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SPECIAL

Big Bang in AI drug development

"The optimisation of antibodies with AI is still years away," says Dr Andreas Evers, Deputy Scientific Director for Antibody Research and Protein Engineering at Merck KGaA. Speaking at PEGS 2024, he points out that the lack of a sufficient amount of clinical data prevents AI systems from being reliably trained for the development of antibodies or ADCs. Preclinical datasets, he adds, remain an inadequate substitute.

Yet investment continues to surge. London-based Arto Ltd reports that nearly half of the US$165bn raised for AI ventures in the first half of 2025 went into drug discovery and life sciences – reflecting the sector's large potential.

At the end of September, Merck KGaA and Siemens AG launched a pilot project integrating all data along the drug development value chain on a single AI platform. The system, LUMA – acquired by Siemens through its US$5.1bn purchase of Dotmatics – aims to streamline processes from hit identification and lead optimisation to GMP production and clinical-trial documentation.

The best results are achieved when humans and machines work together, report researchers at the Max Planck Institute for Human Development in Potsdam. Chinese ML-guided ADC developer BigHat plans to enter Phase I trials next year with its first AI-optimised Antibody Drug Conjugate (ADC) developed on the Milliner ML platform. The company still combines algorithmic and human expertise, partnering with Dutch CRO Synaffix, acquired by Lonza AG in 2023. Founder Floris van Delft credits the partnership to "Lonza's manufacturing reach and Synaffix's ADC platforms" – an approach reflecting Merck and Siemens' integrated model. Futhermore, a team from DKFZ Heidelberg achieved an AUC of 0.94 for early sepsis detection when clinical data from patients were combined with ML-evaluated hyperspectral imaging. The imaging captures inflammation-induced leakage in the microcirculation before first sepsis symptoms appear.

Meanwhile, AI's role in drug screening is expanding. Boehringer Ingelheim and Vienna-based Heartbeat.Bio are combining AI-based image analysis with automated culture and differentiation of Cardiod heart organoids to develop therapeutics for hereditary cardiomyopathies.

In the small-molecule field, Monte Rosa Therapeutics modelled a structural motif shared by E3 ubiquitin-ligase binders to simulate attachment to the beta-sheet G-loop. The work revealed new related binding motifs and around 1,600 potential protein-degraders. To secure exclusive access to the AI-driven discovery platform Queen Novartis AG acquired Monte Rosa in mid-September in a US$5.7bn deal. ■

Evolving Antibody Innovation: New frontiers in cancer R&D

DRUG DISCOVERY Fifty years after the invention of hybridoma technology, biologics have become a cornerstone of oncology drug discovery and development. From the first monoclonal antibody approval in 1995 to today's complex antibody formats and cell-based therapies, biologics are reshaping cancer drug discovery. Yet, despite remarkable progress, the urgent need for novel targets that can exploit recent technological developments remains high.

› Prof. Dr Anton Wellstein, Chief Scientific Officer, Indivumed

One of the striking changes in drug approvals by the US Food and Drug Administration (FDA) is the steadily increasing portion of biologics in the approval portfolio over the past 25 years: In the mid-1990s, only 8% of approved drugs were identified as biologics, a portion that increased ~4-fold to 31% of new approvals in the 2020 to 2024 interval [1]. Most of these biologic drugs are antibodies. While the therapeutic potential of antibodies dates back 100+ years, it was the invention of hybridoma technology 50 years ago that enabled production of monoclonal antibodies as drugs and clinical utility.

