# Wiley Analytical Science MAGAZINE

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LEARN MORE

## Vector Construction

Equipped with a therapeutic antibody's genetic sequence, scientists insert that sequence into a molecular vehicle called a plasmid vector

## Stable Transfection and Selection

Plasmid vectors deliver the desirable DNA construct to thousands of host cells, spurring antibody expression

## Single Cell Depositing and Monoclonality Verification

## Expansion and Characterization

## Scale-Up

Rigorous checks and balances are required to ensure cell line efficiency and viability during scale up

## Master Cell Banking

Selected cell lines are stored in a master cell bank, where they're cryopreserved until future use

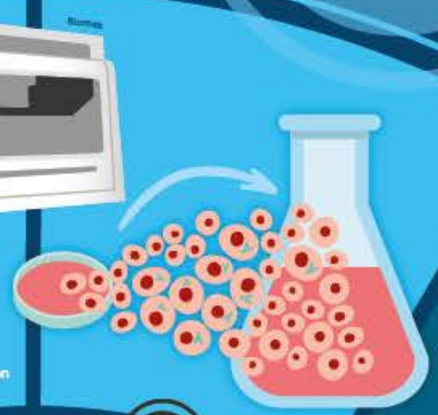
Cell Line Engineering and Selection

Cell Line Characterization

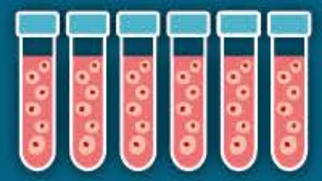
Process Development

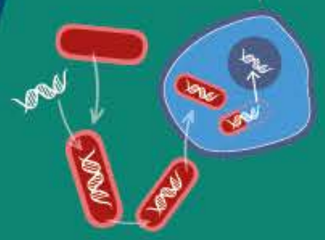












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# Cell Line Development:

## Accelerating Answers with Automation

From generating vaccines and checkpoint inhibitors to developing revolutionary gene therapies, cell line development possesses the power to accelerate innovation in the life sciences. It's a critical cog in the biologics production wheel. Despite advances in technology, manual bottlenecks still plague this workflow. At Beckman Coulter Life Sciences, our goal is to empower and outfit your cell line development workflow with leading-edge automation technology that will inform, unify and accelerate your cell line development workflow, allowing you to produce and select efficient cell lines. But we're more than a technological solution for scientific excellence. Our expert architects in cell line development are here to answer your questions. From antibody engineering to Master Bank Selection, we're here for you at all touchpoints. Explore our array of instrumentation, software, and reagent solutions that'll transform your cell line development workflow into a nimble, efficient and results-driven enterprise.

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Life Sciences

Products and methods described are not intended for use in diagnostic procedures.



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# Content



# Editorial

## Dear Readers,

Wiley Analytical Science Magazine keeps bringing you the latest hot topics in science and we couldn't skip "Drug Discovery", the topic of this issue.

Nowadays, drug discovery rarely occurs as serendipitous as, for example, Penicillin. Yet, through rigorous clinical trials, researchers continue to bring us new ways of treating not only new diseases such as COVID but existing ones, such as cysticercoses. In this issue, we interviewed Maria Elena Bottazzi, Ph.D. who for over 20 years has worked on developing innovative biotechnologies to tackle neglected tropical and emerging diseases (see page 8).

The long and arduous processes of drug discovery have been constantly improved and even automated with artificial intelligence. Now, pharma companies can save costs and manufacture more drugs by selecting better candidates with the help of AI (see page 31).

In this issue, we present Prof. Gunda Georg, who is developing a non-hormonal male contraceptive (page 21); Mathias Hartlieb describes how to create polymers that kill microbes (page 25); and many more.

And don't forget, we are preparing for our second annual Wiley Analytical Science Virtual Conference, which will take place from November 8th to 17th. Also, until October 14th you can vote for Wiley Analytical Science Award 2023. The winners will be announced this autumn at our Wiley Analytical Science Conference.

Would you like to contribute to our magazine? What would you like to read about? For suggestions on research topics and scientists you would like us to interview, please contact us at AnalyticalScience@wiley.com.

**Enjoy the read.**

*Dr. Cecilia Kruszynski*

# At a glance:

## Research updates Pesticides & Pollutants

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### Can a smallpox drug treat monkeypox? Here's what scientists know

As supplies of vaccines against monkeypox remain constrained and the number of people contracting the disease continues to mount, physicians and researchers are looking to the drug tecovirimat for relief. In animals infected with monkeypox, the antiviral has been shown to lower the amount of virus in their bodies and reduce the number of fluid-filled 'pox' lesions forming on their skin.

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### New combination of methods shortens drug search

The use of novel native mass spectrometry methods led to the discovery that cyanobacteria from Caribbean coral reefs produce a group of natural substances that effectively inhibit digestive enzymes.

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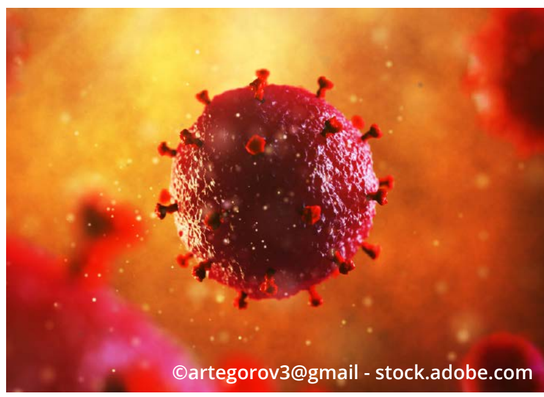
### Two HIV patients appear to have beaten virus, offering hope for cure

A 66-year-old man and a woman in her 70s who beat HIV will help researchers in search for cure for virus that causes AIDS.



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## Could a common diabetes drug ease bipolar disorder?

A half-century-old diabetes drug appears to help treat bipolar disorder by reversing patients' insulin resistance. Bipolar patients who responded to the drug metformin experienced improvement in their mood disorder as their insulin resistance decreased.

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## FDA approves Zonisade

The first and only FDA-approved zonisamide oral liquid formulation offers healthcare providers an important new treatment option for their patients with epilepsy.

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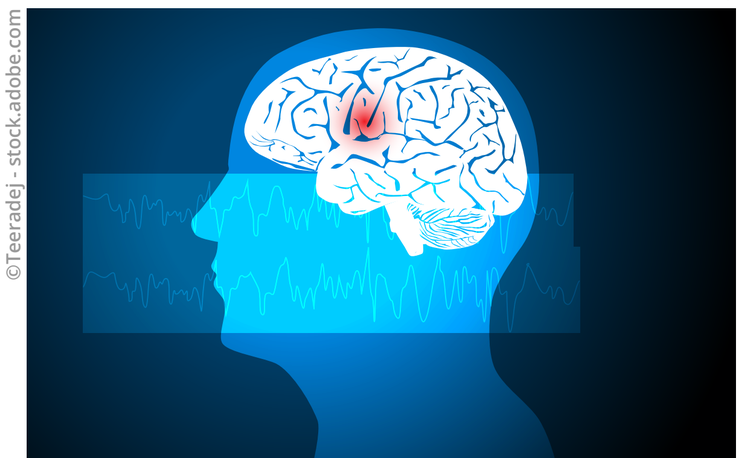

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## China approves first homegrown COVID antiviral

China's drug regulator granted conditional approval on Monday for an HIV drug to be used to treat COVID-19. The drug, Azvudine, developed by Chinese drugmaker Genuine Biotech, is the first oral antiviral for the disease made in China.


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## Pandemic drives largest drop in childhood vaccinations in 30 years

Last year alone, 25 million children missed out on immunizations against infections such as measles and polio, leading to avoidable outbreaks of disease.

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## Two new treatments for Crohn's disease equally effective

The treatments showed roughly equal performance in clinical trials and resulted in clinical remission. This allows clinicians and patients to make treatment choices based on tolerance.

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## The hunt for drugs for mild COVID: scientists seek to treat those at lower risk

People who are unlikely to develop severe COVID-19 have no widely approved medications to ease the illness. Such treatments could reduce the disruption that even mild cases can inflict on people's jobs and family lives.

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## Lipoproteins hide Lyme bacteria from the immune system

Scientists identified two proteins that helped the bacteria evade detection by the human immune system. These findings will inform the development of new therapeutics and vaccine targets for Lyme disease.

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## Malaria vaccine booster prolongs protection

A promising malaria vaccine was up to 80% effective at preventing the disease in young children who received a booster shot one year after their initial dose, exceeding a World Health Organization (WHO) target of 75% efficacy.

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## New reaction facilitates drug discovery

Chemists at ETH Zurich have found a facile method that allows a commonly used building block to be directly converted into other types of important compounds. This expands the possibilities of chemical synthesis and facilitates the search for new pharmaceutically active ingredients.

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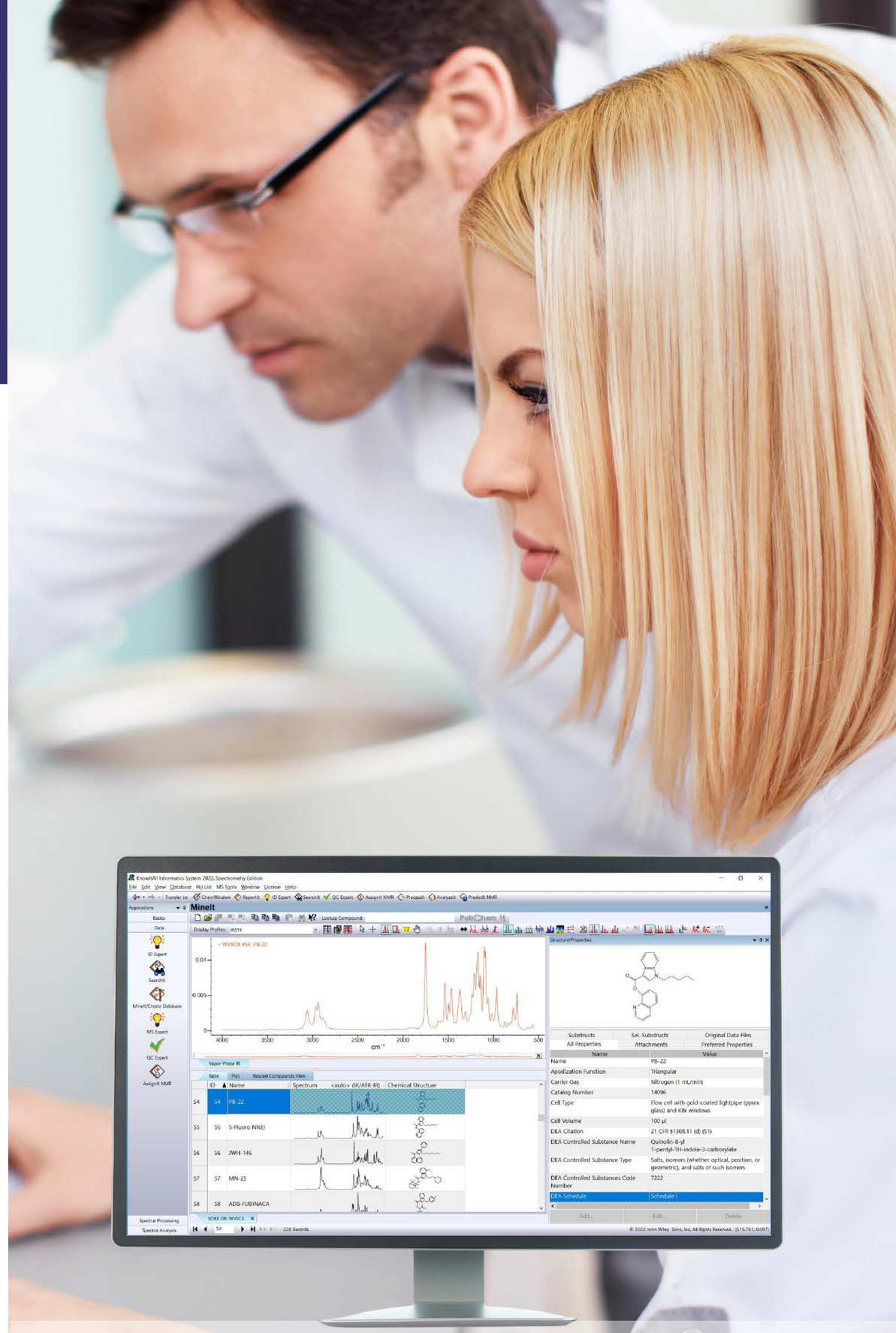


