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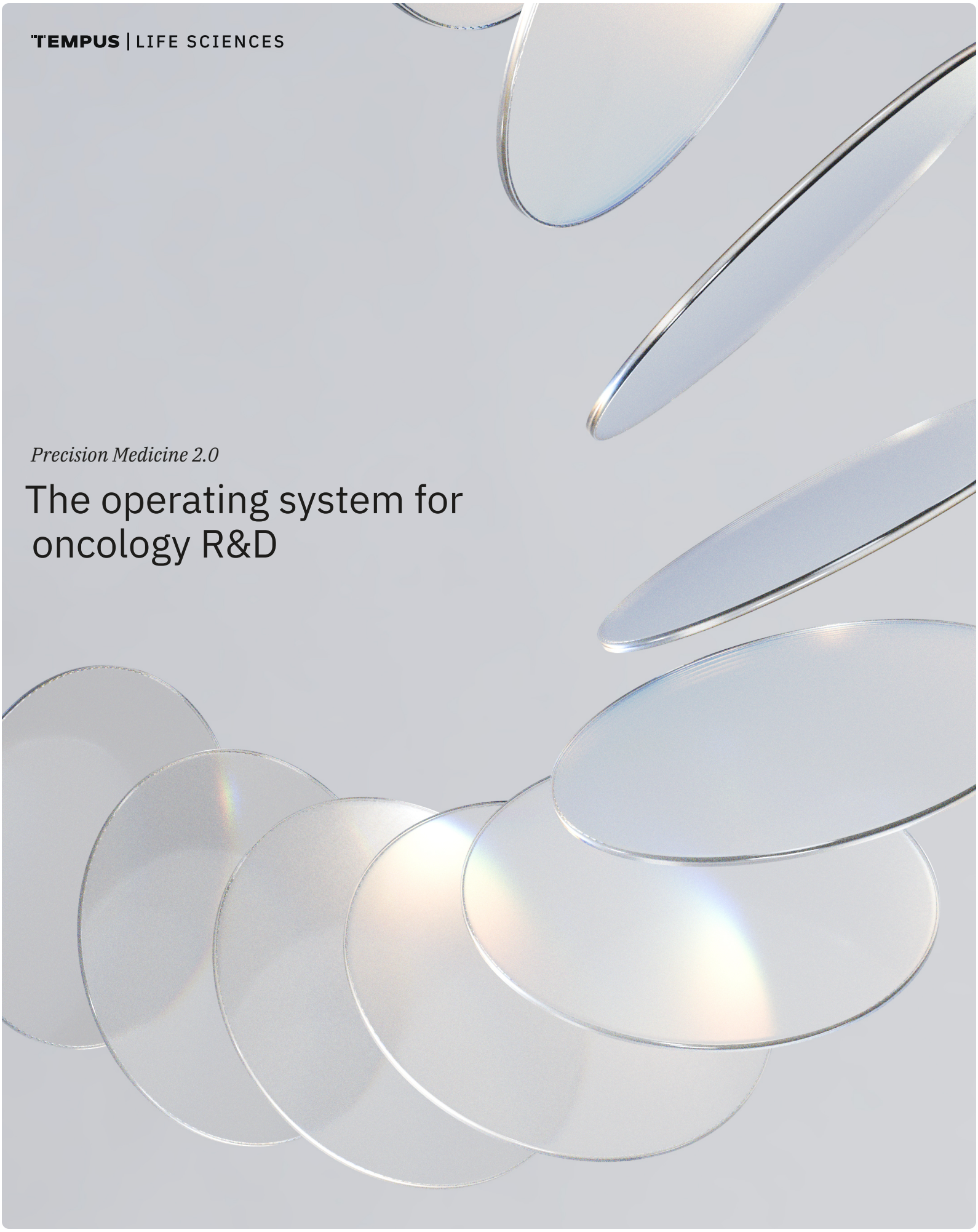
Precision Medicine 2.0

The operating system for oncology R&D



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Please Note: *The information in this white paper is intended for life sciences companies and focuses on research and development applications. It is not intended for clinical use.*

Forward Looking Statements

This white paper contains forward-looking statements within the meaning of Section 27A of the Securities Act of 1933, as amended (the “Securities Act”), and Section 21E of the Securities Exchange Act of 1934, as amended, about Tempus and Tempus’ industry that involve substantial risks and uncertainties. All statements other than statements of historical facts contained in this white paper are forward-looking statements, including, but not limited to, statements regarding the potential for Precision Medicine 2.0 (PM2.0) to redefine cancer care; the expected benefits of an integrated, data-driven approach; and the potential for AI and multi-omic data to accelerate R&D and improve patient outcomes. In some cases, you can identify forward-looking statements because they contain words such as “anticipate,” “believe,” “contemplate,” “continue,” “could,” “estimate,” “expect,” “going to,” “intend,” “may,” “plan,” “potential,” “predict,” “project,” “should,” “target,” “will,” or “would” or the negative of these words or other similar terms or expressions. Tempus cautions you that the foregoing may not include all of the forward-looking statements made in this white paper.

