Not just *another* "AI in Drug Discovery" company.

We are moving beyond the classical paradigm with a more holistic computational platform and a business model to become a central computational hub for pioneering biotech companies.

Polypharmacology

We are the first and only company to query the *entire* proteome using computational biophysics and AI with a validated integrated platform.

With a polypharmacology approach, we design advanced lead molecules with minimal off-target effects, while providing insights into systems biology and structural pharmacogenomics.

Integrated Platform

With Ligand Design and Ligand Express, we have designed advanced leads that minimize off-target activity while ensuring drug-like and ADMET properties.

Our vision is to shorten the time to get better molecules to the clinic with a vision to bring drug discovery down from 7 years to 3 years by 2025.

Proven Business Model

Our goal is to create over 300 programs by 2025 through an innovative partnership model, thereby creating the next wave of molecules entering the clinic in partnership with pharma cos.

We are also continuing to work with global pharma cos. through revenue generating engagements.

Computational biophysics has existed for decades, with AI approaches recently becoming popular. We believe that AI is not the silver bullet - that it's best when it augments computational biophysics.

Garland Marshall forms the image of a molecule while Douglas Covey studies it

DESIGNING DRUGS WITH COMPUTERS

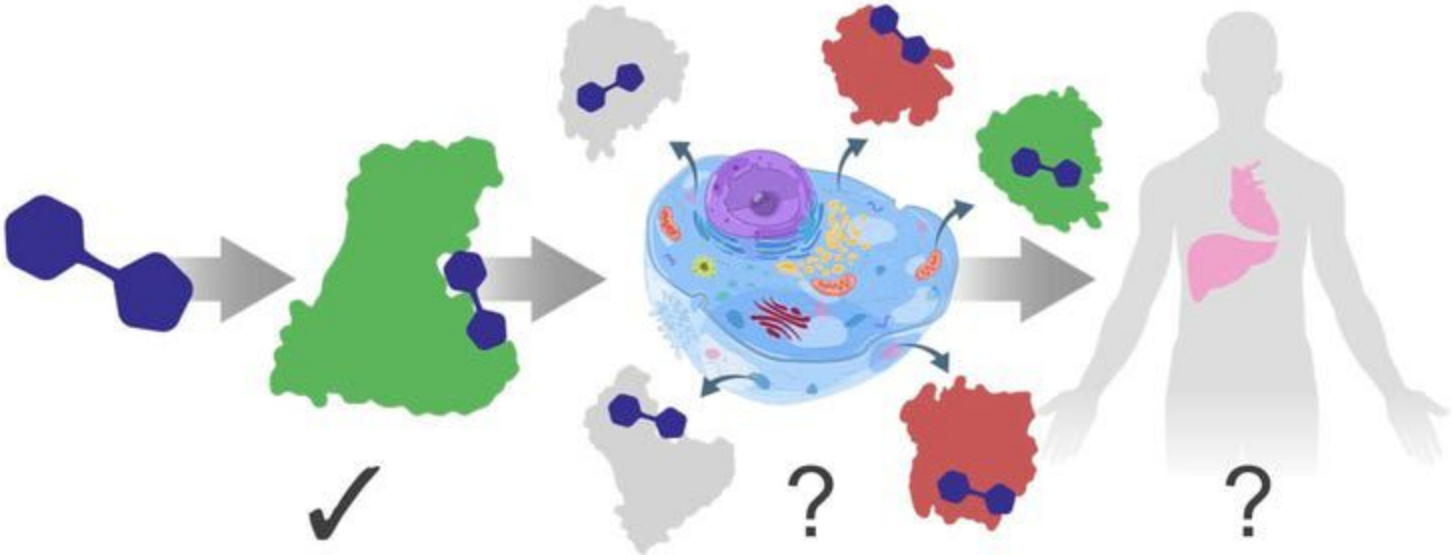
By creating images of molecules on the screen, chemists are learning to tailor drugs to diseases