*Supports multiple techniques and instrument vendor formats to streamline your workflow.*

# Tropical diseases under the microscope

## Maria Elena Bottazzi, Ph.D., the scientist who's made it her life's work to develop innovative biotechnologies to tackle neglected tropical diseases


*Maria Elena Bottazzi is the Associate Dean of the National School of Tropical Medicine, Professor of Pediatrics, and co-director of Texas Children's Hospital Center for Vaccine Development at Baylor College of Medicine in Houston, Texas. For over 20 years, she's worked on developing innovative biotechnologies to tackle neglected tropical and emerging diseases. She's also a world-renowned scientist with an impressive portfolio of work in the field of infectious disease and has been nominated for the 2022 Nobel Peace Prize.*

### At school, the teachers incentivized Bottazzi to pursue the sciences

A scientist with a wide range of expertise, Maria Elena Bottazzi, Ph.D., was fascinated by sciences, math, chemistry, and biology, since she first started school in Italy, where she was born. Daughter of a Honduran diplomat, she moved to Honduras when she was 8 years old. Her teachers at that time were key players in shaping her interest in pursuing a career in the university and higher education. At first, she wanted to study medicine in Honduras. Bottazzi was convinced that this was the best opportunity she had to accomplish her main goal: to help her community. She finished high school in May 1983, however, as the medical school semester only started in January in Honduras, she opted to start a bachelor's degree in Microbiology, which, back in the 80s, was still called Microbiology and Clinical Chemistry, at the National Autonomous University of Honduras.

This was when she realized how difficult it is to understand all the paths and areas the biomedical sciences can offer. “There were so many options of careers and disciplines involved to serve your community and benefit the health of the population that it was difficult to choose from,” she remembers.

Bottazzi was pleasantly surprised that the microbiology curriculum included human, environmental, veterinary, and industrial microbiology topics, and how all were integrated towards the understanding of human, climate, and world health. It was essential for her career that she learned not only the scientific field but also how to operationalize the work towards serving communities. She had to learn how to evaluate the epidemiology and burden of many diseases, while also developing technologies to better diagnose, prevent (i.e., vaccines), and design therapeutic interventions. After this, she never came back to the idea of studying medicine. “Even though I was always interested in the human aspects of things,” she explained “many microbes have this interaction between animal and human health, as does environmental and human health. I basically stayed in microbiology.”

## Working in microbiology

With microbiology, she could interact with physicians and people needing solutions, serve as a public health official, and more importantly, be creative in finding ways to design and discover new technologies. Her first study was to optimize the diagnosis of cysticercoses [1], a parasitic infection that can migrate to your brain and cause several neurological issues, including epilepsy. Previously, in Honduras, there was no easy way of detecting the parasite without the imaging access that we have today. It was possible with invasive techniques, for example, accessing the cerebral spinal fluid, but there was no serological way to detect if you were exposed to the parasite.

This was when she decided, in an interdisciplinary way, to merge parasitology and immunology and apply for graduate programs abroad. Initially intended as a master’s degree, she saw the opportunity to broaden her understanding of host-pathogen relationships by going deep into the molecular aspects and genetics of microbiology, which was not available in Honduras back then. In 1989, she was accepted into a graduate program in the US and that is when she fell in love with academic research.

## Ph.D. studies and serving the community

She obtained a doctorate in Molecular Immunology and Experimental Pathology from the University of Florida. For her Ph.D., Bottazzi was working on understanding the genetic mechanisms of acute myeloid leukemia under the supervision of Dr. Maureen M. Goodenow [2,3]. “Advancing my own academic career and having a Ph.D. degree would give me more flexibility,” says Bottazzi, “but there must be ways that academia can really better serve communities and therefore I started thinking that it's not sufficient to just work in my little world in my lab doing my experiments, I needed to know how to translate those discoveries.”

Thus, the question that popped to mind was “how can I not only develop and discover new ideas but fashion them into real solutions for the communities?” She realized she needed new skills, including understanding the legal framework, and how to manage not only money but people, infrastructure, etc. “How do you really focus on the ethics and the regulatory systems and how do you communicate?”

Early on in a scientist’s career, they learn how to write a manuscript and give a scientific talk at a conference, but never to speak to society. “Not only was I interested in diversifying my knowledge within biomedical fields like immunology, microbiology, biochemistry, but I was interested in diversifying and learning new skills in economics, finances, ethics, and engineering.” When she was a postdoc in Cellular Biology at the University of Miami and Pennsylvania, working with Dr. Richard Assoian, she had an a-ha moment: she started the business administration program at Temple University. First intended as a hobby, it helped her transfer the technologies from academia to the private sector, where the ideas can leave the paper and be distributed to the population.


She still wanted to focus on diseases of poverty as a way to serve her and other countries that still face a lot of tropical disease outbreaks; however, most times she heard that because they are poor people’s diseases it would be difficult to commercialize and advance products. “You rapidly learn that even by trying to push public health gains, eventually, indirectly, maybe in the longer term, the countries recover economic gains because we are raising the health and quality of life of people,” Bottazzi says passionately, “and if you have healthy people, educated people, they are more intellectually engaged and economically productive in society.” She strongly believes that in this way healthy people will work and can contribute to society; rapidly, she knew she wanted to work in the area of global health technology development, specializing in microbiology and specifically emerging and tropical diseases, which brought her back to her Honduran roots.

## Mentors and the importance of disseminating science

Her academic career continued at the George Washington University in Washington DC where she resided for 11 years prior to relocating to Houston in 2011 and where she had randomly stumbled on to the career path of Dr. Peter Hotez, who has now been her science partner for more than 21 years. He is a physician, scientist, and pediatrician, and is totally enamored with parasitology and microbiology. He is also interested in neglected tropical diseases (NTDs) because for many years he worked in Asia; their goals aligned – he was also interested in breaking the paradigm model of how they would develop new interventions and focus on vaccine development.

In the early 2000s, however, a couple of things happened: the United Nations created the Millennium Development Goals (MDGs), where they recognized that for humans to be able to address the issues in the world, including health issues, all nations needed to reduce poverty, increase education, address mortality, etc. And this would include improving the treatments of HIV, malaria, tuberculosis, and other diseases. This allowed Bottazzi and Hotez to bolster and give the other diseases more prominence. In addition, in 2000, the Bill and Melinda Gates Foundation was created: "They understood that product development partnership models could be a good business model for HIV, malaria, NTDs, and other underserved diseases for global health," explained Bottazzi.

At the same time, unfortunately, the 9/11 incident happened and affected the whole biodefense system, which also propelled the creation of centers of excellence to address problems of pandemic biodefense importance. Timely, the Public Library of Sciences (PLoS) open access journals were also created, enabling more open science that could be shareable, and Bottazzi and Hotez invested in disseminating their knowledge [4] "Peter was instrumental in branding the other diseases into neglected tropical diseases, which is a now a term widely used and the launch of PLoS NTDs."

After this, and upon their relocation to Houston in 2011, they ultimately renamed their product development partnership Texas Children's Hospital Center for Vaccine Development at Baylor College of Medicine. They managed to find partnerships moving towards the movement of the decolonization of the vaccine sciences with representation from the countries that had the diseases that needed the interventions.

Those partnerships were key to developing interventions in the countries to remove barriers with their philosophy of open science [5]. They started working with the developing country vaccine manufacturers, starting training programs, and learning the regulatory framework, as she says "because it's not as simple as saying, oh, we're going to do research and that research is going to convert into a product. You have to make it regulatory enabling to meet the global quality."

The most important thing she learned was demand forecasting and how they could educate the community so that they would accept an intervention: "A lot of community engagement shapes the policies that then enable the advancement of these products."

She never forgot that the foundation of her career was to give back to her country, and then serve as a role model, not only as a mentor academically but also personally, and professionally.

## Developing the COVID-19 vaccine

"A decade ago, was the golden years for the NTD, as I called it, where we were able to advance not very rapidly nor with hundreds of millions of dollars, but with very important scientific contributions," Bottazzi remembers. The developments in the last years skyrocketed: a hookworm vaccine, which is currently in phase two clinical trials; schistosomiasis vaccine, which is also in phase two clinical trials; programs in Chagas disease, which are now in the process of manufacturing and will go into the clinic next year; other important diseases that are in current development, such as other helminths, tick-borne diseases (Lyme disease), onchocerciasis (African River Blindness), lymphatic filariasis, and many more.

Even though she always worked with parasitic worms and protozoans, the opportunity to work with viruses emerged around 2010. With a group of virologists, they decided to focus on diseases of pandemic importance, coronaviruses. They selected the target antigen (i.e., the receptor binding domains of the respective spike proteins) with evidence that they would be great vaccine candidates. However, after the SARS and MERS outbreaks, coronaviruses started to be deprioritized and became neglected in comparison to Ebola and Zika virus, for example. Still, they applied for funds from the National Institutes of Health (NIH) and created a consortium, similar to the hookworm, schistosomiasis, and Chagas, which included organizations such as the University of Texas, New York Blood Center, and the US Army that is one of the most concerned parties about global health research and has a vaccine manufacturing pilot facility.

Around 2016, the group had not only advanced the SARS vaccine to a point of a manufactured product but also confirmed with regulatory-enabling experiments that the target – the receptor binding domain of the spike protein, was safe and effective in preclinical models of disease.  However, there was no more priority for these viruses.

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Bottazzi and Hotez opted to keep the program active even without external funding (only with internal institutional funding) because it was a decade of research that could immediately be applied to other pandemic-related viruses. Fortunately, when the COVID-19 outbreak started at end of 2019 – beginning of 2020, a vaccine that took 6 years to develop for SARS was re-engineered in 3 months specifically for the SARS-COV-2. The scientific foundation of the vaccine development was solid, therefore, in a short time, they could expand the partnerships and bring key actors to scale this vaccine, such as Biological E Ltd and Biofarma. “Even if the US was not interested, and we did not receive substantial federal funds, several local foundations believed in our cause and gave us money to advance our research,” she recognizes “And then we expanded our partnerships and brought in real key thinkers to strategize to advance our vaccine into a global health product. Today we have a vaccine that has reached the arms of more than 70 million people.”

## Public trust in scientists: a real policy failure

Bottazzi faced several challenges over the years but never expected what was yet to come. For her, the fact that COVID-19 became a global pandemic was really a policy failure. It wasn't a scientific failure. “I think science was probably the easiest thing for us. We're trained as scientists, and we had a decade of working on a scientific basis for the development of a coronavirus vaccine. Getting financial support is difficult, but everybody has that at one level or another. But what was really difficult was on the policy side. How do you convince the policymakers to support equitable vaccine access policies?”

She explains that it was a policy failure because no country was prepared or valued science, but the problem was even deeper. “Even if you fix the science, fix the investments, fix a little bit the way that you can make policy more flexible, nobody was talking to the society, right? And there was an automatic perception that you were just dictating to society that they needed to use these new RNA or viral vector vaccines and they were never included in the conversation. It's a big lesson.”

Then, the world once again saw how community health is important because an individual decision can impact somebody else. The lesson to learn is definitely to include other voices from society: “It’s not easy to build a plane when you're flying. So yes, there may have been decisions that we made because we didn't know things at that time.” The past 2 years showed a lot of hesitance and fear by the people, and this will most likely affect the future “The fact that also during the pandemic, everything else stopped, for example, all the childhood immunization programs, we're now seeing resurges against not only measles but polio. That's a disaster. It's because people just lost confidence or governments don't have any more money and they can't keep up with their already dire public health systems. We have some tough years to come,” she predicts.