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Introduction

The oncology landscape is shifting, moving beyond the initial promise of precision medicine toward a more integrated, data-driven, and AI-enabled approach: Precision Medicine 2.0 (PM2.0). This evolution reflects not just scientific progress but the growing recognition that the first wave of precision oncology, while transformative, left gaps that still limit therapeutic impact and scalability.[1]

For R&D organizations, understanding this transition is exceptionally timely. While targeted therapies and biomarker-driven approaches have significantly advanced cancer treatment, persistent challenges remain, including low clinical trial success rates, R&D inefficiencies, and difficulties in applying insights across diverse patient populations.[1,2]

Simultaneously, the rapid growth of multi-omic data is converging with the broader adoption of artificial intelligence (AI) and machine learning (ML), enabling researchers to uncover complex patterns across genomics, transcriptomics, pathology, and beyond. This convergence is paving the way for a deeper, systems-level understanding of cancer biology—one that moves beyond single biomarkers toward holistic, predictive models of response.

This white paper provides insights for R&D organizations navigating this transformation, outlining the evolution of PM2.0, its scientific foundations, enabling technologies, market dynamics, and strategic implications.

The evolution of precision medicine

PRECISION MEDICINE 1.0: PROGRESS, PROMISE, AND LIMITATIONS

The first era of precision medicine, referred to here as Precision Medicine 1.0 (PM1.0), centered on a biomarker-driven model: identify a genetic alteration and match it with a targeted therapy. This approach reshaped oncology by demonstrating that molecular insights could lead to more effective, personalized treatments.

The late 1990s marked a pivotal shift in cancer treatment with the FDA's approval of landmark targeted therapies. The era was defined by breakthroughs like rituximab (Rituxan) in 1997 for non-Hodgkin lymphoma and trastuzumab (Herceptin) in 1998 for HER2-positive breast cancer.[3] A subsequent, equally significant moment was the 2001 approval of imatinib for chronic myeloid leukemia (CML), a breakthrough as a small-molecule drug that specifically targeted the BCR-ABL fusion gene. These collective successes reinforced the value of aligning treatments with specific molecular features.[3] Techniques like fluorescence in situ hybridization (FISH) and polymerase chain reaction (PCR) became standard for detecting actionable alterations, particularly in patients with advanced cancers who had exhausted conventional chemotherapy options.[3]

However, as these approaches became more widespread, their limitations also became apparent. PM1.0 represented a significant advance, but it did not fully address the biological complexity of cancer.

Tumor heterogeneity quickly emerged as a major challenge. Cancer is not a single disease, and even within a single patient's tumor, there exists immense molecular diversity, including both spatial and temporal heterogeneity.[4] Even amongst homogeneous tumors, a patient's prior treatment, prognostic features, and clinical history all contribute to the complexity of the disease, which a single biomarker often fails to capture. While a targeted therapy might eliminate drug-sensitive cells, resistant subclones can quickly emerge, leading to rapid relapse after initial response.[5] For example, epidermal growth factor receptor (EGFR) inhibitors are effective in some lung cancers, but their efficacy is reduced when co-occurring mutations such as *TP53* or *KRAS* are present, activating alternative pathways and diminishing drug response.[5] This dynamic emulates a "whack-a-mole" scenario—suppress one mutation, and another emerges.

Clinical trial design inefficiencies also posed challenges. Traditional trials aimed for broad generalizability, which conflicted with the increasingly individualized nature of precision oncology. Recruiting appropriate patients became more difficult, and outcomes were often inconsistent. While innovative concepts like "N-of-1" trials began to emerge, they were difficult to scale and did not fit neatly into established clinical research frameworks.[1]

The limitation of potentially druggable targets became evident as well. Despite breakthroughs, many potential protein targets for precision oncology remain unstudied

or are not effectively druggable by conventional small molecules or antibodies. This is particularly true for complex targets like transcription factors or those exhibiting diverse oncogenic mutations, where a simple "on/off" switch approach is insufficient.[6]

Finally, **PM1.0 was largely reactive**. Most interventions focused on treating advanced disease, rather than predicting risk, preventing progression, or enabling early detection. Molecular profiling was rarely incorporated into earlier settings such as adjuvant or neoadjuvant therapy, limiting its role in curative approaches.[3]

While PM1.0 delivered important scientific milestones—from single biomarker-driven therapies to more refined patient stratification—it also exposed the limitations of a narrowly focused, unintegrated approach. Yet, even as the science advanced, the biopharma development model failed to evolve at the same pace. This mismatch has created a critical bottleneck—one in which breakthroughs in biology struggle to translate into scalable, timely therapeutic advances.

