to diagnosis, these biomarkers are currently under investigation for the prediction of prognosis, monitoring of treatment and identification of those most likely to benefit from the recently developed disease-modifying therapies. Precision medicine in neurology is still at an early phase compared with oncology, but clearly, the principles of precision medicine are becoming more and more integrated in diagnosing neurological diseases, selecting patients in clinical trials, and making decisions for the treatment of neurological diseases (Parvin et al., 2025).

6.3. Chronic myeloid leukemia: adaptive dosing and molecular monitoring

In oncology, chronic myeloid leukemia (CML) is a success story for precision medicine that predates the widespread use of precision medicine as a term, and demonstrates the power of targeting a specific molecular driver. Inhibition of the BCR-ABL1 fusion oncoprotein, which arises from the translocation of the Philadelphia chromosome, is both necessary and sufficient for chronic myeloid leukemia (CML) pathogenesis, and its inhibition by tyrosine kinase inhibitors such as imatinib, dasatinib and nilotinib leads to sustained responses in most patients. The use of molecular monitoring of BCR-ABL1 transcript levels by quantitative polymerase chain reaction allows a very accurate evaluation of the response to treatment and can detect increasing levels of BCR-ABL1 transcripts, which may indicate the development of resistance. This molecular monitoring has led to adaptive dosing strategies, where patients with deep and persistent molecular responses could be candidates for treatment-free remission, meaning that treatment is stopped but molecular monitoring is kept very close. Stable deep molecular response allows for about 50% of patients to stop therapy without a risk of relapse and thus avoid long-term drug toxicities and costs (Sahoo et al., 2024).

Molecular monitoring has allowed for early intervention for patients whose transcript levels are rising, which may include dose modification, changing to other tyrosine kinase inhibitors, or testing them for resistance mutations using sequencing. In oncology, the chronic myeloid leukemia model has helped to shape precision medicine strategies, illustrating the benefit of a well-defined molecular target, sensitive molecular monitoring assays, and a variety of drugs that target the same target but in different binding modes (Sakil & Jabir, 2025).

6.4. Pediatric precision medicine: unique considerations and opportunities

Pediatric precision medicine has unique considerations and opportunities that differ from its applications in adults. Children are at increased risk for genetic and congenital disorders, many of which can be molecularly diagnosed and treated. For neonates with suspected genetic diseases who are critically ill, rapid whole genome sequencing can result in diagnosis within days, with potential for targeted therapy, where appropriate, withdrawal of ineffective therapy and discussion of prognosis with families. In some series, yields over 40% have been reported, significantly higher than the typical rate of diagnosis in adult populations. But there are also specific problems in pediatric precision medicine: rare pediatric diseases might not be attractive to commercial investment in drug development, the formulation of drug products and dosing regimens might need to be adapted to growing and developing bodies, and the ethical issues of genetic testing in minors involve return of results, storage of genetic material as they become independent adults, etc (Schmidt, 2025). Progress is being accelerated by the growing availability of resources that focus on the developing child genome, such as reference datasets that provide information on how gene expression changes throughout development and on the normal variation in expression.

Moreover, the success of gene therapy in SMA and other paediatric genetic diseases shows the impact that precision approaches can have in a monogenic disease with a known molecular pathophysiology. Emerging precision medicine applications involving these various disease categories are summarized in Table 3 including therapeutic modalities, types of biomarkers, and the level of clinical impact. The table shows that there are precision medicine applications with solid clinical promise in oncology, with transplantation and neurology being the most mature, followed by hematology and pediatrics (Sedano et al., 2025). As shown in the table, the different biomarkers for different disease areas and the therapeutic modalities used will differ, but common principles such as molecular characterization and selection of therapy based on biomarkers, as well as monitoring the response to therapy, apply to all disease areas. The clinical impact level is based on evidence quality and guideline inclusion and ranges from established as in the case of chronic myeloid leukemia to

emerging as in the case of pediatric genomic medicine (Serrano, 2023).

Table 3. ***Emerging Applications of Precision Medicine Across Disease Areas***

Disease Area	Therapeutic Modality	Biomarker Type	Clinical Impact Level
Oncology (solid tumors)	Targeted therapy, ADC, immunotherapy	Genomic, protein expression	Established
Hematology (CML)	Tyrosine kinase inhibitors	BCR-ABL1 transcript level	Established
Transplantation	Personalized immunosuppression	CYP3A5 genotype, donor-derived cfDNA	Emerging
Neurology	Plasma-based diagnostics	Phosphorylated tau, NfL, Aβ	Emerging
Pediatrics	Rapid WGS, gene therapy	Pathogenic variants	Emerging

7. From Discovery to Clinical Practice: Implementation Challenges

7.1. The biomarker translation gap

However, the incorporation of new biomarkers into the clinic is still surprisingly slow and inefficient, after many years of intensive biomarker discovery efforts. Over one hundred thousand biomarker studies have been published, and thousands of potential diagnostic, prognostic and predictive markers have been identified in almost every disease. However, only a few have made it through the entire journey from finding to acceptance, guidelines to clinical practice. This gap between discovery and implementation, also known as the biomarker translation gap, is a major hurdle to achieving the promise of precision medicine. There are a number of contributing factors. Many published biomarker studies have small sample sizes, no independent validation cohorts, or have used inappropriate statistical methods that inflate estimates of performance. Well-designed discovery studies can identify biomarkers that are associated with disease status in retrospective series, but are not clinically useful in prospective randomized trials (Shahid & Khattak, 2022).

Another aspect of the translation gap is large investments in discovery and minimal follow-through investments in implementation, as was the case for the penny-farthing problem, which received a large investment in discovery and a low investment in implementation (Aakriti Sharma, Mishra, & Singh, 2024). Although significant investments are made in conducting high throughput omics studies to identify candidate biomarkers, relatively few resources are allocated to method validation, clinical trial infrastructure, regulatory navigation and implementation science needed to get biomarkers to patients. Coordinated actions will be needed to bridge the translation gap, such as prespecified analysis plans for biomarker studies, required independent validation studies for publication acceptance, more funding for implementation research, and regulatory frameworks that understand the specific evidentiary issues that surround biomarker development. The pipeline for implementing the discovery of a biomarker in clinical use is shown in figure 4. As illustrated in the figure, the pathway starts with discovery and initial validation studies, moves forward to analytical validation and clinical validation, and then encounters significant challenges for regulatory approval, reimbursement, and clinical adoption (Aneesh Sharma, Sharma, & Yang, 2023).

Estimated attrition rates are shown in each stage, with most candidate biomarkers terminated in the validation stage because of poor reproducibility, a

lack of prospective data, or commercial reasons. The figure reflects the importance of regulatory fragmentation (diagnostic standards are not harmonized across regulatory jurisdictions) and reimbursement gaps (diagnostic funding is not aligned with therapeutic funding) as key rate limiting factors. The last challenges to the successful implementation are clinician education and integration of the EHR. Identifying these key factors is crucial to formulate strategies which will promote faster biomarker translation (Sherani, Khan, Qayyum, & Hussain, 2024).