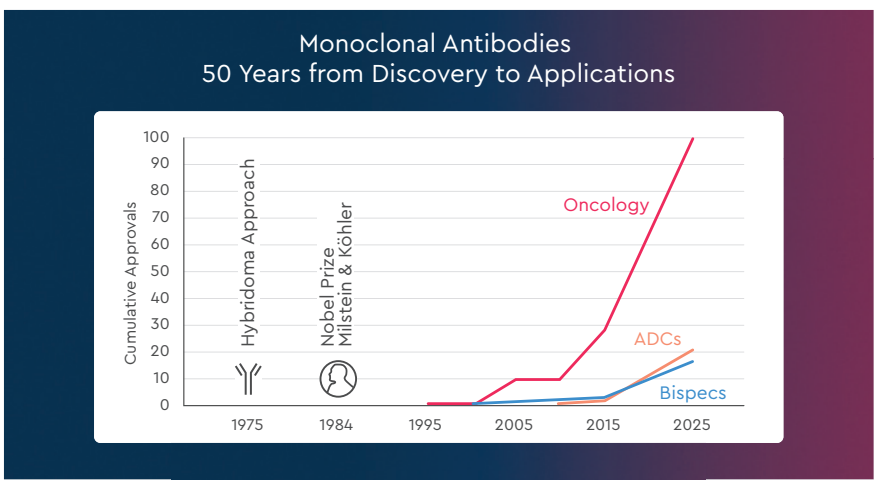
A shift towards antibody-based drugs

In August 1975, Köhler and Milstein published the hybridoma technology and were awarded the Nobel Prize for this work a few years later in 1984. The approach enabled the generation of a single "antibody of predefined specificity" and prompted a revolution in the potential for designing new antibody-based drugs. These biologics can now be generated at any scale with reproducible quality matching chemically defined drugs [2]. This is reflected in their clinical use: The approval of monoclonal antibodies (mAb) for therapy started only 20 years after the initial publication, in 1995 (Figure 1). Today, oncology indications account for about one half (~100) of approved mAb therapeutics worldwide followed closely by autoimmune and infectious disease indications.

Antibodies enter the clinic

The initial generation of antibodies targeted functional pathways similar to a small molecule drug and sought to impact cell function. Some of the biggest successes were the targeting and blockade of growth factor pathways in cancers and the discovery of immune cell activation checkpoints, which can be inhibited by antibodies to activate dormant immune cells. Recent antibody technologies provide a further set of tools to tackle cancers, Antibody Drug Conjugates (ADCs), where a toxic drug is delivered to tumors. This "magic bullet" concept was proposed in the early 1900s by Paul Ehrlich and has been shown to yield significantly improved outcomes over "naked" antibodies in the treatment of cancers, winning approval for ~20 different entities so far.

Another antibody engineering development packs multiple antibody recognition sites into a single antibody molecule. By leveraging two targets, bispecific antibodies can shackle immune cells to cancer cells or hit multiple cancer hallmarks simultaneously and thus increase antibody/tumor selectivity.



Approvals of antibody-based therapies have accelerated sharply since 2000 with oncology dominating the landscape, newer modalities like ADCs and bispecifics gaining momentum [2]

Approval of bispecifics in the last few years is also on the rise due to their treatment efficacy (Figure 1).

Need for novel targets remains

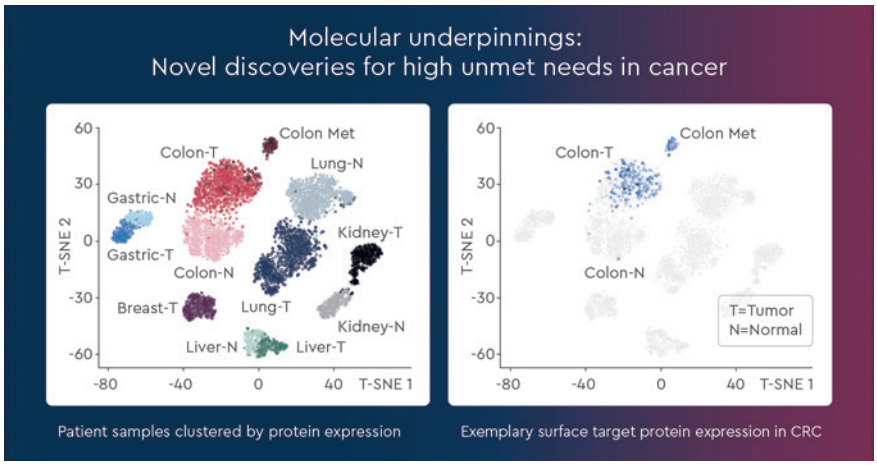
To translate these advances in antibody engineering into breakthrough therapies, the discovery and development of novel targets beyond the usual suspects becomes the key challenge. Luckily, several parallel developments improved our ability to meet these challenges: Molecular analyses of cells and tissues ("omics") became affordable at large scale and the computational power and tools to store and process these complex omics data became ever more refined and cheaper. Thus, it has become feasible to identify those molecules that distinguish cancer from normal cells and adapt antibody targeting to that. Also, rate-limiting growth pathways can be identified and nominated for targeting surface receptors. A technological basis that together with the molecular underpinnings and today's abilities for comprehensive disease understanding will build new frontiers in cancer drug discovery and development.