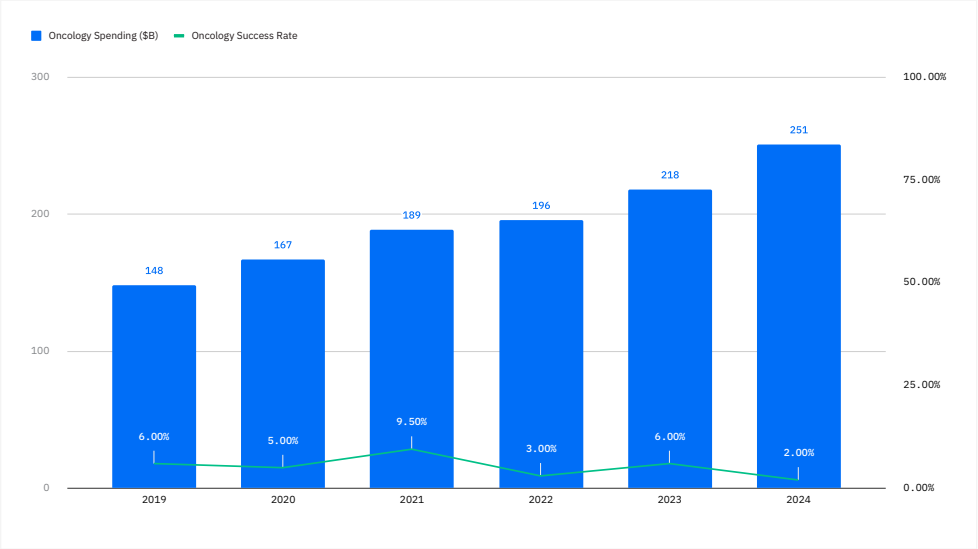
THE "BIOPHARMA BOTTLENECK": INNOVATION WITHOUT BREAKTHROUGH

Over the past couple of decades, the FDA pipeline has reflected a clear shift toward precision oncology. Between June 1998 and January 2024, over 200 novel oncology drugs were approved, with more than 80% classified as targeted therapies and over half as precision oncology agents.[7] This trend has only accelerated: in the five years leading up to January 2024, 75 novel oncology drugs received FDA approval, over 60% of which were precision-based.[7]

However, progress has not come without setbacks. Of the 78 oncology drugs that received accelerated approval from the FDA between 1999 and 2022, 17 (approximately 22%) were later withdrawn, typically because they failed to demonstrate clinical benefit in confirmatory trials.[8] This notable withdrawal rate underscores one of the central challenges of early precision oncology efforts: although therapies may be designed to target specific molecular pathways, real-world outcomes do not always align with initial biomarker-driven expectations.

At the same time, despite record levels of investment—annual oncology R&D spending surged from $148 billion in 2019 to $251 billion in 2024—the composite success rate for oncology drug development programs has remained stubbornly low, averaging just 5.4% from 2019 to 2024, and dropping to only 2% in 2024.[9] This disconnect between innovation and outcomes is often referred to as the "biopharma bottleneck." The causes are multifaceted: rising target complexity, crowded pipelines, and escalating clinical trial costs and timelines.[10] However, a deeper, structural issue persists: the fragmentation of data across the R&D ecosystem.

Figure 1 Global oncology R&D investment vs. clinical trial success rates (2019-2024)[9]



The evolution of precision medicine

Even as precision medicine becomes more widely adopted, essential R&D datasets—clinical, molecular, imaging, and real-world data (RWD)—remain siloed across labs, platforms, and institutions.[11] Without integration, this fragmented data hampers the identification of predictive biomarkers, effective patient stratification, and adaptive trial design—ultimately slowing development, increasing attrition, and impeding the translation of scientific advances into clinical progress.[11]

The traditional R&D model may no longer meet the demands of modern oncology. The complexity of cancer biology revealed by PM1.0 has outpaced our ability to act on it. To break through the bottleneck, biopharma needs a new paradigm—one built for speed, scale, and systems-level insight.

Enter Precision Medicine 2.0

Breaking through the biopharma bottleneck requires more than incremental improvements—it demands a fundamental rethinking of how we approach cancer research and care, with PM2.0 emerging as this new path forward.

CORE SCIENTIFIC PILLARS OF PM2.0

PM2.0 generally consists of four interconnected scientific pillars that collectively enable a systems-level, adaptive, and AI-driven approach to oncology R&D.