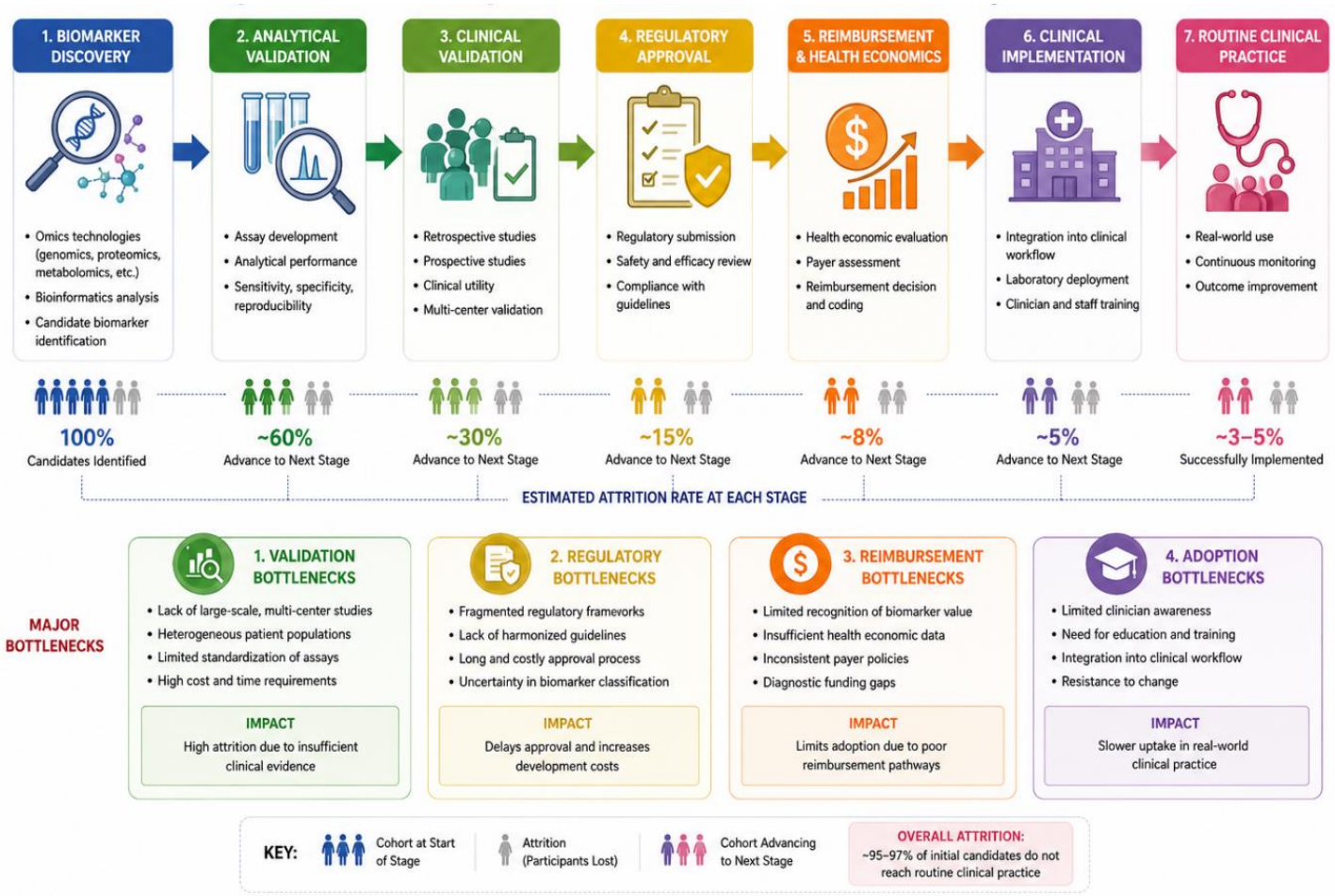

Figure 4. The Implementation Pipeline from Biomarker Discovery to Clinical Practice

7.2. Regulatory and reimbursement barriers

Even if biomarkers can make it through the translation funnel from discovery to validation, significant regulatory and reimbursement hurdles frequently block the way to clinical use. The regulatory structure for therapeutic approval is in place, including pathways for drugs and biologics which include requirements for preclinical toxicology studies, staged clinical trials and manufacturing quality standards. But the frameworks for diagnostic tests, such as companion diagnostics to identify patients who can benefit from targeted therapies, have been historically less standardized, and more fragmented by jurisdictions (Siddiqui, 2024). Laboratory-developed tests in the United States can be marketed without premarket evaluation by the Food and Drug Administration, which may potentially result in differences in analytical and clinical validity from laboratory to laboratory. In Europe, the In Vitro Diagnostic Regulation has established more stringent requirements for

diagnostic test approval, but implementation has been challenging due to capacity constraints and uncertainties about classification. Reimbursement is a huge obstacle in addition to regulatory approval. Almost all health systems have a therapeutic to diagnostic funding ratio imbalance (A. P. Singh, Saxena, Saxena, & Maurya, 2024).

Drugs are usually paid on a scale proportional to their clinical value, and there are big revenue streams to fund development and marketing. In contrast, the reimbursement amounts for many diagnostic tests are insufficient to cover the costs of development or to encourage innovation, although the test result will help inform the costly therapeutic decision. This imbalance has been called the diagnostic funding gap. Precision medicine AI tools are especially complex when it comes to reimbursement, as most payment systems do not have specific payment codes for the outcomes of AI algorithms and have trouble assigning value to avoidable adverse events, or to avoiding unnecessary care (Sherani et al., 2024).

7.3. Diversity in genomic datasets

Precision medicine is facing a scientific and ethical emergency due to the striking lack of diversity in genomic datasets. Genome-wide association study and sequencing projects show that about 86% of the people analysed are of European descent, while only 16% of the world's population is of European origin. Such Eurocentric bias can have significant implications for equitable precision medicine implementation. The frequencies of variants vary significantly among ancestry groups and many clinically important pharmacogenes have frequencies that deviate from European data and could be inaccurate or misleading for other populations. Polygenic risk scores (PRSs), which sum the effects of thousands of variants to predict disease risk, exhibit especially low cross-population portability, meaning that they often yield very different results in groups of non-European ancestry, reflecting differences in the frequency and LD patterns of these populations. These inconsistencies also mean that common variants in non-European populations may not be found in European ones and so may not be used in diagnostics, or for developing targeted therapies. This challenge calls for deliberate efforts to recruit diverse cohorts, community-based participatory research approaches to establish partnerships and trust with underrepresented communities, capacity building in low resource settings, and funding structures that see diversity as a scientific imperative, not an optional add-on (A. P. Singh et al., 2024).