Patient insights guide discovery

The foundation for an in-depth understanding of the underlying biology of cancer and for novel target discovery lies for Indivumed at the very beginning of their R&D approach. Indivumed built a large repository of well curated tumor and adjacent normal tissues focusing on minimal cold ischemia time. A recent study in nature's Cell Death & Disease [5] has demonstrated that numerous differentially expressed proteins are affected by tissue ischemia time and differential expression of many potential tumor targets disappear after 12 minutes. A unique starting point, that makes a difference in novel discoveries.

Large-scale proteomic profiling of thousands of patient samples revealed clear clustering of tumor and normal tissues with a distinct protein expression across cancers and tissue types, with each dot representing one patient (Figure 2a).

With the overlay of the expression of a single cell surface protein across all samples, the protein is detected in about half of the primary and most of the metastatic colorectal cancer (CRC) specimen (Figure 2b). Expression is below detection in other cancers and normal tissues. As a proof-of-principle, this selective expression of the surface protein nominates it as an attractive target for the development of antibody therapeutics such as ADCs.



Analysis of Tumor and Normal tissue protein expression (a) paves the way for target discoveries illustrated by the distinct tumor expression of a surface molecule (b)

Furthermore, the patient-based material contains tumor as well as associated stroma and facilitates definition of surface targets as the basis of bispecific immune cell recruiters discussed above. The tissue specimen-based target discovery approach should increase selectivity toward cancer tissues and reduce the risk for adverse events based on low or lacking expression in healthy tissues.

Combinations for lasting success

Cancer treatment has taught us that combinatorial therapies are needed for the best success and least adverse events and will include small and large molecules. Beyond antibody recognition and targeting of cell surface proteins, understanding the molecular underpinning and the contribution of different drivers of malignancy has provided a plethora of opportunities for combinations that target cancer vulnerabilities. A highly successful field of targeted therapeutics has focused on inhibitors of receptor and intracellular kinases that provide potential partners in treatment combinations with antibodies [3]. Such combination partners would also include recently developed inhibitors of a central driver in different lethal cancers, oncogenic RAS that had evaded discovery of an efficacious inhibitor for decades [4].

Establishing a successful combinatorial treatment paradigm companion to augment antibody targeting is a slow and complex process built on in-depth understanding of the molecular networks targeted as well as expected adverse events. Antibodies have become valuable drugs in a relatively short time due to their potential for innovative drug design that takes advantage of the molecular makeup of cancers and minimizes the risk for adverse effects. Uncovering and validating novel targets for antibody-based drugs and integrating them into the patient care is a promising and exciting frontier that Indivumed is driving. ■

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Pretrained generative AI enters pharmacology

PHARMACOKINETICS A new AI approach called AICMET explores how pharmacokinetic modelling could be accelerated from weeks to hours. In pilot studies, it showed advantages over NLME and neural ODE algorithms, delivering promising predictions from only a few early measurements. Though preliminary, it points towards future applications in adaptive and personalised dosing.

› Dr César Ali Ojeda Marin, University of Potsdam, Dr Ramsés J. Sánchez, University of Bonn

Pharmacology has long relied on pharmacokinetic and pharmacodynamic (PK-PD) models to determine how drugs move through and act in the body. These models are central to preclinical studies and clinical trials, where accurate characterisation of absorption, distribution, metabolism, and elimination is essential for safe and effective dosing. The workhorse of this field has been nonlinear mixed-effects (NLME) modelling. Here, a system of differential equations is specified for each compound, with parameters representing population-level kinetics and patient-specific variability. Training involves estimating these parameters from sparse, irregular trial data – a process that typically requires exten-

sive fine-tuning, making it both tedious and time-consuming. Crucially, the training must be repeated for every new compound, making the process slow and resource-intensive.

Amortised inference offers a breakthrough. Instead of retraining for every new dataset, the model is pretrained once on a large corpus of synthetic pharmacokinetic trajectories. Expert knowledge from systems pharmacology defines these simulations, encoding plausible drug dynamics without using sensitive patient records. At deployment, the model requires only a few empirical data points to adapt – preserving data privacy and enabling a new business model, where companies licence networks and fine-tune them locally without exposing proprietary trial data.

Within this space, two complementary directions are reshaping tabular data and time-series analysis: prior-fitted networks (PFNs), which approximate predictive posteriors for uncertainty-aware forecasting, and foundation inference models (FIMs), which learn to recover the operators driving the dynamics.

Introducing AICMET

The Amortised In-Context Mixed-Effect Transformer (AICMET) is the first framework to introduce these principles into pharmacology. It combines mechanistic PK priors with transformer architectures trained for in-context learning – the same principle powering large language models like ChatGPT. Instead of text prompts, AICMET's prompt is the collective context of trial participants. Conditioned on this context, the model generates calibrated predictions for a new patient after only a handful of early measurements.