Multi-omic systems understanding

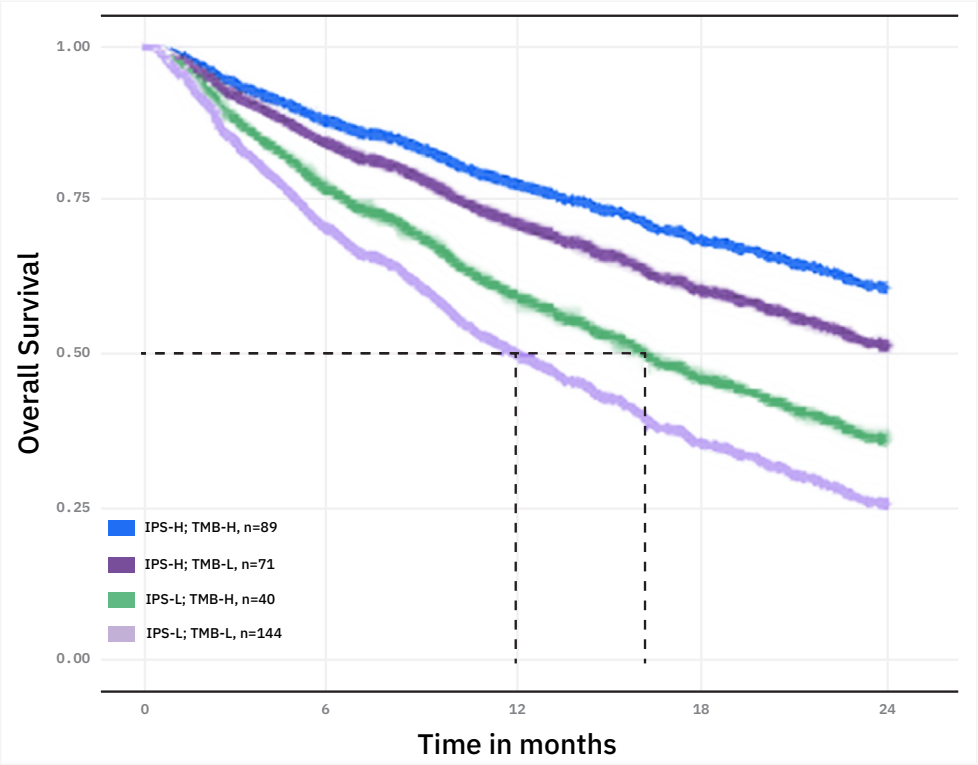
PM2.0 moves beyond the DNA-centric paradigm of precision medicine, embracing a multi-omic approach that integrates genomics, transcriptomics, epigenomics, proteomics, metabolomics, and the microbiome to provide a holistic view of cancer biology, cellular function, and disease mechanisms.[4] Central to this approach is comprehensive profiling of the tumor microenvironment (TME)—a complex ecosystem of cells, signaling molecules, and extracellular components that profoundly influence tumor progression, immune response, and therapeutic outcomes.[12] Multi-omic profiling of the TME is increasingly important for advancing precision immuno-oncology, as current immune checkpoint blockers are ineffective for a majority of patients, underscoring the need for deeper insights into TME mechanisms to improve response rates.[12] Advanced single-cell technologies further enhance this understanding by revealing cellular diversity and rare subpopulations that drive resistance or relapse—insights often missed by bulk sequencing.[13] Ultimately, the integration of multi-omic and clinical data is critical for identifying robust biomarkers and enabling personalized therapy, but it also requires sophisticated computational and AI tools to extract actionable insights from these complex datasets.[4]

An example of this multi-omic approach is the Immune Profile Score (IPS), a novel algorithmic assay developed and validated using Tempus' real-world multimodal database. IPS integrates both DNA- and RNA-based immune biomarkers—leveraging features such as gene expression signatures and immune resistance pathways—to generate a composite score that stratifies patients with advanced solid tumors treated with immune checkpoint inhibitors. In a large, pan-cancer validation cohort, patients classified as IPS-High were found to have a higher real world overall survival (OS) compared to those with an IPS-Low result when treated with ICI-based regimens, and **IPS demonstrated prognostic utility independent of PD-L1, tumor mutational burden (TMB), and microsatellite instability (MSI)**, even when controlling for these variables in multivariable models.[14] Notably, IPS identified patients likely to benefit from immunotherapy even within subgroups considered negative or low by conventional biomarkers, highlighting its value for more precise patient stratification and trial design.[14] IPS adoption has grown in clinical settings, with IPS being ordered on over a third of eligible patients*, reflecting the expanding embrace of multi-omic strategies in the field.

**This statistic refers to patients at institutions for which Tempus' Comprehensive Therapy Selection (CTS) ordering is enabled and represents orders placed between April and June 2025. As of the date of this white paper, CTS ordering is available at select ordering institutions.*

Enter Precision Medicine 2.0

Figure 2 Predicted OS by IPS and TMB (Predicted for 1L; ICI monotherapy; N=344)[14]



AI/ML: The unifying layer of PM2.0

To embrace this next era of precision medicine, AI and ML are increasingly serving as a unifying and transformative layer that integrates complex, multimodal biological and clinical data to generate actionable insights for oncology R&D. By uncovering subtle patterns within vast datasets, AI can help enhance prediction accuracy, reduce diagnostic error, and inform more precise, individualized treatment strategies.[15] These capabilities are particularly valuable in oncology, where traditional drug development is lengthy, high-risk, and resource-intensive—on average taking 10-15 years from discovery to approval.[16] By accelerating target discovery, optimizing trial design, and supporting identification of unproductive candidates earlier, AI has the potential to shorten development timelines, reduce costs, and help de-risk R&D efforts.[17]

AI/ML also enables predictive and adaptive analytics throughout the clinical development process. Predictive models can analyze vast datasets to identify which patients may be more likely to benefit from or meet specific trial criteria, accelerating recruitment.[17] Across the industry, pharmaceutical companies are leveraging AI- and ML-powered analytics to inform and improve site selection strategies—using predictive models to identify clinical sites that are likely to become operational quickly and effectively meet study objectives.[16] AI/ML algorithms can further optimize trial protocols by simulating various scenarios, predicting outcomes, and adjusting parameters in real time, leading to more robust study designs that account for patient variability and improve efficiency and statistical power.[18]

As AI models become more deeply integrated into trial workflows and supporting treatment decisions, ensuring transparency, fairness, and explainability becomes increasingly important.[19] These models must be trained on representative data and designed to minimize bias to build trust among regulators, clinicians, and patients alike.[19] The success of PM2.0 depends not only on predictive power, but also on responsible and interpretable deployment.