7.4. The path forward for clinical implementation

While the challenges to be addressed are significant, as outlined above, the path forward for the implementation of precision medicine is becoming increasingly clear, yet with the sustained commitment from all stakeholders. While ongoing investment in discovery science to find new biomarkers and therapeutics will be necessary, so will be investment in implementation science to understand and overcome implementation barriers. Innovative regulation, such as adaptive pathways, real world evidence frameworks, and parallel review of therapeutics and companion diagnostics can speed up access without compromising safety (A. P. Singh et al., 2024). The economic sustainability depends on reimbursement reform, which includes value-based payment models that take into account how diagnostic tests help improve outcomes while decreasing unnecessary care. Education of clinicians in concepts of genomic medicine, and of genetic counselors to facilitate test interpretation and communication with patients are essential for scaling precision medicine outside of academic medical centers. Education and engagement of patients and the public will be required to develop understanding and trust, which will need to overcome unrealistic expectations and unwarranted fears about genomic medicine. The challenges to implementation are both very real and significant, but not insurmountable, and the benefits to patients are worth the investment (G. Singh, Bajpai, & Bhandari, 2024).

8. The Role of Artificial Intelligence and Data Science

8.1. AI in diagnostic accuracy: pathology, imaging, and predictive modeling

In the field of diagnostic medicine, AI is making a significant impact, from digital pathology and medical imaging to integrated predictive modeling. For some pathological tasks such as detection of mitotic figures, tumor classification and quantification of biomarkers, the performance of deep learning algorithms is comparable or better than a human expert. These algorithms can be taught to pick out the morphology linked to particular molecular modifications, which allows molecular standing to be predicted from the commonplace histology slides without the necessity for further sequencing (G. Singh et al., 2024). For instance, in radiology, CNNs can be trained to identify very faint abnormalities that are not apparent to the human eye, such as tiny lung nodules in a computed tomography (CT) scan or microhemorrhages in a magnetic resonance imaging (MRI) scan or nearly imperceptible fractures in plain radiography (X-rays). AI models are now not only detecting, but also offering a probabilistic differential diagnosis and suggesting further tests if there is uncertainty in a diagnosis. Their incorporation into clinical practice could enhance diagnostic accuracy, minimize inter-observer variability, and alleviate the shortage of pathology and radiology staff. But, achieving this is not without its challenges, as algorithm validation on varied patient groups, integration with EHR systems, and training clinicians to interpret AI results are all crucial aspects of successful implementation (Sedano et al., 2025).

8.2. Machine learning for drug response prediction

One of the most promising applications of machine learning is the prediction of individual patient drug responses, due to the complex and nonlinear relationships between molecular features and clinical outcomes. Conventional methods of response prediction have been based on a single biomarker (e.g. genomic modifications), with only a fraction of the response variability accounted for. By combining hundreds or thousands of features from multiomics data, electronic health records and demographic information, machine learning models can be able to make more accurate, individualised predictions (M. Singh et al., 2025). For instance, gene expression-based models are more effective in predicting response to immunotherapies than PD-L1 expression alone or tumour mutational burden. Likewise, models that combine clinical characteristics with genomic and laboratory information could be used to anticipate the danger of serious adverse reactions to medications, and in doing so, could help to adjust doses or select alternative therapies. When facing longitudinal data from the EHR, RNNs or transformer architectures can be useful to learn temporal patterns that are predictive of disease progression or response to treatment, which may be challenging or impossible for human clinicians to integrate from the serial measurements. Clinical trials testing these models are still ongoing and may be a source of prospective validation of these models, some of which have shown that patient outcomes are better when using algorithm-assisted decision support over traditional approaches (Srivastav, Das, & Srivastava, 2024).

8.3. Integration of electronic health records with multiomics data

Multiomics data must be integrated with electronic health record data to give a comprehensive view of a patient's health trajectories and to realize the full potential of AI in precision medicine. A wealth of longitudinal information exists within EHRs, such as diagnoses, procedures, medication history, laboratory results, vital signs, and clinical notes, that play a role in interpreting genomic and other molecular data. But, the interoperability of such disparate data types is far from trivial in terms of both technical and organizational challenges. EHRs may lack structured data, data may be inconsistently encoded, or the data might be incompatible among different health care systems. In clinical notes, unstructured data must be processed using natural language processing to glean its meaning, but is made challenging by variable documentation styles, abbreviations, and implicit

data, which is hard to algorithmically capture. Data sharing between institutions is challenging due to privacy and security considerations, but federated learning can be used to train models on decentralized data without centralization (Stojanovska, 2025). Yet, trailblazing health care delivery organizations have started to adopt integrated data platforms that integrate genomics data with imaging, laboratory and clinical data for each patient and are available in real time for decision support at the point of care (Sundari, Rishitha, Majety, & Vegiraju, 2025).

Figure 5 shows a precision medicine workflow implemented with AI, which combines these different data. The workflow starts with the collection of patient data from different sources like genomics, medical imaging, electronic health records or lifestyle monitoring devices as depicted in the figure. These data are fed into machine learning algorithms that classify the diseases, select treatments, and predict outcomes. One important aspect that is represented in the figure is the iterative nature of learning, where predictions are checked against observed results, and the model is improved over time as more data is collected. This continuous improvement can lead to more precise recommendations with experience using more patients and varied clinical situations (Tabery, 2023). The figure highlights that AI is not meant to replace clinical decision-making but to complement it, offering probabilistic predictions and decision support that are meant to guide rather than dictate clinical decisions. To integrate AI into everyday clinical practice, factors like usability, explainability, and trust must be considered.