*Interview conducted by Dr. Cecilia Kruszynski, editor at Wiley Analytical Science.*

## References


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[2] *Ambrose MR, Bottazzi ME, Goodenow MM. Expression of the c-ski proto-oncogene during cell cycle arrest and myogenic differentiation. DNA and cell biology. 1995;14(8):701-7. Epub 1995/08/01.*

[3] *Bottazzi ME, Goodenow MM, Moscovici MG, Moscovici C. BM2L is a spontaneous leukemogenic variant of a non-leukemogenic v-myb-transformed myeloid cell line. Oncogene. 1993; 8:731-6. Epub 1993/03/01.*

[4] *https://journals.plos.org/plosntds/*

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# Mass spectrometry in the pharmaceutical industry

## A fundamental analytical method in drug development

Health is a fundamental need of mankind. The pharmaceutical industry develops and supplies drugs for new therapies for the care of patients. From an analytical point of view, modern mass spectrometry has become an indispensable instrument in the pharmaceutical industry. It is an efficient tool that is used for chemical analysis across almost all stages of drug development (Fig. 1) in order to gain fundamental insights at the molecular level or to make key decisions in the drug development process.

## Applications of mass spectrometry

Mass spectrometry is an analytical technique for measuring the mass per charge of ions. With knowledge of the ion type (e.g., [M+H]+, [M]+, [M-H]-, [M+2H]2+, [M+Na]+, etc.), the technique provides the measured mass of molecules. MS has been rapidly developed in the last decades thus specific solutions and commercial instruments currently exist for a large number of different applications. The measurement of mass as an intrinsic property of molecules is used to characterize chemical compounds, e.g., reaction products in chemical synthesis, environmental analysis, biomolecules in biochemistry, doping controls, and medicinal chemistry to identify substances from the body.

## Chromatography as separation system before MS

For the analysis of complex mixtures, MS systems are often directly coupled with chromatography. While liquid chromatography-MS (LC-MS) is typical for dissolved analytes, volatile components can be efficiently analyzed with gas chromatography-MS (GC-MS).

In LC-MS, electrospray ionization (ESI) results in a soft ion formation where large biopolymers such as proteins, polysaccharides, and oligonucleotides can be analyzed completely intact.

Molecule sizes range from small molecules via small drugs such as aspirin, peptides, and insulins to proteins, such as antibodies and intact protein complexes.

In contrast, electron impact ionization, which is typical in GC coupling, results in reproducible compound-specific fragmentation due to the unstable radical cations generated. This is advantageous in the case of unknown components since comparison of the measured spectra with spectral libraries allows efficient structure determination of molecules.

## Understanding a disease – biomarkers and targeting

For a pathological understanding of a disease, a scientific model is needed that provides in-depth information at the cellular and microbiological levels. There, in the interaction of biomolecules, proteins with their individual structure play a central role as molecular tools. The proteome as a sum of the proteins in the system under consideration is in focus in the discovery of functional biomarkers for diseases.

In drug development, often the first step is to find a suitable target in the disease process. In the most straightforward case, if a patient is partially or completely deficient in a particular substance, that substance can be administered as a drug. Examples are the hormone insulin for diabetics, the enzyme lactase for people with lactose intolerance, and coagulation factors for hemophilia patients. In most cases, the points of attack in the disease process must first be identified in order to be able to develop a specific active ingredient; it is the search for a target. Frequent targets are proteins that function as enzymes or receptors.

## Dr. Jürgen Schäfer

studied chemistry in Frankfurt. After his PhD thesis on ion formation in the MALDI process with Prof. Karas, he worked on the discovery of new protein biomarkers at Industriepark Höchst starting in 2000 and developed the isobaric tandem mass tag technology. Since 2009, his focus as a mass spectrometry lab manager has been on drug discovery of small molecules, peptides, insulins, proteins and antibodies. Since 2018, he has been a guest lecturer at Provadis University with the Mass Spectrometry Specialty Analytics lecture.

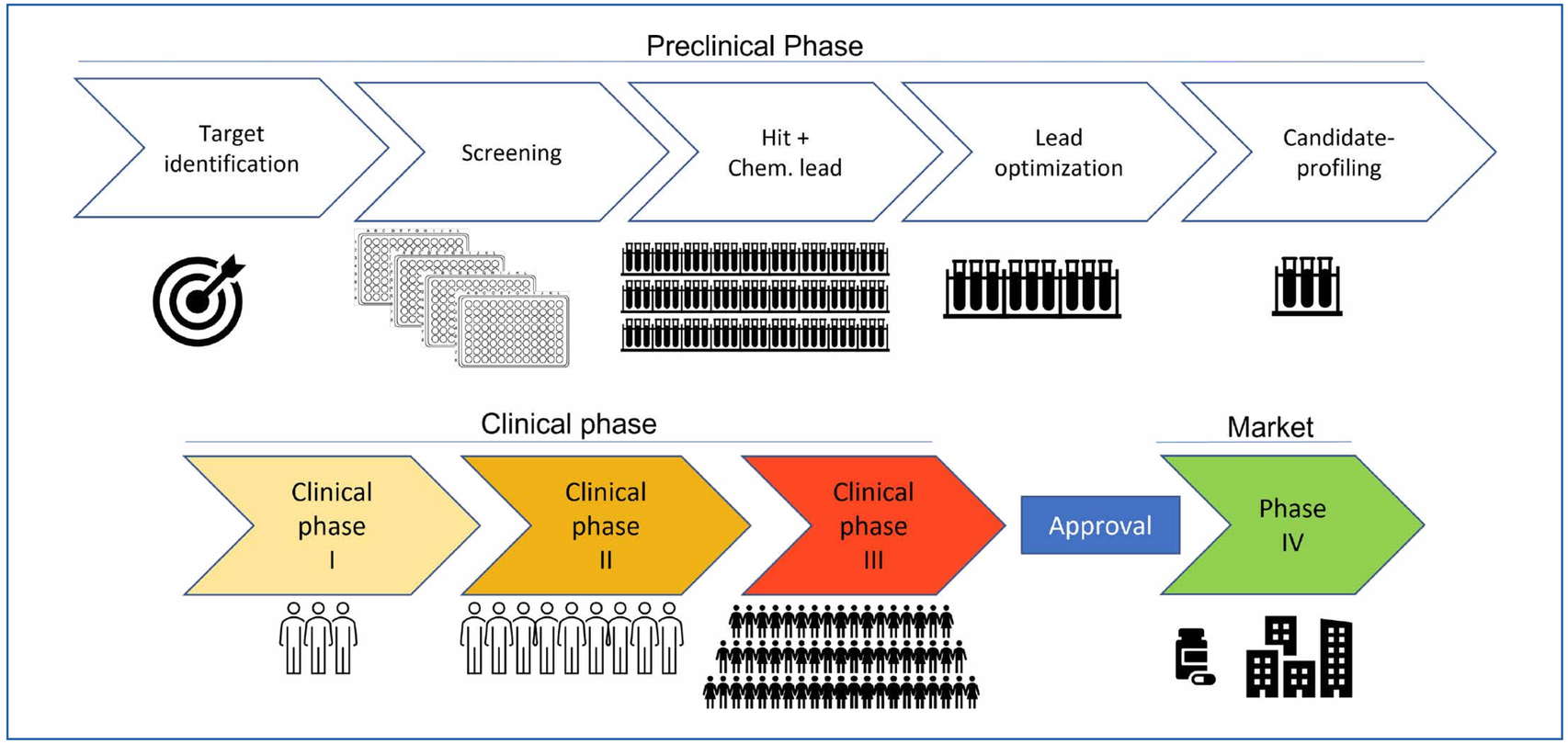


*Fig. 1: Flow chart for drug development in the pharmaceutical industry.*

## Proteomics provides microbiological insights

Proteomics technologies are used in the discovery of significant differences in the proteome of diseased patients and normal volunteers. Two-dimensional protein gels, on which the separated proteins were visualized as color markers, have been displaced by mass spectrometric techniques that detect thousands of proteins. Identification and quantification of disease-regulated proteins are performed after enzymatic cleavage at the peptide level with automated data acquisition of numerous spectra and fragment spectra (MS and MS/MS) and subsequent comparison with protein databases comprising all proteins of the species of interest. The isobaric multiplex analysis strategy is particularly efficient, allowing up to 18 different samples to be labeled with different isobaric isotope markers and then analyzed together in a single chromatographic run. This allows complex biological series experiments to be measured in a single chromatographic LC-MS run, saving time and eliminating the need for computationally intensive adjustment of the varying retention time of individual experiments. The data sets contain the dynamics of thousands of proteins.

These techniques not only find statistically significant regulated biomarkers with diagnostic utility, but also potential therapeutic targets.

The proteomics boom has driven the development of efficient mass spectrometers, leading to a range of fast, high-resolution MS/MS capable instruments: time-of-flight mass spectrometers with their high data acquisition rate up to 200 Hz and Orbitrap detector instruments with high resolving power of 1 million. The combination of collision-induced (CID) and electron-induced (ETD) fragmentation in one instrument can automatically perform the most favorable MS/MS conditions adjusted according to peptide size. The high sensitivity of the instruments now makes it possible to obtain quantitative protein data from the systematic analysis of single cells (single-cell proteomics).



## Search for active ingredients

Once a target has been identified, the search starts for an active ingredient that interacts intensively with the target and achieves the desired effect. If molecules naturally exist in the organism that binds to the target, this form can be used as an active ingredient (ligand-based drug design). Virtual screening is the search for suitable binding partners for 3D protein models on the computer according to the lock-and-key principle. In high-throughput screening (HTS), several thousand compounds are tested for binding to the target in miniaturized microtiter plates. Special reagents enable inexpensive optical readout of the screens. Mass spectrometric detection has advantages in the selectivity and number of targets. Automated solid-phase extraction (SPME) is used as a fast separation method to enable high throughput.

HTS hits can be used to derive lead structures that are further optimized for specific properties, such as protein binding, and in animal studies of tolerability, absorption, metabolism, distribution, and excretion (lead optimization).

## Cellular proteomics

Based on the knowledge that proteins are more thermostable with respect to aggregation when the appropriate ligand binds to them, a melting curve can be derived from temperature-dependent series of measurements of the amount of soluble protein. With quantitative mass spectrometry, thousands of proteins can be detected from the level of intact cells (Thermal Protein Profiling – TPP), and thus fundamental biological studies can be performed. For drug candidates, data on efficacy and also potential incompatibilities are derived from the protein binding properties.

## Metabolism and pharmacokinetics

The degradation of the active agents of a drug in the body must be understood qualitatively and quantitatively. In the structural characterization of metabolites, precise mass determinations are essential, allowing unambiguous identification of the molecular formula, as well as conclusive fragment spectra.

Once the chemical structures of the metabolites have been clarified, triple quadrupole mass spectrometers, which are sensitive and selectively tuned to the respective molecules, are used on a large scale in the investigation of the pharmacokinetics of the active substances. In this Multi Reaction Monitoring mode (MRM), a particularly broad linear range over five orders of magnitude is available.


## Imaging mass spectrometry

In the analysis of drug distribution in tissue sections with imaging mass spectrometry (MS imaging – MSI), the focused laser in matrix-assisted laser desorption/ionization enables a particularly high spatial resolution of a few micrometers. Unlike classical radio imaging, in which an image of the radioactive radiation distribution is obtained after administration of a radiolabeled drug, MSI allows a distribution image to be generated from the data for each separately detectable mass, so that drug and metabolites can be visualized completely independently of each other. Valuable detailed information can be traced from the spatial distribution at high resolution.

## Regulatory documents – characterization of biopharmaceuticals

Drug regulatory authorities require extensive state-of-the-art characterization studies for the approval of biopharmaceuticals. For example, for antibodies with MS, the amino acid sequence is confirmed, the correct linkage of the disulfide bridges is checked, the glycans are characterized, as well as their quantitative distribution. Other critical quality attributes include oxidation of methionine side chains or deamidation of acidic amino acids asparagine and glutamine, respectively.

Proteins originating from the host cells of antibody production (host cell proteins – HCP) should not be found in the product, they are quantified by MS. For antibodies chemically modified with an active substance, the drug/antibody ratio is measured by MS.