Beyond trial design, AI is increasingly being used to support the creation of novel therapeutics.[20] By processing vast multimodal datasets, AI can predict new drug-target interactions, often outperforming traditional methods.[20] Some pharma R&D teams are integrating multimodal data, systems biology, and patient-derived organoid (PDO) models with AI/ML to help identify and validate new drug targets, enabling iterative testing and

potentially reducing risk in the discovery process.[21] This integrated strategy may help accelerate the translation of AI-derived insights into potential therapies, particularly for cancers that are resistant to existing treatments, and may help prioritize the most promising candidates for further development.

AI is increasingly being used to support the monitoring of tumor evolution in real time, detecting genetic variants that signal emerging resistance to therapies.[20] This approach may allow clinicians to consider switching second-line therapies before clinical relapse occurs, thereby enabling more adaptive treatment strategies.[20] While specific, well-known resistance alterations like the EGFR T790M variant can be identified through standard analysis, AI algorithms can analyze complex data from liquid biopsies to help detect rare genetic variants and novel alterations that may influence resistance.[20] This allows for a more comprehensive understanding of a tumor's dynamic evolution, helping to identify emerging clones that might be resistant to current regimens before clinical relapse occurs.[20] This deeper level of insight may then prompt a timely adjustment to therapy, such as switching to osimertinib to combat a specific variant.[20]

Ultimately, AI/ML serves as the connective tissue in PM2.0, unifying disparate data streams into a cohesive, actionable insights network. This integration, from early discovery and trial optimization to real-time treatment adaptation, is powered by AI/ML's capacity for continuous learning and adaptation. As more de-identified data are incorporated, these models become more refined, potentially leading to more precise insights and improved care.

Modeling the “whole patient”

PM2.0 moves beyond a reductionist view of cancer, one that breaks the disease down into individual components like tumor suppressors and oncogenes, to a comprehensive understanding of the "whole patient" as a dynamic biological system. This requires advanced modeling that integrates spatial, temporal, and systemic dimensions of disease. Spatial biology techniques now provide high-resolution views of the tumor microenvironment (TME), allowing researchers to map the location of cells, transcripts, and proteins within intact tissues, revealing how spatial arrangement influences tumor progression, immune infiltration, and therapeutic response—insights that go far beyond the average signals of bulk molecular analysis.[22] For example, spatial analysis can distinguish the organization and proximity of immune cells within the tumor microenvironment, which may be a critical factor in predicting immunotherapy effectiveness.[23] At the same time, temporal modeling—often enabled by longitudinal profiling through technologies like liquid biopsies—tracks the dynamic evolution of tumors, monitoring changes in clonal composition, cellular phenotypes, and the TME in real time as the disease progresses or responds to therapy.[24,25] This dynamic perspective is fundamental to adaptive therapy, where treatment schedules are adjusted based on the tumor’s evolving response.[25]

Systemic modeling further extends this approach by incorporating the patient’s genetic, molecular, environmental, and lifestyle factors. Digital twin (DT) technology exemplifies this frontier, creating dynamic virtual replicas of patients that enable researchers to simulate disease progression and treatment responses, thereby facilitating personalized and optimized interventions before they are applied in the clinic.[26] The integration of AI is crucial in developing these sophisticated models, supporting a shift from static, isolated analyses to a holistic, systems-level understanding of cancer within the patient's biological context.

ENABLING TECHNOLOGIES AND MODALITIES

New-age technologies and modalities are what make the scientific pillars of PM2.0 actionable. These advanced tools form the operational foundation for integrated, adaptive, and data-driven oncology R&D and care.

Next-generation sequencing (NGS) and comprehensive genomic profiling (CGP)

NGS and CGP are foundational to PM2.0—not as endpoints, but as enablers of deeper biological insight, scalable testing, and adaptive decision-making. By consolidating key

genomic signals—mutations, fusions, copy number changes, and complex signatures like TMB and MSI—into a single, multiplexed readout, these technologies can reduce the amount of tissue required for testing , thereby broadening clinical utility across solid and liquid biopsy platforms.

In practice, CGP supports more than just biomarker identification; it may inform treatment strategies, improve trial stratification, and enable monitoring of disease evolution through serial sampling. Retrospective analyses and prospective studies, including the PANGEA trial, suggest a consistent association between CGP-guided interventions and improved clinical outcomes, particularly when interpreted within multidisciplinary frameworks like molecular tumor boards.[27] In the context of PM2.0, CGP represents a scalable gateway to multimodal integration, not a standalone solution.