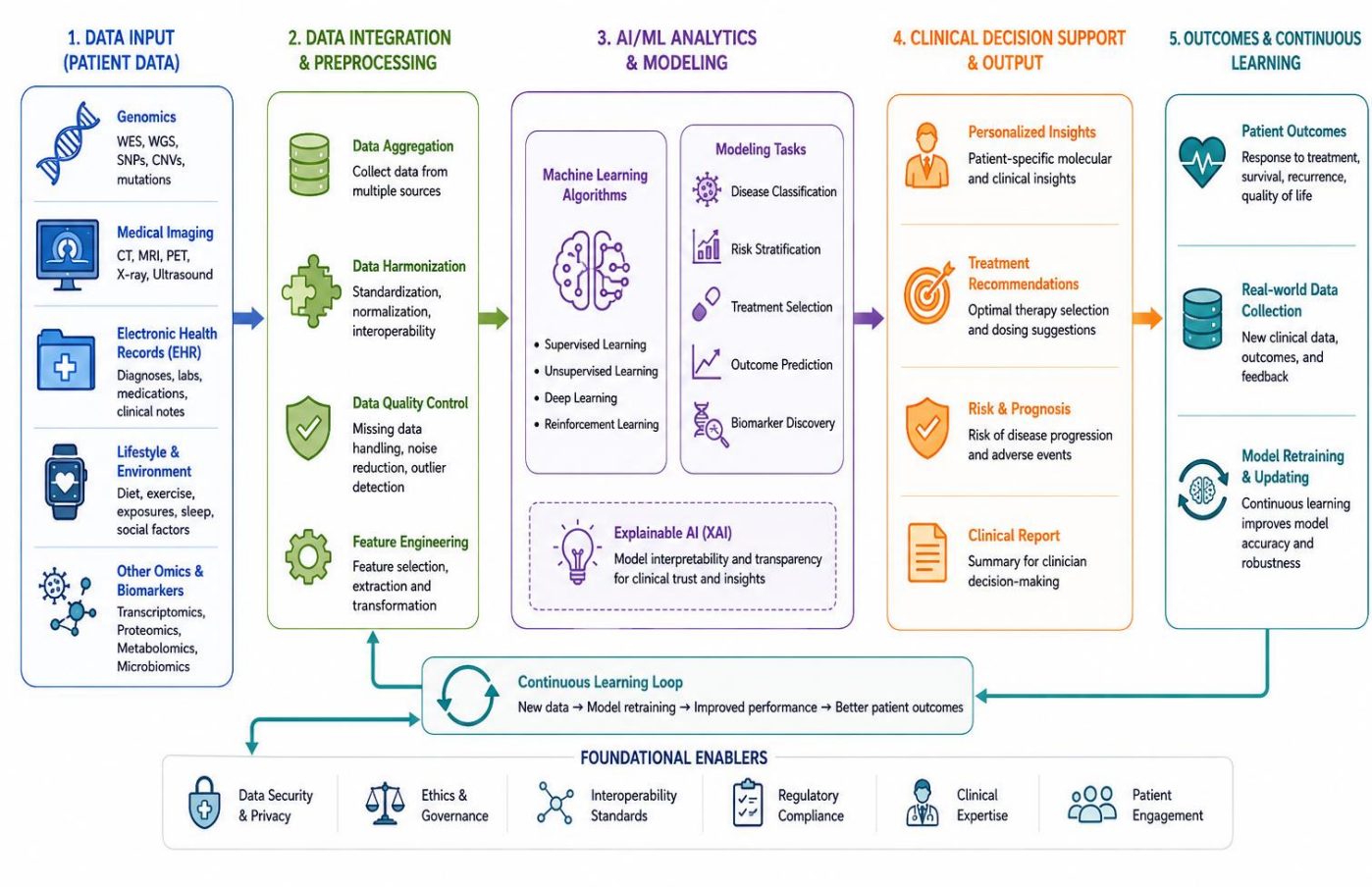

Figure 5. ***AI-Enabled Precision Medicine Workflow***

8.4. Algorithm-assisted precision dosing8.4

Precision dosing, which is powered by algorithm, is one tangible use of AI that is already enhancing patient results in a number of therapeutic areas. Initial dose selection is traditionally based on population average pharmacokinetic parameters, with empirical dose adjustments made based on therapeutic drug monitoring or clinical response. Algorithm-assisted methods use the individual patient data such as genotype, demographic parameters, measures of organ functions and drug concentrations to make personalized dose recommendations based upon a Bayesian forecasting model or a machine learning model. Algorithm-assisted dosing has been proven for warfarin, a narrow therapeutic index drug with high genomic and environmental variability, to decrease time in subtherapeutic or supratherapeutic range, as compared to standard dosing. Algorithmic dosing results in higher target attainments and less nephrotoxicity with vancomycin and aminoglycoside antibiotics (Tagoe, Quainoo, Clotworthy, Ofori, & Amponsah, 2025). In transplant recipients, algorithm based dosing of immunosuppressants that includes therapeutic drug monitoring and genotype of the cytochrome P450 3A5 gene also decreases rejection episodes and drug toxicity. These algorithms have been incorporated into EHRs with clinical decision support (CDS) alerts, and have been seen to improve adoption and clinical outcomes, although alert fatigue and integration into the workflow are issues (Taheri & Bakhtiari, 2024).

As AI continues to evolve and be integrated into precision medicine, its potential capabilities will grow more powerful, such as the ability to process multimodal data, which combines genomic sequences, medical imaging data, clinical text, and time-series data (Yeung et al., 2023). Generative AI models can help in generating reports, patient communication, and matching clinical trials. Sequential treatment decisions could be optimized using reinforcement learning, which could learn from past treatment results to suggest personalized treatment sequences over time. The goal of causal machine learning is to go beyond prediction to causal inference which is estimating the effect of a specific intervention for an individual patient (Tawfik et al., 2023). But, much work lies ahead to ensure that this future becomes a reality, such as algorithm bias, explainability, algorithm validation and regulation of algorithms that are continually learning. To achieve equitable and safe use of AI tools in improving patient outcomes, collaboration between computer scientists, clinicians, regulators, and patients is essential (Tawfik et al., 2023).

9. Future Perspectives and Unanswered Questions

9.1. Toward predictive and preventive healthcare models

Precision medicine is not just about treatment matching to patients with known disease; it is a paradigm shift that will ultimately bring about predictive and preventive medicine. This model involves the detailed molecular characterisation of individuals early in life, so that a baseline is set for future assessment on an individual basis. High-risk groups for certain diseases are targeted for specific prevention, such as lifestyle changes, more frequent surveillance, pharmacologic prophylaxis and even gene therapy for monogenic disease with high penetrance (Tesi et al., 2023). While this transition from reactive to proactive medicine has the potential to lower disease burden and health care costs, it presents some significant issues related to overdiagnosis, adverse psychological effects of risk information, and economic considerations of intervening in healthy populations.

9.2. The genotype-first or "reverse phenotyping" approach

The traditional approach to medical genetics has been a phenotype-driven one, where patients with certain clinical features were first sent for genetic testing, which may lead to a molecular diagnosis. This paradigm is reversed with the genotype-first or reverse phenotyping approach, which starts with sequencing the genome of unselected individuals and then deep phenotyping selected individuals with specific genotypes of interest. This strategy has been very successful in identifying novel genotype-phenotype

relationships, identifying individuals carrying pathogenic variants, but without classical clinical features, and elucidating complete penetrance and expressivity of genetic disorders (TumkurSattar, Abushoumi, Al Dobayan, & Al-Ghamdi, 2023). Population-scale sequencing projects involving genotype-first approaches have redefined estimates of genotype-phenotype correlation for many conditions in which some well-defined pathogenic variants have had significantly reduced penetrance than was previously thought from clinically ascertained cohorts (Usmani, Watada, & Usmani, 2024).

9.3. Precision nano-oncology: smart delivery systems and theranostic platforms

Nanotech and precision medicine have started to converge, which could herald a new era in drug delivery and diagnostic imaging. Precision nano-oncology is a field that combines smart delivery systems to selectively release therapeutic payloads in the presence of specific tumor-associated stimuli, such as acidic pH, enzymatic activity, and reducing conditions found in cancer cells. Theranostic nanoparticles are designed to combine both diagnostic and therapeutic effects in one platform, which allows real-time tracking of the drug delivery and release (Vij, 2024). Conventional chemotherapeutics, nucleic acid-based drugs, or immunomodulatory drugs can be encapsulated in tumor-targeted nanoparticles to deliver more of the drug to the tumor and less to the rest of the body than conventional drug delivery. Scalability, batch to batch consistency and other regulatory hurdles for combination drug-device products must be overcome for clinical translation of these technologies (Tawfik et al., 2023).

9.4. International harmonization of regulatory frameworks

Greater international harmonization of regulatory frameworks for precision medicine are needed, given the global nature of drug development and biomarker discovery. The status quo of the fragmented regulatory landscape leads to inefficiencies, access delays for patients, and uncertainty for developers (Tabery, 2023). Examples of areas where harmonization is needed encompass standards for validation and approval of companion diagnostics, standards for evidentiary requirements for tissue-agnostic indications, framework for evaluating multi-marker tests and algorithmic classifiers, and strategies for regulating software as a medical device. International collaboration, such as the International Medical Device Regulators Forum and the International Coalition for Medicines Regulatory Cooperation, is seeking alignment, although it has not been as fast or as strong as many stakeholders would like (Voss, 2024).