## Ion mobility spectrometry as a new MS separation dimension (IMS-MS)

While detection in mass spectrometry takes place in a vacuum, ion mobility is based on the interaction of ions in an inert gas stream depending on their cross-sectional area. Isomeric compounds that have identical masses can thus be fed to the mass analyzer separately in time and quantified independently. This opens up a new dimension of molecular characterization in mass spectrometry. This still young, dynamically growing technique is advancing numerous applications. Circular IMS arrays offer multiple runs as an option to achieve high resolution. The separation of isomer molecular ions of oligosaccharides and protein complexes of different cross-sectional areas is evident. Similarly, background noise can be minimized in this way, improving the quality of spectra and fragment spectra. Operated as an ion trap, ion mobility can collect precursor ions to be fragmented in a sorted manner during the fragmentation of multiple chromatographically coeluting ions, thus minimizing losses. This in particular is very useful in proteomics experiments.

## Summary

In the pharmaceutical industry, mass spectrometry provides a view of the molecular level in the development of new drugs. At different stages of development, mass spectrometric analytical results provide important input for the necessary decisions leading to a successful, tolerable, and effective drug substance.

## Author

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# Non-hormonal **male** contraception

**Interview with Prof. Gunda Georg about her discovery of a contraceptive that effectively prevents pregnancy in mice**

*Prof. Gunda Georg has dedicated over 20 years toward developing a male contraceptive that would be effective, reversible, safe, and affordable, reports Róisín Murtagh, editor for Wiley Analytical Science.*

**Can you describe the processes involved in the non-hormonal male contraceptive?**

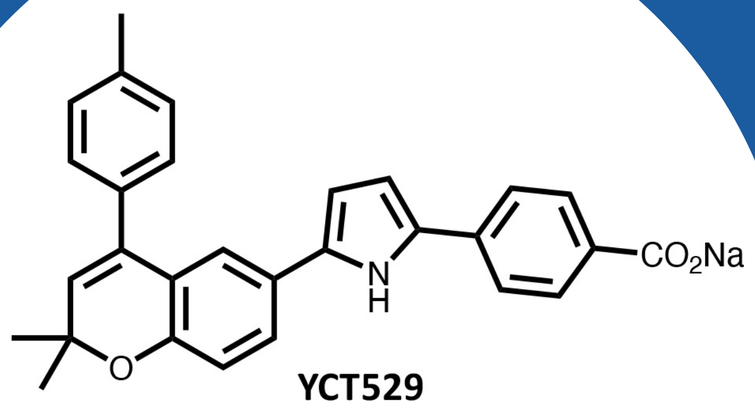
***Gunda Georg:*** In a typical drug discovery process, the first step is target validation, which is also required for a male contraceptive agent. This can be done by creating a knock-out (KO) mouse that lacks an essential biomolecule required for male fertility. If the KO mouse is healthy but sterile, then one can assume that a molecule that is interfering with the biological function of the said biomolecule, could become a contraceptive drug.

After target validation, one must find chemical matter. This can be done by several methods such as virtual high throughput screening, high throughput screening of compound collections, including DNA-encoded libraries, or one can start with existing compounds that target the same or similar proteins.

Next, one needs to go through a typical drug discovery and development process that is used for all drug discovery projects. The chemical matter needs to be improved for potency, selectivity, physicochemical properties, *in vivo* activity, and off-target effects. This process involves the synthesis and evaluation of many compounds in multiple assays.

For a contraceptive agent, proof of the effectiveness of an optimized compound is obtained by a mating trial that is typically performed in mice or rats to show that infertility can be achieved after drug administration and that fertility is regained after drug treatment is discontinued.

Our compound YCT529, which was discovered by my research team at the University of Minnesota in the Institute for Therapeutics Discovery and Development, showed 99% effectiveness in preventing pregnancies and full recovery of fertility in mice. This was shown by our collaborators, reproductive biologists Debra Wolgemuth and Sanny Chung at Columbia University. YCT529 works by reducing sperm counts to infertility levels. These tests indicated that this is an effective and safe drug candidate at therapeutic doses. However, additional toxicological tests need to be conducted to gain FDA approval to initiate a clinical trial. This is very expensive and cannot be done by an academic lab. We were fortunate that the company Your Choice Therapeutics (YCT), licensed our compound and is in the process of gathering the data required for submission of an application to the FDA. Studies carried out by YCT subsequently showed the effectiveness of YCT529 in non-human primates, which is a very good predictor of effectiveness in humans.



YCT529

**What do we have to consider when discussing male contraception methods?**

***G. Georg:*** Male contraception with an oral pharmaceutical is a new concept that will require discussion and education. Acceptance will vary widely and depend on various factors, such as attitudes towards sexuality and contraception, geography, culture, or religious beliefs. A recent unpublished survey of 2,000 men, 18–50 years of age, showed that over three-quarters of men were willing to use a new male contraceptive. This result was strongly related to gender-equity attitudes. Other prior research showed that men are willing to try a male contraceptive. It was also reported that women trust their male partners to take contraceptives. Current methods for men are limited to condoms and vasectomy, which can be an irreversible process. Additional methods for male contraception would provide couples with additional choices for contracepting to better share the responsibility for family planning. It also will provide reproductive autonomy to men.

**What are the main challenges in male contraceptive therapy?**

***G. Georg:*** Contraceptive drugs must be effective, reversible, very safe, and affordable. This is exceedingly difficult to accomplish for any drug and takes time and an investment of significant resources.

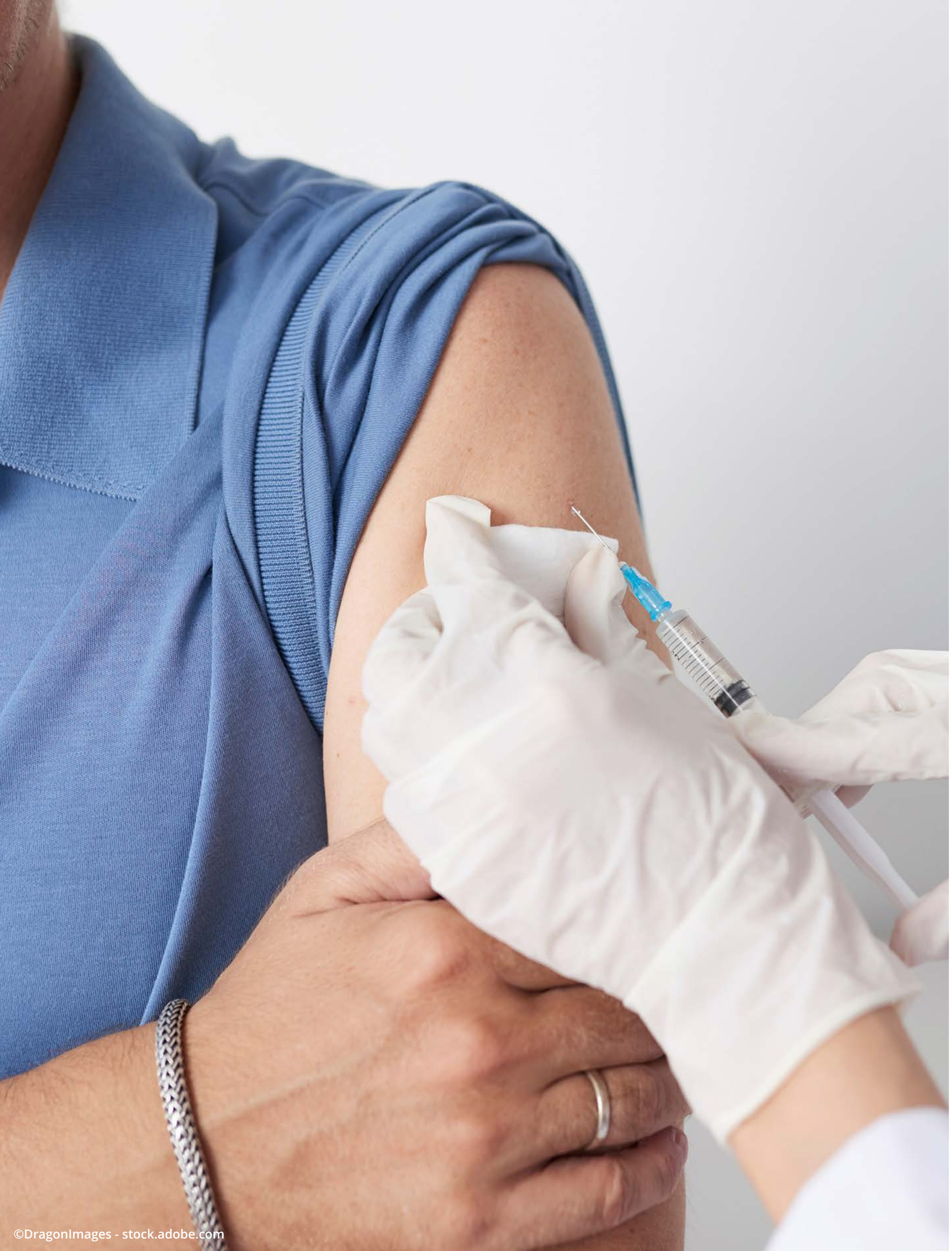
Another challenge is that no major pharmaceutical company currently has an active program to discover a male contraceptive agent. Only a few academic labs are currently involved in this type of research, and these groups have far fewer resources than a company.

**What analytical/lab techniques are used?**

***G. Georg:*** We design compounds computationally using structure-based drug design and taking advantage of published research. The synthesis of the compound requires organic chemistry methods. We use a fluorescent resonance energy transfer (FRET) assay to determine selectivity for the three retinoic acid receptors, RAR-alpha, RAR-beta, and RAR-gamma to identify an antagonist that is selective for RAR-alpha. We characterize all newly synthesized compounds for identity and purity. For confirmation of identity, we use nuclear magnetic resonance and mass spectrometry. We conduct purity analysis using HPLC with several different solvent systems and elemental analysis. Since the synthesis of our drug candidate involves metal-catalyzed steps, we analyze the final product for trace metal residues by ICP-MS. For in vivo pharmacokinetic studies we use UPLC/MS/MS analysis.

## Prof. Gunda Georg

She earned a B.S. in pharmacy and a Ph.D. in Medicinal Chemistry from Philipps Universität Marburg, Germany. After postdoctoral studies (University of Ottawa in Canada), she became a faculty member in the Department of Medicinal Chemistry at the University of Kansas. Since 2007 she is a University of Minnesota Professor and leads the Institute for Therapeutics Discovery and Development. She was Editor-in-Chief of The Journal of Medicinal Chemistry (2012-2020). She is an AAAS Fellow, and an American Chemical Society Fellow. In 2017 she was elected to the Hall of Fame of the Medicinal Chemistry Division of the ACS. In 2020 she received the Alfred Burger Award in Medicinal Chemistry from the American Chemical Society.




**What was your biggest challenge in developing the technology?**

***G. Georg:*** Our biggest challenge was that we had limited resources to carry out the required tests to identify the best out of the many compounds that we synthesized.

**What results were the most unexpected/surprising during the developmental process?**

***G. Georg:*** My research group and I have worked on non-hormonal male contraception for about 20 years on several projects and therefore during the discovery phase of YCT529 we were surprised how well this compound performed in all our tests compared to others that we have investigated so far.

**Have you assessed how likely people are to accept this type of therapy compared to hormonal therapy?**

***G. Georg:*** If we can show that a non-hormonal contraceptive does not have the side effects of hormonal therapy, we trust that men will find this therapy acceptable.

**What other technologies are you currently developing?**

***G. Georg:*** We are working on finding second-generation retinoic acid receptor antagonists and inhibitors for several other validated male contraceptive targets. Cyclin-dependent kinase 2, testis-specific bromodomain, testis-specific serine/threonine kinases, CatSper, and Na, K-ATPase.