Radiomics, pathomics, and immunogenomics

AI is being used in precision oncology to enable the extraction and integration of high-dimensional data from imaging, pathology, and genomics. In radiomics, AI algorithms analyze features from CT, MRI, and PET/CT scans to uncover imaging biomarkers that may reflect tumor heterogeneity, immune cell infiltration, and likely treatment response, supporting non-invasive, real-time assessment of the tumor microenvironment.[28] For example, a recent study developed and prospectively validated a radiomics signature for CD8+ T cells that could predict clinical outcomes in patients receiving immunotherapy, demonstrating the potential of AI-driven imaging biomarkers to guide immunotherapy decisions.[28] Pathomics leverages AI to deeply analyze digital pathology images, revealing subtle microenvironmental and morphological features that may inform biomarker discovery and help predict which patients may benefit from specific therapies. In immunogenomics, AI processes large-scale genomic and transcriptomic data to identify predictive biomarkers for immunotherapy response and disease prognosis, enabling more personalized treatment strategies. The convergence of these AI-powered 'omics' approaches is helping accelerate the translation of precision medicine into clinical practice by improving the speed, accuracy, and personalization of cancer care.[28]

Real-world evidence (RWE) generation

RWE—derived from diverse RWD sources such as electronic health records (EHRs), registries, claims data, and digital health technologies—is increasingly vital for PM2.0.[29] RWE complements traditional clinical trials by providing external validity, supporting patient stratification, early signal detection, and regulatory decision-making, while often reducing resource requirements and timelines.[29] In emerging economies, RWE has been used to contextualize patient profiles, inform treatment choices, and optimize dosing strategies, as demonstrated by the HOLA study, which used registry data to reveal treatment patterns and comorbidities among multiple myeloma patients in Latin America.[29]

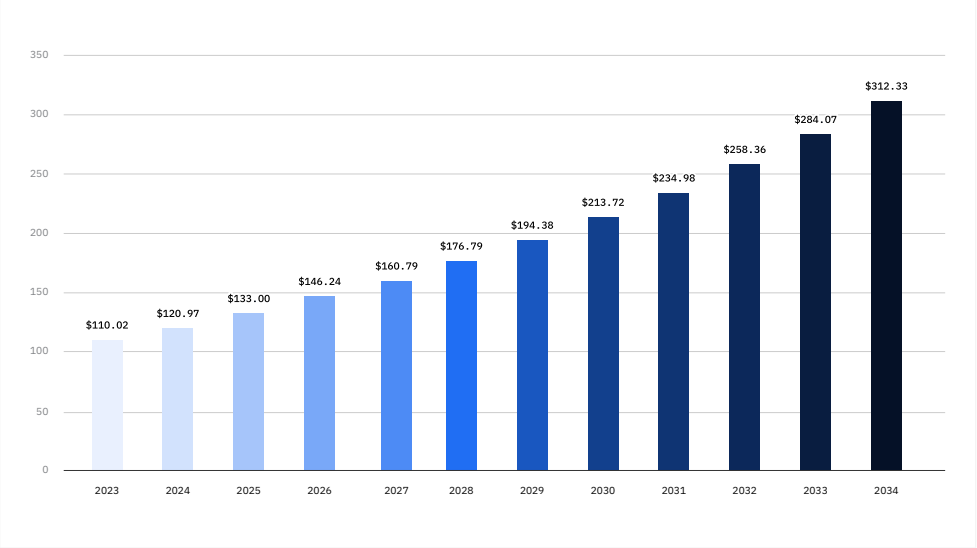
The value of RWE is fundamentally dependent on the quality, completeness, and harmonization of the underlying RWD.[30,31] Only with robust, well-curated, and standardized datasets can RWE generate reliable evidence to inform regulatory submissions, post-market surveillance, and label expansion—an approach increasingly recognized and encouraged by agencies such as the Food and Drug Administration (FDA) and European Medicines Agency (EMA).[30,32] RWE is also being used to construct external control arms for clinical trials, support health economic and outcomes research, and inform payer and policy decisions.[31] As the adoption of RWE accelerates, ensuring data quality, harmonization, and appropriate data governance will be critical to realizing its full potential in advancing precision oncology.