9.5. Open data platforms and precompetitive collaboration

Precision medicine research is so complex and large in scope that no single institution or company is able to handle it alone, requiring open data platforms and precompetitive collaboration. To ensure the responsible sharing of genomic and phenotypic information beyond institutional and national boundaries, there are initiatives like the Global Alliance for Genomics and Health, the European Genome-phenome Archive and the Database of Genotypes and Phenotypes (Waaje, Karim, Roshid, Yeamin, & Meem, 2025). Precompetitive consortia such as the Structural Genomics Consortium and the Accelerating Medicines Partnership (AMP) unite industry, academia, and non-profit groups to engage in basic research on drug targets to be shared freely. While these models are collaborative, they have helped to speed up discovery and decrease duplication of effort, but they do need to be mindful of data governance, data privacy, and benefit-sharing with research participants and their communities (Weerasinghe, Pathirana, Jayasuriya, & Warnakulasooriya, 2021).

10. Conclusion:

The shift of precision therapeutics from theory to practice is one of the most important paradigm changes in the history of medicine. The systematic identification of genomic variants that impact disease susceptibility, disease progression and treatment response has been made possible by the foundation laid by the Human Genome Project. The advent of next generation and long read

sequencing has led to more widespread access to comprehensive genomic profiling and existing pharmacogenomic implementation programs have been adopted to guide prescribing across a number of therapeutic areas to millions of patients. Combining multiple layers of omics data, facilitated by artificial intelligence and advanced bioinformatics techniques, is painting ever more comprehensive molecular images of each patient. Precision oncology is the most advanced area, and new modalities such as antibody-drug conjugates, HIF-2α inhibitors, and functional drug testing platforms are showing tremendous clinical success. Examples of such applications, other than oncology, such as transplantation, neurology, and pediatrics, among others, demonstrate the wide applicability of precision medicine concepts.

But, there are many obstacles that need to be overcome if precision medicine is to fulfil its promise. The biomarker translation gap remains a hurdle in making the leap from discovery to clinical use. Regulatory fragmentation and reimbursement constraints pose economic hurdles that are especially hard on diagnostic innovation. It is striking how little diversity exists in current genomic reference datasets, which run the risk of widening rather than narrowing health gaps. Solving these issues will take continued investment, creative regulation, reimbursement, workforce development, and a continued commitment to equity.

Predictive, preventive, personalized and participatory medicine, as envisioned by those who advocate for it, is a lofty goal but one that is becoming more and more real. This vision requires integrated efforts from academia, industry, healthcare systems, regulators and patient communities. The scientific underpinning is strong, the technological tools are becoming more powerful and the clinical evidence base is growing. It is no longer a question of if precision medicine will revolutionize medicine, but rather when, how and how much. The promise of precision therapeutics holds hope for improved outcomes and fewer harms for patients with cancer, rare diseases, adverse drug reactions and the myriad other diseases where one-size-fits-all has failed. The work of making that promise a reality goes on.

REFERENCES

Aarif, K. M., Hasan, V. M. Y., Alam, A., Ali, K. S., & Pakruddin, B. (2025). Decoding DNA: deep learning's impact on genomic exploration. In *Deep learning in genetics and genomics* (pp. 77-95): Elsevier.

AbuAlrob, M. A., Itbaisha, A., & Mesraoua, B. (2025). Unlocking new frontiers in epilepsy through AI: From seizure prediction to personalized medicine. *Epilepsy & Behavior, 166*, 110327.

Addissouky, T., Ali, M., El Sayed, I. E. T., & Wang, Y. (2023). Revolutionary innovations in diabetes research: from biomarkers to genomic medicine. *Iranian journal of diabetes and obesity*.

Adeghe, E. P., Okolo, C. A., & Ojeyinka, O. T. (2024). The role of big data in healthcare: A review of implications for patient outcomes and treatment personalization. *World Journal of Biology Pharmacy and Health Sciences, 17*(3), 198-204.

Ahmed, F. (2024). Genomics and bioinformatics: integrating data for better genetic insights. *Frontiers in Biotechnology and Genetics, 1*(2), 126-146.

Ahmed, M. S., Das, P. J., & Mandal, S. 26 PHARMACY OF TOMORROW: NAVIGATING INNOVATIONS IN TECHNOLOGY, PERSONALIZED MEDICINE, AND NANOTECHNOLOGY. *INNOVATIVE RESEARCH*, 179.

Alhajahjeh, A., & Nazha, A. (2024). Unlocking the potential of artificial intelligence in acute myeloid leukemia and myelodysplastic syndromes. *Current Hematologic Malignancy Reports, 19*(1), 9-17.

Ali, A., Al-Rimy, B. A. S., Tin, T. T., Altamimi, S. N., Qasem, S. N., & Saeed, F. (2023). Empowering precision medicine: Unlocking revolutionary insights through blockchain-enabled federated learning and electronic medical records. *Sensors, 23*(17), 7476.

Ali, H. (2023). Artificial intelligence in multi-omics data integration: Advancing precision medicine, biomarker discovery and genomic-driven disease interventions. *Int J Sci Res Arch, 8*(1), 1012-1030.

Allen, B. (2024). The promise of explainable AI in digital health for precision medicine: a systematic review. *Journal of personalized medicine, 14*(3), 277.

Arianpour, A. (2024). Unlocking the Power of Patient Data: A Catalyst for Precision Medicine. *Inside Precision Medicine, 11*(3), 32-34.

ASLAM, S., MASOUD, M. S., ASHFAQ, U. A., ANSARI, M.-u. R., NAHID, N., IMRAN, M., . . . QASIM, M. (2024). Genomic tools and technologies: revolutionizing livestock improvement. *ANIMAL PRODUCTION and HEALTH*, 46.

Attaran, S., & Attaran, M. (2024). Advancing healthcare through the integration of digital twins technology: Personalized medicine's next frontier. *Future Internet, 16*(12), 477.

Ayoola, F., Oladele, S., & Faline, P. (2024). The Role of Machine Learning in Revolutionizing Healthcare.

Aziz, M., Asif, M., Ullah, I., Salma, U., Sial, N. T., Qamar, S., . . . Dahesh, S. M. (2025). Personalized Treatment in Oncological Therapeutics: Unlocking Targeted Cancer Treatment.

Bajjash Alhadi, T. M., Mohamed Albager, A. H., Alotaibi, W. F., Aljurayan, R. M., Nasser Al Nasser, I. N., Alshahrani, A. A., . . . Hussein Al-Yami, S. A. (2023). Biopharmaceuticals: Unlocking The Potential Of Biological Therapies. *Journal of Namibian Studies, 36*.

Balasubramanyam, A., Ramesh, R., Sudheer, R., & Honnavalli, P. B. (2024). Revolutionizing healthcare: A review unveiling the transformative power of digital twins. *IEEE Access, 12*, 69652-69676.