# The matter of SHAPE

## Polymers against the silent pandemic

*Antimicrobial resistance is an increasingly serious threat, endangering our public global health. Antimicrobial polymers are a promising type of material that could help to solve this issue in the future.*

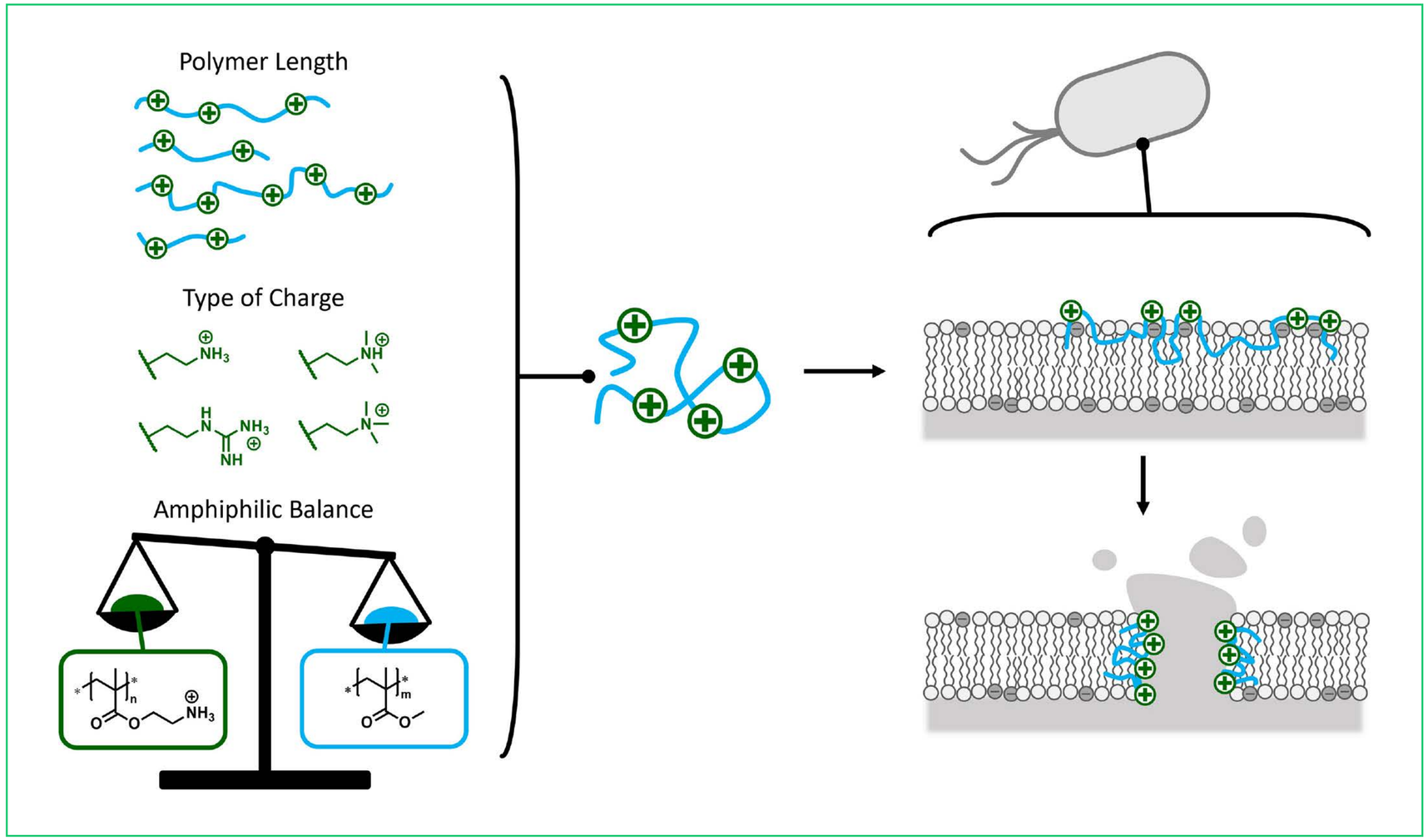



*Fig. 1: Important structural aspects in antimicrobial polymers and schematic representation of their interaction with bacterial cell membranes.*

## Antibiotics and antimicrobial resistance

One of the most remarkable scientific milestones from the last century was the discovery of Penicillin by Alexander Fleming [1]. When Fleming returned from his holiday in 1928, sorting through old petri dishes, he noted that one of them was covered in mold (*Penicillium notatum*), which had killed the bacteria (*Staphylococcus*) that were supposed to grow in it. It wasn't until the mid 1940's that the drug was, after significant effort, commercialized as the first antibiotic [2]. Since then, antibiotics evolved as a corner stone of modern medicine. Many of today's medical procedures: surgeries, chemotherapy, transplantations, etc. are virtually impossible without effective measures against bacterial infections [3]. Likewise, curing life threatening illnesses such as pneumonia, tuberculosis, gonorrhoea, blood poisoning, or foodborne diseases is only possible with working antimicrobials.

However, the age of antibiotics in coming to an end [4]. Antimicrobial resistance (AMR), the ability of bacteria to develop countermeasures against antibiotics, is spreading worldwide. AMR is silently and slowly, but consistently leading mankind into a post antibiotic era, in which we will lose a significant share of medical progress. The harbingers of these developments are already obvious, with almost 5 million deaths associated with bacterial AMR in 2019 [5]. And while overuse and misuse of antibiotics is driving AMR worldwide, the antibiotic pipeline is running dry, with only few new drug candidates for priority pathogens [6].

## Antimicrobial polymers

A possible solution to this silent pandemic is the development of new antibacterial drugs, that are unsusceptible toward AMR. Antimicrobial polymers (APs), mimicking naturally occurring antimicrobial peptides (AMPs), are promising candidates [7]. In sharp contrast to conventional antibiotics, they do not have a specific target, but rather attack the bacterial cell membrane [8]. The advantage of this comparably unspecific mechanism is the high threshold for resistance development and its unsensitivity toward conventional resistance mechanisms. Hence, if successfully implemented as antimicrobial drugs, APs could be used more freely and to combat resistance pathogens.

APs are generally comprised of a combination of cationic and hydrophobic units enabling them to kill bacterial cells. Cationic charges result in an affinity to the bacterial cell envelope, while hydrophobic units damage and destroy the cellular membrane, killing the microorganism (Fig. 1). Amongst other factors, the ratio between these parameters, the amphiphilic balance is of utmost importance for their activity and selectivity. But also their length, chemical identity, as well as the organization of functional subunits are detrimental for their activity (Fig. 1) [9]. A key challenge in this regard is the selectivity of APs: due to their unspecific mode of action, they usually affect not only bacterial, but also mammalian cells, resulting in unspecific toxicity for the host/patient. It is of paramount importance to overcome this issue when aiming for a future clinical application of APs.

## A matter of shape – polymer topology and architecture

AMPs, which are the blueprint for APs, are often organized in short β-sheet structures comprising a facial amphiphilicity [10], i.e., cationic charges and hydrophobic units are preferentially presented on opposing sides of the peptide. When the first APs were developed two decades ago, they were designed to resemble AMPs, also regarding their shape. It was however soon discovered that also unordered random polymer coils could arrange themselves when in contact with bacterial membranes and form dynamic facial amphiphilic structures [11]. As such, the majority of investigated APs in the last decades were linear copolymers with a random mixture of functional subunits [12].

However, in recent years focus was in part shifted to polymer architecture and topology in APs again. One aspect that seems to influence AP performance drastically is the segregation of functional subunits/monomers [13]. Indeed when cationic and hydrophobic groups are separated within distinct segments of the polymers, activity as well as selectivity is increased (Fig. 2) [14]. These findings are in part a result of the altered physico-chemical properties of these APs. For instance, global hydrophobicity of the polymer could be modulated, with random copolymers being more hydrophilic than block copolymers.


## Matthias Hartlieb

studied chemistry at the Friedrich-Schiller-University of Jena, where he also received his PhD in 2015. He proceeded to work as a postdoctoral research fellow at the University of Warwick, England, followed by a position at the Helmholtz Zentrum Geesthacht, Germany. Since 2019, he leads an independent research group at the University of Potsdam, which is funded by the Emmy Noether program of the DFG since 2021. His interests range from controlled polymerization techniques to biomaterials, with a focus on antimicrobial polymers.

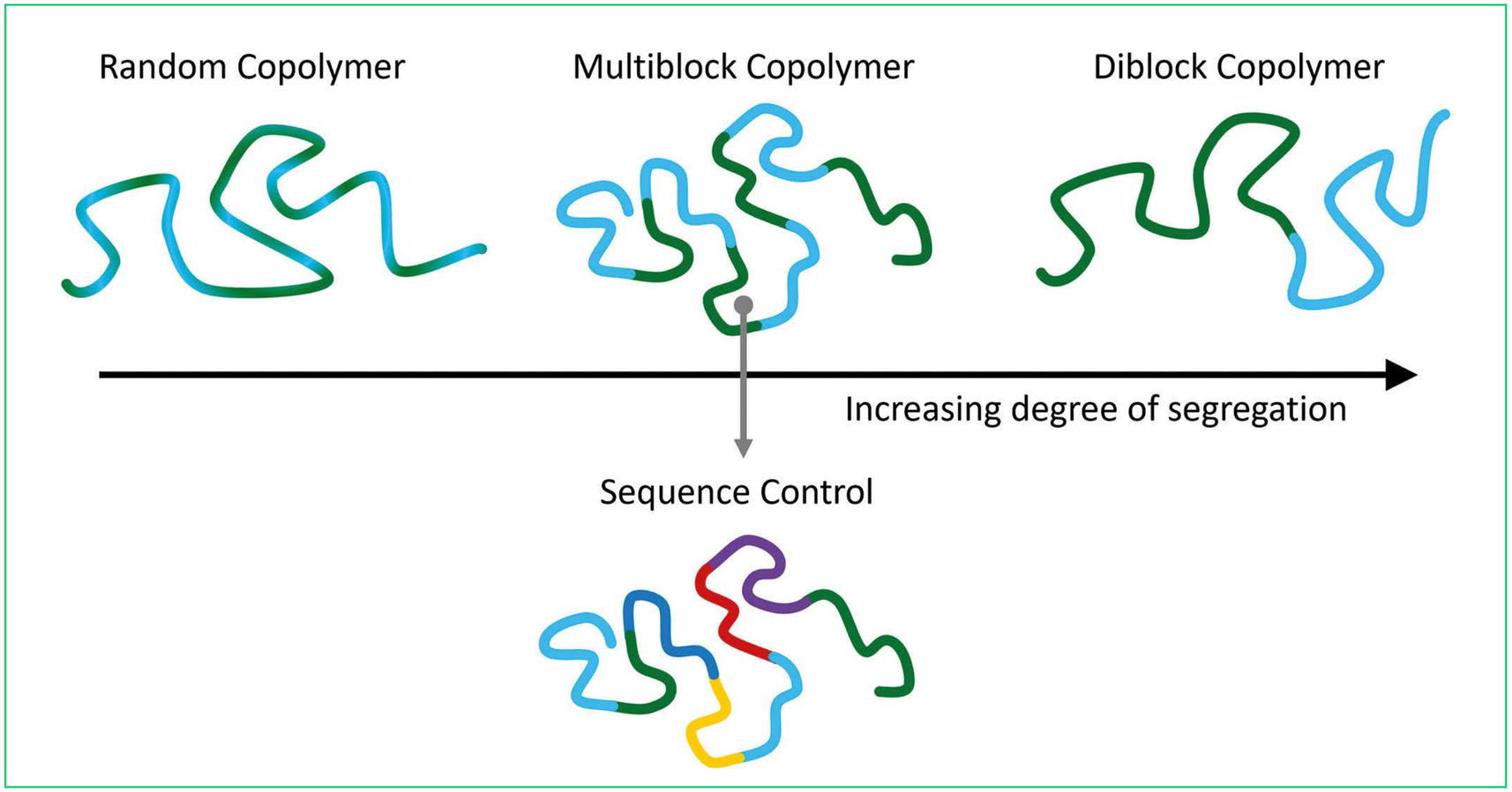



*Fig. 2: Schematic representation of segmentation and sequence control in APs by variation of the polymer architecture.*

By decreasing the length of segments in a multiblock copolymer architecture, this property and the biological activity could be modulated and optimized [14]. Controlling the sequence in such block copolymers can in turn even lead to selective activity toward certain bacteria strains [15]. Here hydrophilic monomers were introduced as a third building block and the block sequence within was varied. However, there is no general strategy in designing such APs and the polymer structure has to be adjusted to the respective purpose. For instance when targeting intracellular S. aureus infections, diblock copolymers are superior in their performance when compared to random and multiblock copolymers [16].