Current landscape and strategic shifts

MARKET TRENDS AND INVESTMENT GROWTH

The oncology market remains one of the world's largest and most competitive pharmaceutical sectors.[33] The global precision oncology market was valued at $120.97 billion in 2024 and is projected to grow to approximately $312.33 billion by 2034, representing a compound annual growth rate (CAGR) of 9.95% over the forecast period.[34] This robust growth is driven by rising cancer incidence, demand for more predictive R&D pipelines, and continuous technological advancements—particularly in AI-driven diagnostics and targeted therapies.[34] Targeted therapies now hold the largest share of the market, reflecting the continued shift toward precision-based treatment approaches.[34] In 2023, North America accounted for over 43% of global revenue, driven by the widespread adoption of advanced diagnostic technologies.[34]

Figure 3 Global precision oncology market size and forecast (2024-2034)[34]



How pharma and researchers are responding

Pharmaceutical and biotech companies are strategically reorienting investments toward AI and multi-omics as critical enablers of PM2.0.[35,36] Reflecting this trend, Tempus recently entered into multi-year collaborations with AstraZeneca and Pathos AI, involving $200 million in combined data licensing and model development fees. These organizations are jointly developing a multimodal foundation model in oncology, which can be used to generate biological insights, uncover novel targets, and support therapeutic development in oncology.[37] Tempus' de-identified clinical and molecular data will be used to develop the model.[37] Other recent work has demonstrated how integrating large-scale clinical and molecular datasets with phenomic and transcriptomic analyses may help automate the selection of preclinical models, support prediction of mechanisms of action, and assist in optimizing lead compounds.[38] This enables target-agnostic discovery and more efficient advancement of novel small molecule therapeutics.[38] Collectively, these initiatives exemplify a broader industry movement to leverage data and technology to streamline trial operations, enhance enrollment efficiency, and bridge the gap between innovation and real-world adoption in oncology care.

Meanwhile, academic medical centers are implementing PM2.0 approaches through integrated research, advanced diagnostics, and collaborative programs.[39,40,41] Recent real-world studies were conducted by leveraging CGP and NGS, along with multimodal clinical data, to identify actionable variants, match patients to targeted therapies, and improve adherence to evolving clinical guidelines across diverse cancer types.[39,40] These efforts not only may enhance diagnostic accuracy and treatment personalization but also may help expand access to guideline-driven care and support the adoption of new precision oncology strategies in both well-resourced and resource-limited settings.[39,40]

Current landscape and strategic shifts

Cross-sector collaboration is beneficial for navigating the complexity and data intensity of PM2.0. Public-private partnerships (PPPs) bring together government, academia, industry, and non-profits with the aim of accelerating translation of research into clinical impact.[41] The FDA Oncology Center of Excellence (OCE) supports these efforts through initiatives such as the Precision Oncology Program, Oncology Real World Evidence Program, Project Orbis (for global regulatory collaboration), and Project Pragmatica (which integrates real-world practice into trials).[42] These collaborative models may help address the challenges of PM2.0, accelerate discovery, and improve patient access.

Together, these market shifts and collaborative models may support a more *adaptive*, *data-driven*, and *patient-centered* future.

Discussion and future outlook

The journey from PM1.0 to PM2.0 marks an evolution in oncology R&D, as the field shifts from single-biomarker approaches to a systems-level model. Driven by the convergence of multi-omic data and advanced AI/ML capabilities, the next wave of precision medicine is emerging as an “operating system” for oncology, uniting diverse data streams with holistic patient insights.[15] This new paradigm may help break through the "biopharma bottleneck," supporting the discovery and delivery of transformative therapies.

Ultimately, PM2.0 is poised to redefine cancer care, helping to establish personalized, adaptive, and effective treatments as the standard of care. Achieving these goals may require investment in integrated, AI-enabled infrastructure and cross-sector collaboration and ensuring equitable and ethical deployment. By doing so, we may help improve patient outcomes and move toward a future where cancer is increasingly understood, predicted, and overcome.

Tempus solutions to enable Precision Medicine 2.0

Tempus delivers an integrated platform of multimodal data, advanced analytics, and AI-driven applications to support the next era of precision oncology. Our solutions help life sciences companies accelerate research, optimize clinical development, and inform commercialization strategies across every stage of the drug lifecycle. For more information on how Tempus can support your R&D initiatives, visit tempus.com/life-sciences.

REAL-WORLD DATA

Access one of the world's largest oncology multimodal real-world databases, linking DNA, RNA, H&E images, and other clinical, imaging, and molecular data to uncover insights across the R&D continuum. **Tempus Lens** offers the full power of Tempus data at your fingertips and both code-based and no-code analytical solutions to help accelerate time-to-insights.

350+ petabytes of data

8M+ de-identified research records

~1.5M records with matched clinical data linked with genomic information

BIOLOGICAL MODELING

Utilize our model systems, such as fixed or custom panel PDO screens, to interrogate disease biology and generate multimodal data insights. These models are a key component of **Tempus Loop**, our proprietary platform that integrates RWD, PDOs, and AI/ML to rapidly uncover insights for pre-clinical therapeutic development and help validate actionable targets. To further enhance discovery and characterization, Tempus also provides single-cell RNA sequencing and spatial transcriptomics to map cell populations and to better characterize the relationships between molecular profiles and therapeutic response.

~1K tumor-derived organoids across a range of indications

NEXT-GENERATION SEQUENCING

Comprehensive genomic profiling services, including solid tissue and liquid biopsy testing, as well as whole transcriptome RNA, MRD, hereditary, and whole exome sequencing, in addition to treatment response monitoring.