Bhatia, A., Kumar, A., Kumar, R., & Jain, V. (2025). Medications and the Role of Tailored Healthcare. In *Smart Healthcare, Clinical Diagnostics, and Bioprinting Solutions for Modern Medicine* (pp. 165-192): IGI Global Scientific Publishing.

Borawake, D., Shaikh, R. J., Shaikh, N. P., & Wadghule, A. S. (2025). Future of Precision Medicine with AI: Shaping the Future of Personalised Healthcare. *Biopress Journal of Computational Life Sciences (BJCLS), 1*(03), 7-20.

Chacon, J., Faizuddin, F., McKee, J. C., Sheikh, A., Vasquez Jr, V. M., Gadad, S. S., . . . Dhandayuthapani, S. (2025). Unlocking the microbial symphony: The interplay of human microbiota in cancer immunotherapy response. *Cancers, 17*(5), 813.

Channi, H. K., Sandhu, R., Kaur, M., & Ghai, D. (2025). Precision medicine and personalized treatment. In *Advancing Healthcare through Decision Intelligence* (pp. 151-174): Elsevier.

Chaudhary, U., Ali, M. F., Kumar, A., Sharma, A., & Jayakody, D. N. K. (2025). Unleashing the power of wireless communication in healthcare by empowering patient care and connectivity: A comprehensive survey. *IEEE Access*.

Chauhan, A. S., Singh, R., Priyadarshi, N., Twala, B., Suthar, S., & Swami, S. (2024). Unleashing the power of advanced technologies for revolutionary medical imaging: pioneering the healthcare frontier with artificial intelligence. *Discover Artificial Intelligence, 4*(1), 58.

Chen, Y.-M., Hsiao, T.-H., Lin, C.-H., & Fann, Y. C. (2025). Unlocking precision medicine: clinical applications of integrating health records, genetics, and immunology through artificial intelligence. *Journal of Biomedical Science, 32*(1), 16.

Chigozie, V. U., Aniokete, C. U., Ogbonna, P. I., & Iroha, R. I. (2025). Transforming antimicrobial resistance mitigation: the genomic revolution in one health and public health. *Discover Applied Sciences, 7*(10), 1187.

Chrysanthakopoulou, D., & Koutsojannis, C. (2025). Unlocking the power of digital twins in personalized healthcare. *World J Adv Res Rev, 25*(2), 1193-1199.

Cioroboiu, C., & Popescu, R. (2024). Genetic Health. *A Glimpse at Medicine in the Future*, 79.

Darwish, A. S. K. (2025). Harnessing AI for Revolutionary Healthcare Transformation in Nanotechnology. In *Nanotechnology For Medicine* (pp. 364-385): CRC Press.

Das, S., Roy, R., Sarkar, A., Bose, R., Sarkar, I., & Roy, S. (2025). *Revolutionizing Healthcare: Synergistic Integration of Genomics, Clinical Decision Support Systems, and Advanced Machine Learning for Precision Medicine.* Paper presented at the 2025 AI-Driven Smart Healthcare for Society 5.0.

Desta, G. M., & Aserese, M. B. (2024). Revolutionizing Personalized Medicine: Synergy with Multi-Omics Data Generation, Main Hurdles, and Future Perspectives.

Dimple, M. " Revolutionizing Personalized Medicine with Digital Twin Technology.

Domadiya, D. H. (2024). Revolutionizing Healthcare: Unleashing the Power of Machine Learning for Patient-Centric Solutions. *Shodh Sari-An Int. Multidiscip. J, 3*(02), 64-76.

Ehyaei Rad, N. (2025). Synthetic Biology in Genomics: Redefining Genetic Engineering and Its Applications in Personalized Medicine. *Advanced Therapies Journal, 7*(22), 61-69.

Eskandar, K. (2023). Artificial intelligence in healthcare: explore the applications of AI in various medical domains, such as medical imaging, diagnosis, drug discovery, and patient care. *Series Med Sci, 4*(1), 37-53.

Falkner, S. The Intelligent Revolution in Healthcare: AI and Biosensors Leading the Way. *Arch Adv Art Intel Data Sci Mach Learn 2025; 1 (1): 1, 13.*

Fatima, G., Siddiqui, Z., & Parvez, S. (2024). AI and precision medicine: paving the way for future treatment.

Fon, T. E., Kenneth, Y. A., Ndofor, A. E., Veranso, L. J. T., Nkongwa, N. S., & Achungu, C. R. (2024). Genomic revolution in parasitology: Unlocking the mysteries of parasites.

Frascarelli, C., Bonizzi, G., Musico, C. R., Mane, E., Cassi, C., Guerini Rocco, E., . . . Reggiani Bonetti, L. (2023). Revolutionizing cancer research: the impact of artificial intelligence in digital biobanking. *Journal of personalized medicine, 13*(9), 1390.

Fu, S. W., Tang, C., Tan, X., & Srivastava, S. (2024). Liquid biopsy for early cancer detection: technological revolutions and clinical dilemma. *Expert Review of Molecular Diagnostics, 24*(10), 937-955.

Geanta, M., Boata, A., Cucos, B., Cioroboiu, C., & Popescu, R. (2024). Genetic Health. In *A Glimpse at Medicine in the Future* (pp. 79-91): Springer.

Ghebrehiwet, I., Zaki, N., Damseh, R., & Mohamad, M. S. (2024). Revolutionizing personalized medicine with generative AI: a systematic review. *Artificial Intelligence Review, 57*(5), 128.

Goswami, S., & Sharma, S. (2024). *Artificial intelligence, quantum computing and cloud computing enabled personalized medicine in next generation sequencing bioinformatics.* Paper presented at the 2024 IEEE International conference on interdisciplinary approaches in technology and management for social innovation (IATMSI).

Gouripur, K. (2024). The impact of artificial intelligence on healthcare: A revolution in progress. *The North and West London Journal of General Practice, 10*(1).

Gupta, S. (2024). AI-metagenomics fusion: paving the way for precision Microbiomics. In *Genomic Intelligence* (pp. 319-328): CRC Press.

Han, X., Cai, C., Deng, W., Shi, Y., Li, L., Wang, C., . . . Fang, B. (2024). Landscape of human organoids: Ideal model in clinics and research. *The Innovation, 5*(3).

Harrison, J. (2024). Impact of the Genomics Revolution on Drug Development and Personalized Medicine in Pharmaceutics. *IJIPE-International Journal of Innovation in Pharmacy Education, 1*(1).

Heesen, P., Schelling, G., Birbaumer, M., Jäger, R., Bode, B., Studer, G., & Fuchs, B. (2024). Real-world-time data and RCT synergy: advancing personalized medicine and sarcoma care through digital innovation. *Cancers, 16*(14), 2516.

Husnain, A., Rasool, S., Saeed, A., & Hussain, H. K. (2023). Revolutionizing pharmaceutical research: Harnessing machine learning for a paradigm shift in drug discovery. *International Journal of Multidisciplinary Sciences and Arts, 2*(4), 149-157.

Hussain, K. (2024). Revolutionizing healthcare: The impact of artificial intelligence on patient care, diagnosis, and treatment.