Discover Magazine
August, 1981

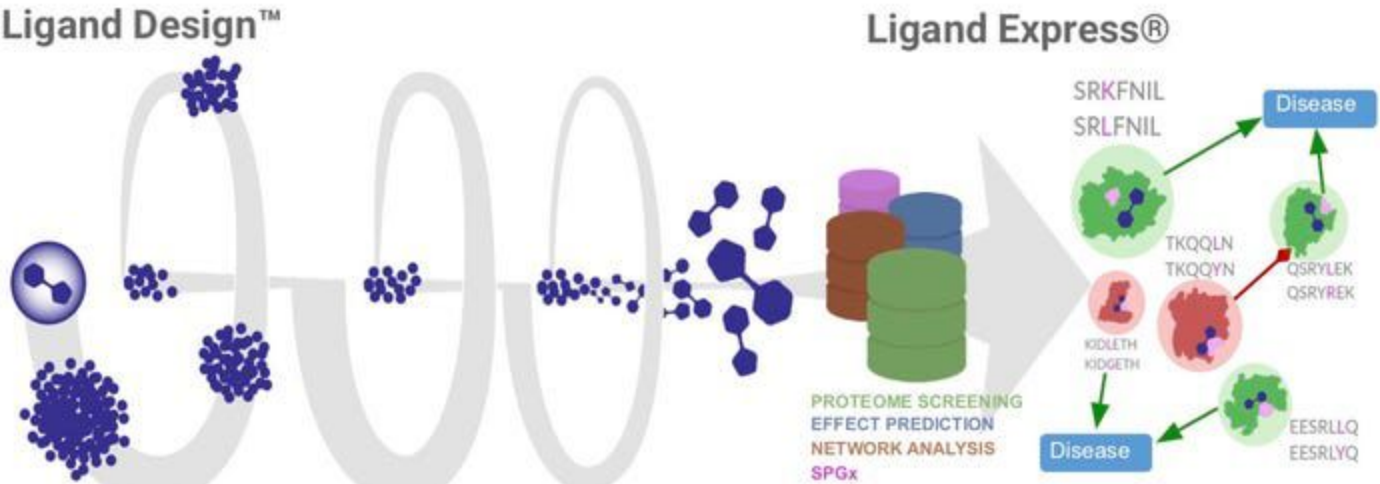
BenchSci
Sept, 2019

Most AI companies are focused on the "one target, one drug" paradigm and do not consider the impact of off-target interactions. We are focused on a drug's ***polypharmacology***.

Polypharmacology recognizes that therapeutic activity occurs via the modulation of multiple targets. Our appreciation of polypharmacology drives the design and characterization of safer and more efficacious molecules, increasing the likelihood of a drug's downstream success.



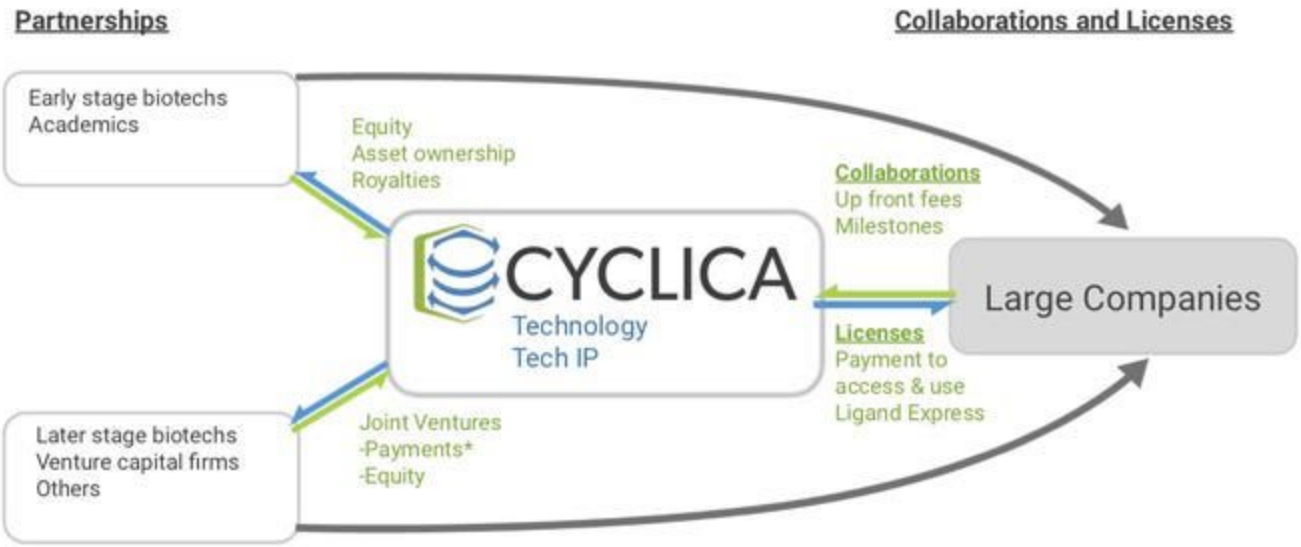
Our platform opens new opportunities for drug discovery, including multi-objective drug design, lead optimization, target deconvolution, and drug repurposing for small molecules, including PROTACS.