A further aspect that has shown promising results is the renunciation of a linear polymer topology in APs. Indeed it was demonstrated that a multivalent presentation of linear APs within a star-shaped copolymers [17], or within bottle brush copolymers [18-20] is beneficial for their performance (Fig. 3). When arranged into a bottle brush topology, antimicrobial activity was boosted and unspecific toxicity decreased [19], a result of the altered physico-chemical properties within the confinement, but likely also attributed to their specific shape [20]. Also degradation of bottle brush polymers to smaller macromolecules was able to deactivate APs [18].

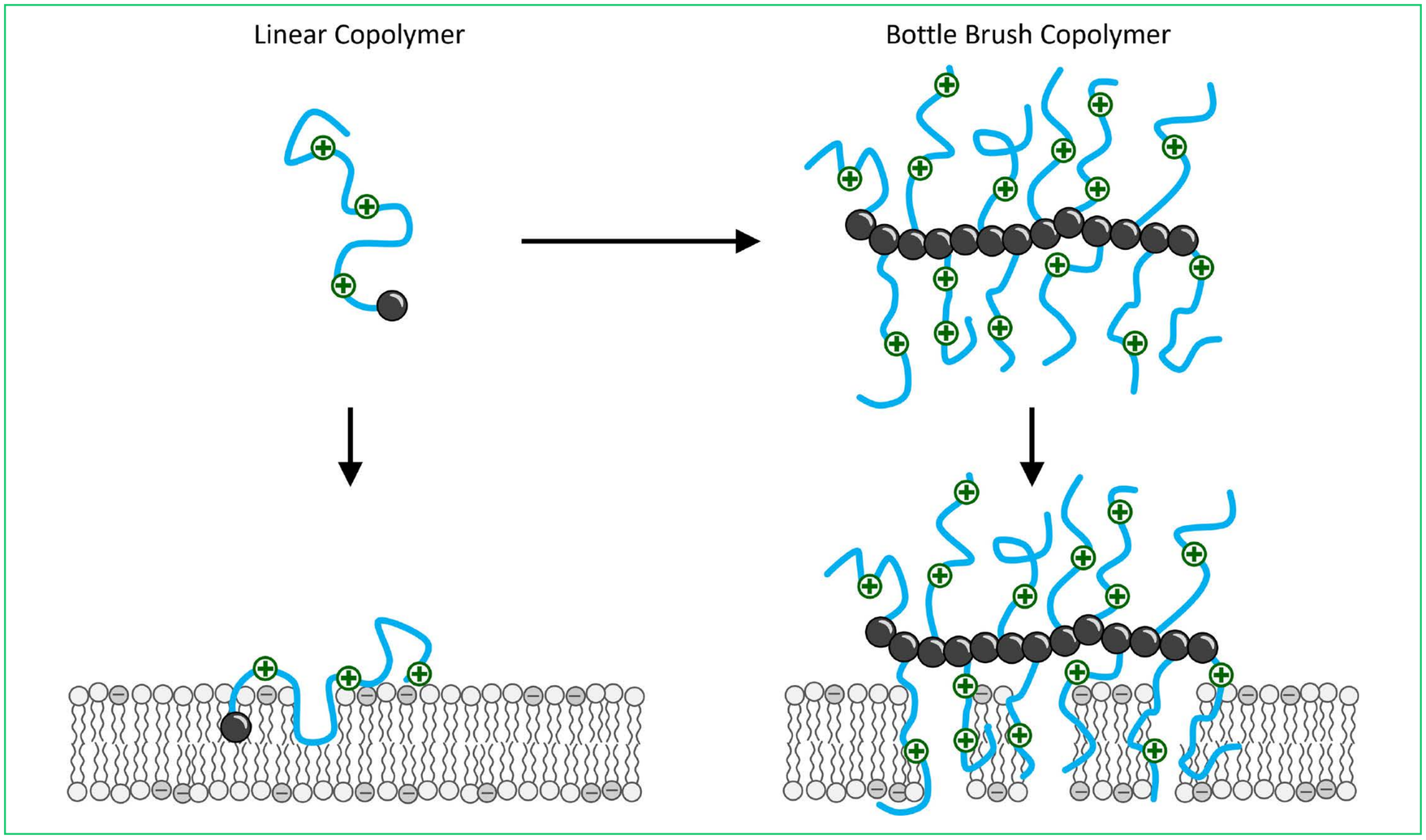



*Fig. 3: Schematic representation of the advantages of a bottle brush topology in APs.*

## Outlook

Of course, topology and sequence control are only two of multiple aspects that show promise in creating APs suitable for clinical applications. Active targeting, the use of smart polymers or drug delivery of APs are for instance further research areas that have received little attention yet. It is of utmost importance to continue research in this area to create new antimicrobials to face the ever-increasing threat of AMR.

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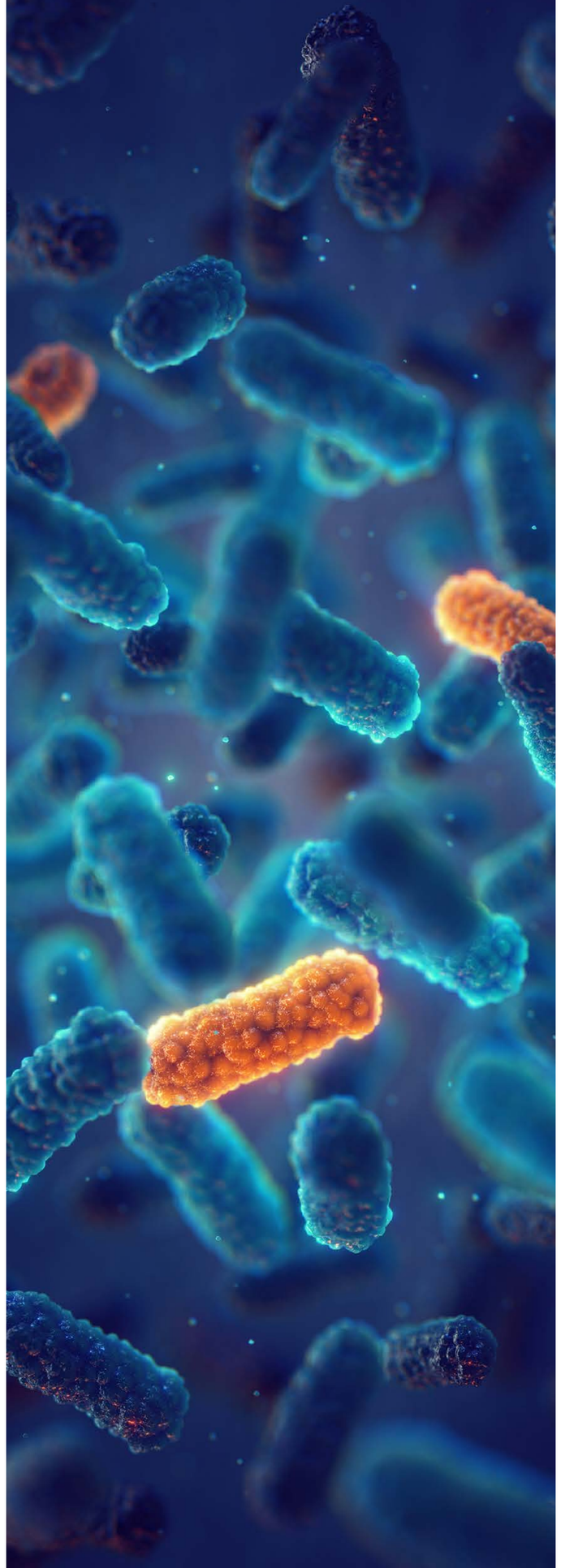




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# AI-ASSISTED
# Drug Discovery

## Interview with Ronald Dorenbos, Executive Director Business Development, Logica at Charles River Laboratories.

### Can you tell me a bit about yourself? - who you are and what you've done

My name is Ronald Dorenbos. I'm originally from the Netherlands, have a Ph.D. in microbiology and did a Postdoc in Neuroscience, focusing on Parkinson's Disease at Harvard Medical School. After moving into the industry over 15 years ago, I started consulting for small and mid-sized pharma and biotech companies providing strategy, commercialization, and business development services before migrating to big pharma where I was involved in leading projects around strategy, technology, and innovation. In that capacity, I have worked for companies that include Pfizer, Sanofi, and Takeda. More than 10 years ago, I got involved with Cyclofluidic, a small company using algorithms in combination with automated microfluidic synthesis and biochemical assays to automate drug discovery. Although nobody talked about AI at the time, this was my first interaction with the field of computational drug discovery. I have been fascinated with the field ever since and it is incredible to see the flight the field has taken over the last 10 years.

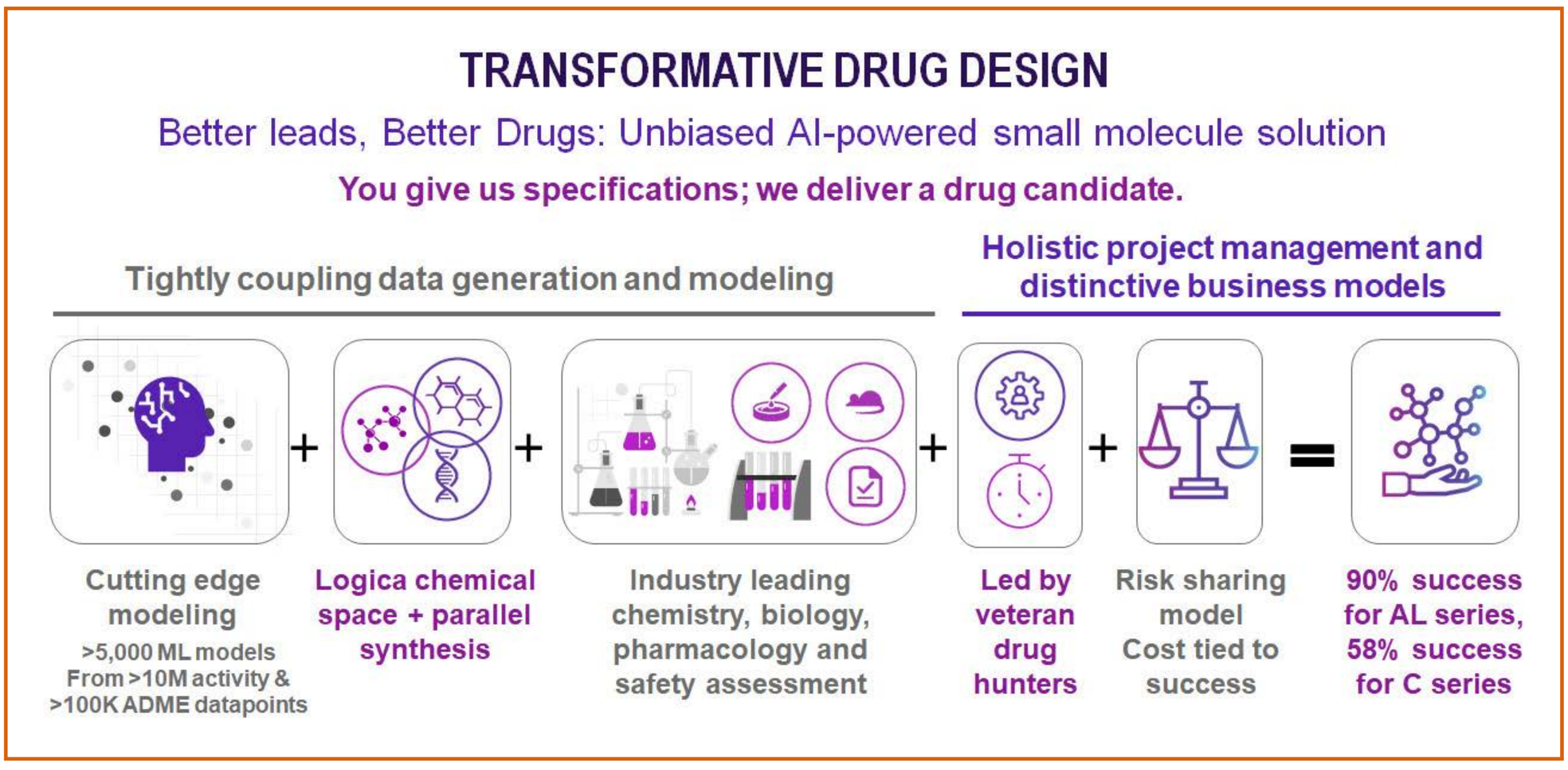


*Figure 1: Overview of different aspects of Logica that make the platform unique*

## How did the idea to use AI-powered computation to develop and increase drug discovery arise?

For the last few decades, the pharma industry has been plagued by increasing costs for the development of new drugs. The increasing complexity of advanced treatments and investment into drugs that do not make it successfully to market makes R&D ever more expensive and estimates for bringing a new drug to market range from US$1.3 to US$2.8 billion. The complexity of drug development and the huge amounts of data that are being generated in the process make drug discovery and development an ideal area for the application of computational tools. With AI and machine learning algorithms becoming more sophisticated, quite a number of people and companies concluded that it made sense to apply these technological platforms to the process of drug discovery and development to increase the chances of success and shorten the time from discovery of a target to the development of a new drug. If anything, the last 10 years have shown that AI cannot do it alone. Drug discovery needs to be approached through both AI and traditional techniques to tackle the many challenges that are an integral part of the process. This is where Logica comes in.