10 NGS tests to support clinical trial and research sequencing

OMICS SOLUTIONS

A wide range of disease-agnostic technologies, including methylation testing, genotyping, proteomics, and single-cell sequencing.

8-day average TAT for genotyping tests

9-day average TAT for methylation tests

CLINICAL TRIALS SOLUTIONS

The Tempus TIME program combines data, technology, and operations to power patient matching and help increase site engagement for your clinical trials.

40K+ patients identified for potential enrollment into clinical trials in our network

1.5K+ clinical trials have been active

~10 business days for just-in-time (JIT) trial activation

AI ALGORITHM DEVELOPMENT AND DEPLOYMENT

Harness multimodal data, AI/ML, and bioinformatics to help develop, validate, and deploy molecular algorithms.

CARE GAP CLOSURE

Tempus Next notifies providers of care gaps at the point of care. The platform is designed to improve adherence to guideline-based care by identifying patients who may benefit from precision care pathways.

60+ algorithms to identify potential care gaps across 15 cardiovascular diseases

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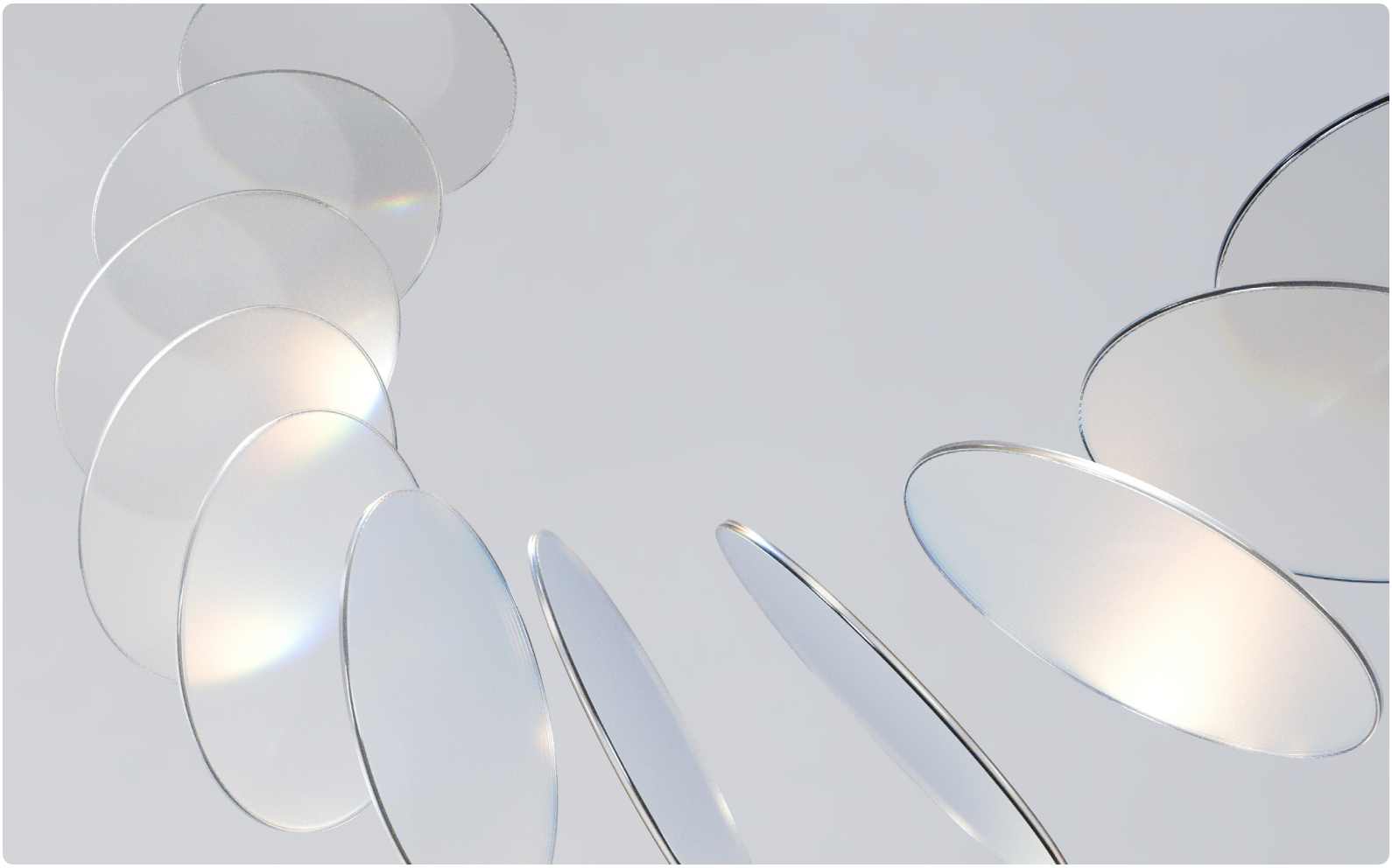

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95%

of the top 20 pharma companies have partnered with Tempus[43]

250+

biopharma partnerships

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