Ikwelle, T. A., Ihim, A. C., Ozuruoke, D. F., Obi, P. C., Obi, C. U., Onuora, I. J., . . . Romanus, O. O. (2025). Multi-Omics Integration in Personalized Medicine: Advancing Laboratory Diagnostics and Precision Therapeutics in the Era of Individualized Healthcare. *Journal of Drug Delivery & Therapeutics, 15*(5).

Jabbar Basha, S. A., KP, K., Angel, M., Yadavalli, V., Nagaraju, G. V., & Ramu, J. (2024). The Role of Artificial Intelligence in Precision Medicine: Bridging Data Science and Patient Care. *Frontiers in Health Informatics, 13*(8).

Jain, N. EMERGING TRENDS IN BIOTECHNOLOGY: UNLOCKING THE FUTURE. *BIOPROCESS ENGINEERING, 85*.

Khan, S. N., Danishuddin, Khan, M. W. A., Guarnera, L., & Akhtar, S. M. F. (2025). Multi-modal AI in precision medicine: integrating genomics, imaging, and EHR data for clinical insights. *Frontiers in Artificial Intelligence, 8*, 1743921.

Khare, N., & Khare, P. (2024). Personalised medicine and molecular docking: tailoring drug discovery for individual patients. In *Unravelling Molecular Docking-From Theory to Practice*: IntechOpen.

Khondakar, K. R., Tripathi, D., Mazumdar, H., Ahuja, K., & Kaushik, A. (2024). Tailored MXenes and graphene as efficient telemedicine platforms for personalized health wellness. *Materials Advances, 5*(10), 4091-4111.

Kolanu, N. D. (2024). CRISPR–Cas9 gene editing: curing genetic diseases by inherited epigenetic modifications. *Global medical genetics, 11*(01), 113-122.

LB, K., S, V., Kotei, E., Gadde, A., Kothamasu, G. A., & Nallabantu, S. C. (2024). AI and the next medical revolution: Deep learning's uncharted healthcare promise. *Engineering Research Express, 6*(2), 022202.

Maleki Varnosfaderani, S., & Forouzanfar, M. (2024). The role of AI in hospitals and clinics: transforming healthcare in the 21st century. *Bioengineering, 11*(4), 337.

Mandala, G., Reddy, R., Nishanth, A., Yasmeen, Z., & Maguluri, K. K. (2023). AI and ml in healthcare: redefining diagnostics, treatment, and personalized medicine. *International Journal of Applied Engineering & Technology, 5*(S6).

Mazumdar, H., Khondakar, K. R., Das, S., Halder, A., & Kaushik, A. (2025). Artificial intelligence for personalized nanomedicine; from material selection to patient outcomes. *Expert Opinion on Drug Delivery, 22*(1), 85-108.

Mohammadi, A. T., Amini, K., Mojtahedzadeh, M., Arjipour, M., Mehrpooya, M., Mahdilou, M., & Ghanbarzadeh, E. (2024). *Exploring Boundless Horizons: Medicine and Pharmacy*: Nobel Sciences.

Mohammadi, A. T., Far, Y. K., Amini, K., Mehranfar, S., Sofiani, T. P., Razmi, M., . . . Bozorgi, M. (2024). *Nano revolution: unleashing the power of nanotechnology in healthcare*: Nobel Sciences.

Mohammadi, A. T., Far, Y. K., Fathi, H., Zareii, D., Shekarian, N., Kazemi, A., . . . Sofiani, T. P. (2024). *BioPharma Revolution: Exploring the Nexus of Biotechnology and Pharmacology*: Nobel Sciences.

Molla, G., & Bitew, M. (2024). Revolutionizing personalized medicine: synergy with multi-omics data generation, main hurdles, and future perspectives. *Biomedicines, 12*(12), 2750.

Molla, G., & Bitew, M. (2025). The future of cancer diagnosis and treatment: Unlocking the power of biomarkers and personalized molecular-targeted therapies. *Journal of Molecular Pathology, 6*(3), 20.

Muminov, O., Muradov, S., Numonov, D., Ibragimova, E., Norjigitov, A., & Yusupov, D. (2025). *AI and ML in Genomic Research: Unlocking the Potential of Precision Medicine.* Paper presented at the 2025 International Conference on Frontier Technologies and Solutions (ICFTS).

Naithani, K., Tiwari, S., Chauhan, A. S., & Wadawadagi, R. S. (2025). Smart health revolution: Unleashing the power of AI, electronic health records and the IoT for sustainable systems. In *Big Data Analytics and Intelligent Applications for Smart and Secure Healthcare Services* (pp. 129-156): CRC Press.

Nguyen, A. M., Rivera, A. M., & Gualtieri, L. (2023). A new health care paradigm: the power of digital health and e-patients. *Mayo Clinic Proceedings: Digital Health, 1*(3), 203-209.

Nori, L. P., Lohitha, M., Vadapalli, R. R., Bonthagarala, B., Nagineni, S. R., & Kalidindi, V. R. (2025). Revolutionizing Healthcare: The Impact of AI on Precision Medicine. *International Journal of Pharmaceutical Investigation, 15*(2).

Normanno, N., Apostolidis, K., de Lorenzo, F., Beer, P. A., Henderson, R., Sullivan, R., . . . Lawler, M. (2022). *Cancer biomarkers in the era of precision oncology: addressing the needs of patients and health systems.* Paper presented at the Seminars in cancer biology.

Onciul, R., Tataru, C.-I., Dumitru, A. V., Crivoi, C., Serban, M., Covache-Busuioc, R.-A., . . . Toader, C. (2025). Artificial intelligence and neuroscience: Transformative synergies in brain research and clinical applications. *Journal of Clinical Medicine, 14*(2), 550.

Ozcelik, F., Dundar, M. S., Yildirim, A. B., Henehan, G., Vicente, O., Sánchez-Alcázar, J. A., . . . Karanfilska, D. P. (2024). The impact and future of artificial intelligence in medical genetics and molecular medicine: an ongoing revolution. *Functional & integrative genomics, 24*(4), 138.

Pamulaparthyv, S. (2022). Realizing the potential of AI in improving health outcomes: strategies for effective implementation. *ESP Journal of Engineering & Technology Advancements*.

Pan, K. (2024). The Future of Personalized Medicine: How Genomics is Revolutionizing Patient Care. *International Journal of Recent Engineering Science-IJRES, 11*.

Panahi, O. (2025). The Role of Personalized Medicine in Modern Healthcare.

Parisi, G. F., Terlizzi, V., Manti, S., Papale, M., Pecora, G., Presti, S., . . . Leonardi, S. (2025). Cutting-edge advances in cystic fibrosis: from gene therapy to personalized medicine and holistic management. *Genes, 16*(4), 402.

Parvin, N., Joo, S. W., Jung, J. H., & Mandal, T. K. (2025). Multimodal AI in biomedicine: pioneering the future of biomaterials, diagnostics, and personalized healthcare. *Nanomaterials, 15*(12), 895.