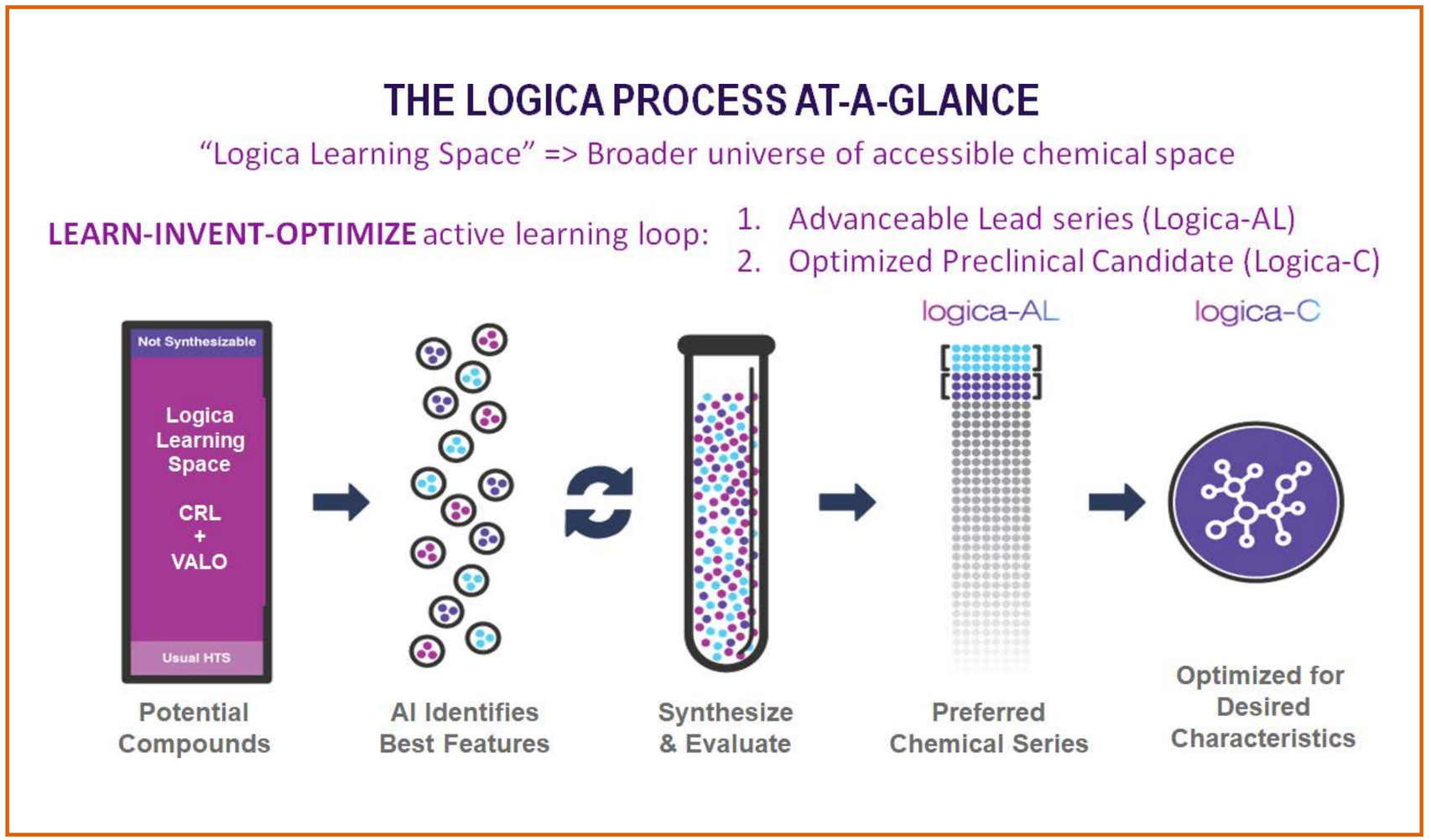


*Figure 2: Starting with a unique chemical universe (the Logica Learning Space that excludes non-synthesizable compounds), AI is used to learn by probing the biology and in this way develop models that are bespoke for the problem at hand. These bespoke models are then being used to identify the best features and create novel models. In parallel, compounds are being synthesized and evaluated and results being fed back to the algorithms (active learning loop). Repeating this process eventually leads to preferred chemical series of higher value and quality that set the stage for Logica C in which molecules are further optimized and de-risked through a combination of wet lab experiments and AI.*

## What is Logica? How does it work?

Logica is a platform resulting of a collaboration between two giants in their own industries: Valo, with close to 20 years of experience in the AI Drug Discovery space, and Charles River Labs as one of the leading end-to-end preclinical CROs and with almost eight decades of history. The two companies combine industry-proven platforms from the modern as well as from the traditional world and in that way create a transformative way of doing drug discovery. Logica starts with a unique universe of accessible chemical space, excluding non-synthesizable compounds. This space is being used to LEARN about the target and create bespoke models that are then used in the INVENT phase to develop a highly valuable and qualitative lead series, which concludes the first phase of Logica, Logica AL. During this phase, more than one advanceable lead series is produced. The lead series of Logica AL set the stage for the second phase, Logica C, or the OPTIMIZE phase. During Logica C, molecules are further optimized for the criteria that were defined in collaboration with the client at the beginning of the project. It is this phase that leads to the IND-enabling candidate compound that is in line with the target product profile of the desired molecule. With Logica, this process, which usually takes 36 months or more, is executed within 18 to 27 months. Logica does not only save time here, but because of the highly de-risked molecules that result from this process, the likelihood that these molecules will progress through the clinical trial phases is as well significantly higher, which ultimately brings these molecules faster to the market and faster to the patient.

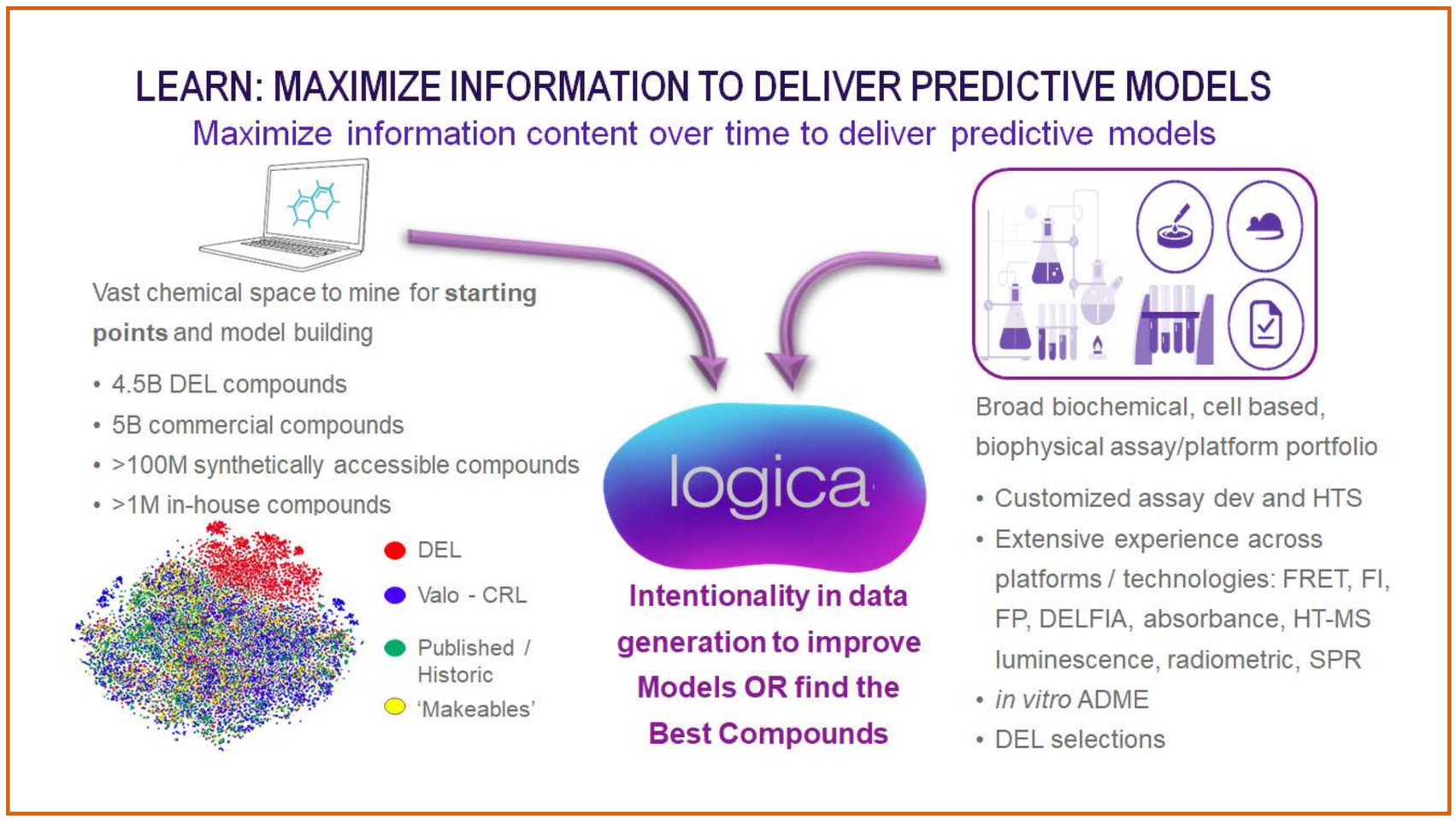


*Figure 3: Logica brings together the best of both worlds: cutting edge AI and modeling capabilities of Valo with the end-to-end preclinical CRO experience of Charles River Labs.*

## What can this be applied to?

The Logica platform can be used for the development of small molecules for a large variety of target classes. One can think of targets such as kinases, GPCRs, and ion channels, but the Logica platform may also be applied to discover small molecules targeting proteases, epigenetic targets, protein-protein interactions, phosphatases, and RNA, although the latter examples may be more challenging. We will also be able to include target classes that have not been drugged before and we are currently in conversation with some companies to do just that.

## What analytical/lab techniques are used in this technology?

The Logica platform has an unprecedented arsenal of analytical and lab technologies at its disposal. This includes a wide range of biochemical, cell-based, and biophysical assays and platforms. Furthermore, it has access to extensive experience across platforms and technologies, such as FRET, FI, FP, DELFIA, absorbance, HT-MS, luminescence, radiometry, and SPR. Added to this is the availability of in vitro ADME and access to extensive DNA-encoded libraries. Combined with the experienced drug hunters that Logica brings to the projects, and people with decades of experience in the industry, the platform is well-positioned to assist with bringing new molecules to market, emphasized by success rates for Logica AL and Logica C of 90% and 58%, respectively.