Initial benchmarks indicate that AICMET not only outperforms NLME and neural ODE baselines in prediction capabilities, but also shows the potential to generalise to drug metabolites without redesigning models. Most importantly, it compresses the model-development cycle from weeks to seconds, pointing towards what we call "zero-shot dosing." While these results are preliminary, they open the door to a new paradigm of adaptive, data-efficient and privacy-preserving pharmacology.

The implications are profound. By turning context into computation, AICMET makes dosing prediction flexible, data-efficient and privacy-preserving. It opens the door to adaptive clinical trials that adjust in real time, regulatory submissions backed by calibrated uncertainty estimates, and personalised regimens that scale across compounds and populations.

And pharmacology is only one proving ground. Amortised and foundation inference models represent a broader shift in science: replacing dataset-specific model fitting with pretrained inference engines that generalise across stochastic processes. From biology to physics, this paradigm promises to make inference itself a reusable foundation – transforming not just drug dosing, but the practice of modelling across disciplines. ■

Screening test

PANCREATIC CANCER Nasdaq-listed Mainz BioMed NV has announced encouraging results for its multivariate RNA liquid biopsy test for pancreatic cancer, exclusively in-licensed from Liquid Biosciences Inc in March. In a small feasibility study involving 30 blood samples, the test demonstrated a 100% sensitivity and 95% specificity, highlighting its potential as a tool for early detection of one of the most lethal cancers.

The test leverages a panel of 18 RNA biomarkers, analysed using Liquid Biosciences' EMERGE platform and AI algorithm. Unlike traditional approaches that focus on individual markers, the machine learning model evaluates combinations of normalised expression profiles to generate a risk score. This score is then compared to a defined cutoff, classifying patients as "increased risk" or "no evidence of tumour." The methodology also reportedly allows detection of precancerous lesions, although the company has not disclosed quantitative results.

These results are particularly notable given the historical limitations of pancreatic cancer detection via liquid biopsy. Previously, only metastatic (Stage IV) disease could be reliably detected with 80–95% accuracy, while early-stage tumours (Stage I) were identified with a mere 1–2% sensitivity using single-marker assays.

Despite being hailed as "sensational" by Benzinga.com, the results are preliminary. Larger studies are required to validate the findings across diverse patient populations before the FDA can consider the test as clinically evidential. Mainz BioMed intends to pursue such validation, aiming to position the assay as a screening tool for high-risk groups, enabling earlier intervention and potentially improving outcomes.

The company plans to expand clinical evaluation through its PancAlert programme, finalising the selection of PCR-detectable biomarkers and assessing performance across multiple cancer stages. ■

Sepsis diagnosis: culture-free, rapid and non-invasive

AI Pattern recognition is often cited as a major strength of AI tools. European Biotechnology spoke with Dr Maximilian Dietrich from Heidelberg University Hospital about how this can be used to evaluate changes in microcirculation that indicate sepsis. Together with colleagues, he has developed a method that could revolutionise sepsis screening.

EuroBiotech_Could you briefly explain how your method works and what role AI pattern recognition plays in this process?
Dietrich_*Our non-invasive method utilises a medically approved hyperspectral camera to capture reflectance spectra of the skin, allowing us to analyse microcirculatory changes using AI. These changes are early indicators of sepsis. No reliable technical approach is currently available in clinical practice to objectively assess microcirculation, although hyperspectral imaging shows promise as a potential solution. Since 2020, we have been working with a device developed by Diaspective Vision GmbH, which can spatially resolve both tissue oxygenation and water content, thereby quantifying capillary leak. Our partners, the Division of Intelligent Medical Systems at the German Cancer Research Center (DKFZ) in Heidelberg – specialising in AI-based image data analysis – collaborated with us throughout the project. Encouraged by the promising results on pilot study data, we proceeded to conduct a monocentric study involving more than 500 patients. Encouraged by the promising results, we proceeded to conduct a monocentric study involving more than 500 patients.*

EuroBiotech_What were the results?
Dietrich_*In this monocentric study, we included critically ill patients admitted to our intensive care unit. Approximately one-third of the patients had sepsis according to clinical criteria. Recognising sepsis in critically ill patients is significantly more challenging than distinguishing it from healthy controls, demanding a highly discriminative method. We decided to include only ICU patient data for the training and validation analysis, as an AI can only be as good as the data used for training sets. Using our AI-based image analysis method, we achieved an AUC of 0.8; when incorporating clinical parameters, we reached an AUC of 0.94 for identifying sepsis. We were also able to predict mortality with high accuracy using this method (AUC 0.72). A limitation of our study is that the method has not yet been validated on external datasets. We plan to continue validation efforts, including collaborations with other hospitals. After thorough external validation, we believe this method could be well suited for screening at-risk patients, for example in emergency departments.*

PD DR MAXIMILIAN DIETRICH, anesthesiologist and intensivist at the University Hospital Heidelberg with a research focus on sepsis.