Paulson, D., & Johnson, A. (2025). Integrating Artificial Intelligence with Genomic and Biomarker Data for the Advancement of Personalized Therapeutics in a Human-Centric Framework.

Rajuroy, A. AI in Precision Medicine Decoding Genomic Data, Personalizing Treatment, and Safeguarding Data Privacy.

Saeed, M. (2024). Integrating genomic data into clinical practice: implications for precision medicine. *Emerging Trends in Medicine, 1*(2), 57-62.

Sahoo, O. S., Aidasani, H., Nayek, A., Tripathi, S., Talukdar, J., Gul, A., . . . Karmakar, S. (2024). Role of next-generation sequencing in revolutionizing healthcare for cancer management. *MedComm–Future Medicine, 3*(4), e70001.

Sakil, M., & Jabir, M. (2025). AI in Precision Oncology: Revolutionizing Early Diagnosis, Imaging and Targeted Therapies. *Paradise, 1*(1), 1-10.

Schmidt, R. (2025). Unlocking the Code of Innovation: TRIZ Theory's Blueprint for Precision Medicine Breakthroughs. In *Innovations in Healthcare and Outcome Measurement: New Approaches for a Healthy Lifestyle* (pp. 3-18): Springer.

Sedano, R., Solitano, V., Vuyyuru, S. K., Yuan, Y., Hanžel, J., Ma, C., . . . Jairath, V. (2025). Artificial intelligence to revolutionize IBD clinical trials: a comprehensive review. *Therapeutic advances in gastroenterology, 18*, 17562848251321915.

Serrano, P. (2023). On a Positive Note: Current Genetic Strategies Promises a Revolutionary Transformation for the Future of Medicine. *University of Ottawa Journal of Medicine, 13*(S1).

Shahid, A. H., & Khattak, W. A. (2022). Improving patient care with machine learning: A game-changer for healthcare. *Applied Research in Artificial Intelligence and Cloud Computing, 5*(1), 150-163.

Sharma, A., Mishra, S. S., & Singh, S. (2024). Gene Therapy, OMICS Approaches, and Translational Neurodegenerative Models: Recent Advancements and Future Perspectives. In *Neurodegenerative Diseases* (pp. 206-223): CRC Press.

Sharma, A., Sharma, R., & Yang, C.-H. (2023). *Revolutionizing Healthcare: Case Studies of AI Algorithms Transforming the Field of Medicine.* Paper presented at the International Conference on Security and Information Technologies with AI, Internet Computing and Big-data Applications.

Sherani, A. M. K., Khan, M., Qayyum, M. U., & Hussain, H. K. (2024). Synergizing AI and Healthcare: Pioneering advances in cancer medicine for personalized treatment. *International Journal of Multidisciplinary Sciences and Arts, 3*(2), 270-277.

Siddiqui, F. (2024). The Role of Genomic Medicine in Cancer Treatment and Diagnosis. *Frontiers in Biotechnology and Genetics, 1*(2), 166-183.

Singh, A. P., Saxena, R., Saxena, S., & Maurya, N. K. (2024). Artificial intelligence revolution in healthcare: transforming diagnosis, treatment, and patient care. *Asian Journal of Advances in Research, 7*(1), 241-263.

Singh, G., Bajpai, A., & Bhandari, D. (2024). THE FUTURE OF HEALTHCARE: ADVANCEMENTS IN PRECISION MEDICINE AND PERSONALIZED TREATMENT.

Singh, M., Gupta, S., Bhardwaj, P., Tripathi, R., Mishra, J., & Bhardwaj, R. (2025). *Integrating artificial intelligence and robotics for advancements in personalized medicine within life science.* Paper presented at the AIP Conference Proceedings.

Srivastav, A. K., Das, P., & Srivastava, A. K. (2024). Healthcare Revolution. In *Biotech and IoT: An Introduction Using Cloud-Driven Labs* (pp. 75-113): Springer.

Stojanovska, M. (2025). Pharmacogenomics Unleashed: Navigating the Intersection of DNA and Drug Therapies. In *Advances in Forensic Biology and DNA Typing* (pp. 305-323): CRC Press.

Sundari, M. S., Rishitha, K., Majety, S., & Vegiraju, K. (2025). Precision Medicine and Clinical Applications. In *From Genes to Algorithms: Navigating the Biotechnology Data Revolution* (pp. 176-200): Bentham Science Publishers.

Tabery, J. (2023). *Tyranny of the gene: Personalized medicine and its threat to public health*: Knopf.

Tagoe, B., Quainoo, L., Clotworthy, D., Ofori, E. K., & Amponsah, S. K. (2025). Advanced Diagnostics for Personalized Medicine: A New Paradigm. In *Diagnostic Advances in Precision Medicine and Drug Development* (pp. 153-169): CRC Press.

Taheri, Z., & Bakhtiari, P. (2024). Revolutionizing Cancer Care: Artificial Intelligence and Genetic-Based Precision Medicine Transforming Treatment Strategies. *International Journal of BioLife Sciences (IJBLS), 3*(3), 238-243.

Tawfik, S. M., Elhosseiny, A. A., Galal, A. A., William, M. B., Qansuwa, E., Elbaz, R. M., & Salama, M. (2023). Health inequity in genomic personalized medicine in underrepresented populations: a look at the current evidence. *Functional & integrative genomics, 23*(1), 54.

Tesi, B., Boileau, C., Boycott, K. M., Canaud, G., Caulfield, M., Choukair, D., . . . Wirta, V. (2023). Precision medicine in rare diseases: What is next? *Journal of Internal Medicine, 294*(4), 397-412.

TumkurSattar, A. H., Abushoumi, F., Al Dobayan, Z., & Al-Ghamdi, F. (2023). Investigate how genetic variations impact drug response and explore the integration of pharmacogenomics into clinical practice. *European Journal of Cardiovascular Medicine, 13*(4).

Usmani, U. A., Watada, J., & Usmani, A. Y. (2024). *Revolutionizing Healthcare and Pharma: Unleashing the Power of AI for Precision Medicine, Diagnostics, and Therapeutics Optimization*. Paper presented at the International Conference on Intelligent Information Hiding and Multimedia Signal Processing.

Vij, R. (2024). Revolutionizing Healthcare: Unleashing the Power of Digital Health. In *Federated Deep Learning for Healthcare* (pp. 17-30): CRC Press.

Voss, A. (2024). *Health in the Digital Age: The Rise of Personalized Medicine*: eBookIt. com.

Waaje, A., Karim, R., Roshid, M. M., Yeamin, B., & Meem, T. N. (2025). Integration of industry 4.0 with personalized medicine: A shift of the paradigm in healthcare. In *AI-driven personalized healthcare solutions* (pp. 27-70): IGI Global Scientific Publishing.

Weerasinghe, D., Pathirana, T., Jayasuriya, M., & Warnakulasooriya, R. (2021). PERSONALIZED MEDICINE THROUGH AI-BASED GENOMIC ANALYSIS.

Yeung, A. W. K., Torkamani, A., Butte, A. J., Glicksberg, B. S., Schuller, B., Rodriguez, B., . . . Peng, H. (2023). The promise of digital healthcare technologies. *Frontiers in public health, 11*, 1196596.