## What was the biggest challenge you came across during the development of this technology?

Getting the algorithms right is the first small step – rethinking the process and focusing it on value creation and making it as large-scale lab-native as it is cloud-native is the harder, more important step to achieve true closed-loop discovery. A significant challenge then was the creation of a real integrated drug discovery engine that not only combined the modern with the traditional, but that truly merged the two approaches so that the two became interdependent. It is marrying data gen and modeling in a way that inserts intentionality to achieve something previously unthinkable in our trial-and-error pharma world: we know the value of an experiment before we perform it by knowing quantitatively what it will teach our models.

Another challenge we are currently facing is the fact that over the last five to 10 years, a plethora of companies in the pharma and biotech industries have poured millions of dollars into the AI drug discovery field. Although maybe not intentionally, some of the companies leading the field made promises and raised expectations that ultimately were not realized. As a result, many companies in our industry are now reluctant to step into another 'AI deal'. In this respect, it helps that Logica offers a unique business model in which companies only pay a small amount upfront and the rest of the payment is tied to the success of the platform and its deliverables. The fact that we are willing to share the risk also shows how convinced we are about the exceptional capabilities of Logica.

## How cost-effective is the process compared to former techniques?

At first sight, the cost may seem comparable to traditional methods but using a risk-sharing model means that clients pay just a small amount upfront and only pay more when the platform successfully delivers the desired lead series or IND-enabling compounds. Furthermore, when one looks down the development pathway and journey of a molecule through pre-clinical and then clinical development, the Logica platform offers significant savings for two reasons, the first one being the fact that the platform takes only 18 to 27 months to go from scratch to an IND-enabling candidate, whereas the traditional route takes at least 36 months. The second reason, however, is more impactful. For any molecule to get to market it needs to go through clinical trials and candidate molecules coming from the Logica platform are not only developed in a record time, but they are also of significantly better quality and highly de-risked.

This means that chances of success when entering clinical trials improve dramatically. Since the patent life of a drug starts around the time that a molecule enters the clinic, any delays or problems during the clinical trials will delay the time to market to the patient and will shorten the patent life of the drug. On average, about nine out of 10 candidate therapies fail somewhere between phase I and regulatory approval. Anything we can do to increase the success rate is a huge win. It is here where the Logica platform offers a huge advantage when compared to traditional methods.

## Are there plans for improving the technology/ future outlook?

The nature of the platform means that there is a continuous feedback loop from the algorithms to the wet lab experiments and vice versa. Every time the platform is being used for a project the knowledge gained will improve the technology and hopefully shorten the time it takes from start to finish. In the future, other developments related to the use of AI in drug discovery may become part of the platform. In this respect, one can think of the use of AI to identify targets, elucidate protein structures, predict the success rate of chemical reactions, etc. Furthermore, when AI evolves and becomes better at predicting outcomes, for information that we can now only gain through experiments in the lab, it may be possible to scale down this lab-based work or eliminate it altogether, therefore decreasing the costs and speeding up the process. The future will also see more automation of different parts of the process and more focus on the reasons for attrition to decrease failure rates. No matter what the future holds, it is a given that the field of discovering, designing, and developing new medicines will change dramatically and I am confident that the Logica platform will have a significant role to play in this transformation.

## LINKS TO ADDITIONAL INFORMATION:

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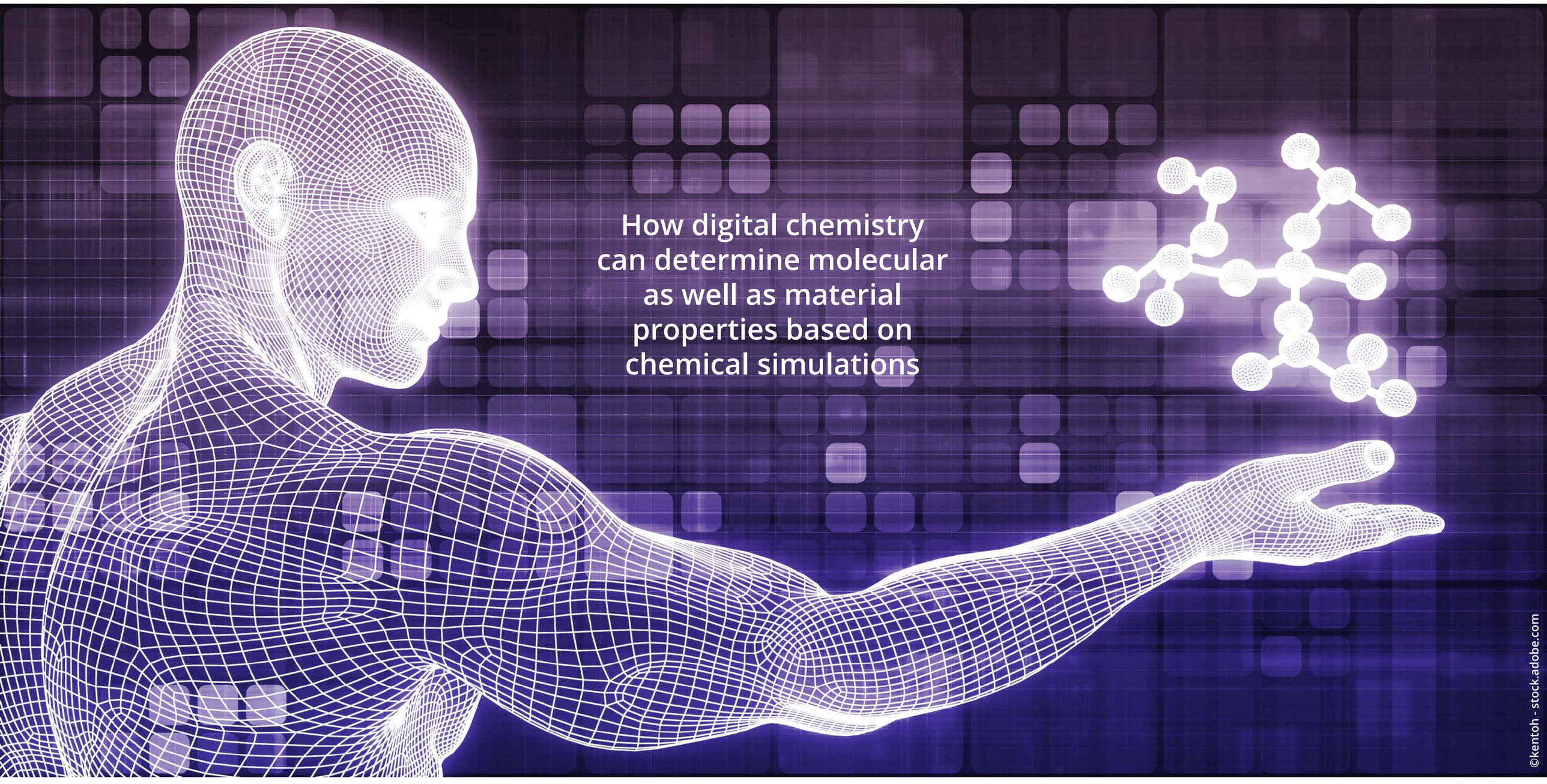
# SIMULATING




chemical solutions with software

*Predicting chemical reactions, simulating a wide variety of spectra, and determining molecular to complex material properties based on quantum chemical simulations and optimizing them by modifying chemical structures – what sounds like a digital chemistry lab has become a reality thanks to Quantistry's software. Learn more about the start-up founded by Marcel Quennet and Vincent Pohl in 2019:*


**What exactly is your software about?**

***M. Quennet:*** Our software is a simulation solution in the field of computational chemistry – a digital chemistry laboratory, so to say. Among other things, it offers the possibility of predicting chemical reactions, simulating a wide variety of spectra, and of course – which is one of the most important points from the point of view of many of our customers – determining molecular as well as material properties based on quantum chemical simulations. Furthermore, it can be used to optimize these parameters by modifying the chemical structures. Exciting use cases are also, for example, the simulation of viscosities and mechanical properties, such as compression moduli or surface interactions. Nowadays, many of these analyses are still carried out purely in the laboratory, although simulations would often be the better alternative in direct comparison.

**What are the biggest advantages?**
**What makes the software unique?**

***V. Pohl:*** Several factors come together here: on the one hand, our solution is an intuitive, browser-based web application that is designed for people who have had so far little to no contact with computational chemistry and IT. What may sound obvious at first, is a real novelty with regard to this field. The fact is that existing applications in the field of chemical simulation are extremely user-unfriendly. Even experts need weeks, or even months, to really get through that kind of software. We think this needs to be much easier and we see in our own product that this is principally possible. Unlike alternative solutions, we also supply the required computing capacity, which is complemented by consulting with our computational chemists.

## Marcel Quennet

started as an IT consultant in Berlin after completing his doctorate in chemistry at Freie Universität Berlin. In his PhD, he worked on simulations of novel solar cells and thermoelectrics, among other things.

**What aspects in terms of sustainability does the software offer?**

***M. Quennet:*** Simulations are basically more sustainable in direct comparison to purely laboratory-based R&D. By dispensing with chemical starting materials and avoiding chemical waste, as it is required or produced in classical experiments, the environmental balance of the entire development process is optimized. In addition, the energy requirements of a laboratory are significantly higher than those of a simulation. In addition, cloud-based software is ecologically much more efficient than on-premise resources – such as HPC clusters – due to its dynamic scaling of HPC resources.

**Software always means some form of automation of workflows. At what point does your solution deliver added value in this context?**

***V. Pohl:*** Chemical simulations are usually a complex matter, which requires special expert knowledge. Therefore, it is not surprising that there are only a few people who have the skill set to adequately use software like that. At the same time, however, the demand for simulations is relatively high, simply because they can save money and time.

Our approach is to make the knowledge of these simulation experts available to other colleagues. We do this by enabling these experts to create simulation workflows, which are basically templates for digital test series. These workflows can then be used by other non-simulation colleagues without any expert knowledge.

## Vincent Pohl

received his PhD from Freie Universität Berlin in theoretical chemistry with a focus on fundamental quantum mechanics and molecular electronics. As part of his PhD, he developed open-source software for visualizing complex chemical and physical data.

All they have to do is to select the structure that needs to be analyzed. This allows us to strengthen collaboration within the company and significantly improve the flow of information and data storage within companies.

**Who do you want to reach with your innovation? Who is it aimed at specifically?**

***M. Quennet:*** Our solution is primarily relevant for companies with a strong focus on R&D in the area of material development. We are arousing particular interest in the semiconductor industry, the development of high-tech materials, and the petrochemical industry. But our software also offers clear advantages for battery and fuel cell development.

**Your startup was founded in 2019. Where did the inspiration come from? How did the company come to be founded?**

***M. Quennet:*** Basically, we had a great interest in computational chemistry right from the start and focused our studies accordingly on this subject area, from our bachelor's theses to our PhDs. To be honest, in the beginning, we simply couldn't understand why laboratory work was not supported much more by simulations even though there was already enough computing capacity available.

***V. Pohl:*** Yes. And the idea of founding a company out of this need developed step by step and became very concrete as soon as our dissertations were about to be finished.

## Quantistry

was founded in 2019 to integrate chemical simulations more closely into the everyday work of chemical research and development – easier, faster, and cheaper. In this context, Quantistry develops a highly intuitive and innovative computational chemistry platform – the Quantistry Lab. Quantistry was awarded as one of the top 6 out of 500 startups nationwide in 2020, participating in the Startup Scale program of BMWi's Digital Hub Initiative

**What are your plans for the future? What goals and further developments would you like to achieve?**

***M. Quennet:*** As usual, we were very focused on product development and raising venture capital for the first two years after founding. In the meantime, we have achieved very important milestones in both areas and are now entering the market with our product and having talks with (potential) customers. Accordingly, 2022 is clearly dominated by the goal of expanding our customer base and going beyond the DACH region in the process.

***V.Pohl:*** Of course, we will continue to work on our software and we keep on developing numerous features to make our solution even more attractive in the future and to offer our customers further added value.

*The interview was conducted by Corinna Herbst, editor of GIT Labor-Fachzeitschrift.*

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