EuroBiotech_ How does your test compare to clinical assessment based on the Sepsis-3 criteria (SOFA/qSOFA), supplemented by laboratory parameters and wet-lab tests that also measure microcirculation changes?
Dietrich_*Currently, no single biomarker test or scoring system can unequivocally identify sepsis without clinical evaluation and expertise. The SOFA score is the standard for diagnosing organ failure but is complex to obtain. As a result, various clinical scores are used for screening, such as the qSOFA, which assesses increased respiratory rate, severely reduced systolic blood pressure, and altered mental status. However, qSOFA has the drawback of often identifying sepsis patients only at a late stage, when they are already severely ill. Earlier-acting scores such as NEWS or MEWS require various clinical parameters that must first be collected. While innovative laboratory biomarkers are essential for enhancing sepsis diagnosis, their reliance on sample collection means results are not immediately available. In terms of speed, our non-invasive method offers a clear advantage –once a device with integrated AI-based analysis is available—since image acquisition takes only a few seconds. However, such a system can only be developed in cooperation with industry partners. Ultimately, all methods are complementary, aiming to achieve the highest possible diagnostic certainty: upon admission, risk assessment with hyperspectral imaging (AI) could be followed by clinical scoring and biomarker testing as needed.* ■

Picture: © University Hospital Heidelberg

AI for Transition AI for Change

CONFERENCE Leading experts from industry and academia unite to shape a circular future for renewable carbon with help of artificial intelligence at the AI Circular Economy Conference, 4-5 March, 2026 in Cologne and online.

Artificial intelligence (AI) is no longer just a technological trend; it is a transformative force that is accelerating the transition from fossil fuels to renewable carbon sources in the chemical and materials industry. This represents one of the greatest industrial challenges since the beginning of the industrial revolution, requiring the most advanced digital solutions available. AI is emerging as the key enabler of this transformation.

Recognising the transformative power of artificial intelligence, nova-Institute is actively shaping this development by holding this conference. The AI Circular Economy Conference will bring together all relevant stakeholders to discuss the need for AI solutions in a circular economy in the chemistry and materials sector and to match these needs with technical solutions from scientists and developers.

Featuring top experts in AI development, chemical and plastics manufacturing, biotechnology, agriculture, recycling and sustainability, this interdisciplinary event will explore the latest developments in the field.

Topics include, but are not limited to, the following:

- High-tech innovators are delivering cutting-edge AI solutions for science and industry.
- Chemical and plastics producers are using AI to innovate more quickly, efficiently, and sustainably.
- The agricultural and biomass sectors are using AI in precision farming to increase yields, lower the environmental impacts and close the loop on material flows.
- Cutting-edge applications of AI, including AI-assisted modelling of CCU processes and catalysts, optimisation of CO_2 capture, and the design of novel chemical pathways such as those involving electrochemistry.
- Use of AI for process control and optimisation in depolymerisation, advanced waste stream sorting and feedstock analysis, as well as quality assurance of recycled materials.

The High-Level Advisory Board ensures a comprehensive, balanced programme. It unites leading experts from chemicals, materials, AI, and digital solutions-representing global software firms and practitioners in process optimisation, predictive maintenance, supply chain forecasting, data analytics, and industrial AI. nova-Institute adds decades of expertise in renewable carbon, bioeconomy, circular economy, and sustainability. ■

Join

Nova-Institute proudly presents its new highlight event, bringing together the best innovators, researchers, and practitioners

of this fundamental digital transformation in the renewable economy. Join us at this groundbreaking conference to explore how advanced AI tools and applications are shaping the future of circular and sustainable chemicals and materials by unlocking the full potential of renewable carbon from biomass, carbon capture utilisation (CCU), and recycling. We are curious to learn whether our stakeholders share this view.

Michael Carus,
CEO and Founder nova-Institute

Dr. Lars Börger,
CEO nova-Institute

› QUICK FACTS

Venue Information
AI Circular Economy Conference 2026
Maternushaus
Cologne, Germany (and online)
4-5 March 2026
www.ai-circulareconomy.eu

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