Our integrated drug discovery platform is powered by MatchMaker™, a deep learning model to identify drug-target interactions across the entire known proteome, and POEM™, a general purpose machine learning engine that has been implemented to design for ADMET properties.

Big pharma companies are increasingly looking to biotech companies for discovery opportunities. We believe that the future of pharma is in the hands of innovative biotech companies

Our partnership models create a diversified portfolio of assets across multiple indications that will usher in a tidal wave of molecules into the clinic in the next 3 to 5 years. These partnerships will also provide a robust pipeline directly to larger companies for clinical development.



Our business model has been adopted in the industry, and contributed to the research efforts of early stage biotech, research institutes, and multinational companies globally.

Tieös Pharmaceuticals

"The molecules we've synthesized have shown good solubility, multitargeted biophysical interaction and have evidenced good safety, efficacy and pharmacokinetics in our in vivo models." He adds that his team has "been blown away by what we are seeing."

- Dr. Arun Anand, Founder and CEO, Tieös Pharma
(as written in Nature Medicine)

"...artificial intelligence applications like Ligand Express® will provide important insights to enhance how we think about target identification to support phenotypic screening and off-target profiling in general…[Their] technology fits well into our increasing focus on phenotypic high-throughput screening, adding a target deconvolution method that takes 3D target information into account, which is a unique feature. "

- Dr. Friedrich Rippmann, Director of Computational Chemistry & Biology
(as mentioned in Nature Medicine and GEN)

Merck KGaA
Darmstadt, Germany

UNIVERSITY OF TORONTO

"We are extremely pleased to be working with Cyclica...our collaboration represents a unique approach that unites two completely novel and complementary approaches…[to] accelerate our ability to build novel EGFR inhibitors...and will thus speed up their implementation in the clinic."

- Dr. Igor Stagljar, Professor, University of Toronto

We have grown our business and technology by assembling a team guided by experienced business leaders in pharma R&D, computational biophysics, AI, and strategic partnerships.

- Operational since 2014, based in Toronto, a global epicenter for AI and scientific research
- Technology developed and patented at Cyclica (2014 - ongoing); strong IP position
- Validated and commercialized (2015 - ongoing); working with many top 50 pharma, biotech, and academia
- 35 employees; computational scientists, experimentalists, data scientists, software developers

We have been capital efficient to date as we validated our technologies, platforms and business model. We have achieved our milestones and are primed for global scale and impact.

Seeking: CAD$20M in a Series B round of financing to expand our biotech partnerships and Joint Ventures & pharma deals globally, deliver on R&D roadmap, bolster IP portfolio, and enhance ops.

From: Investors with a strong understanding of healthcare, life sciences and technology, who share our vision of transforming the discovery of better medicines with a computationally centric approach, and who are dedicated to supporting our commercial and R&D strategy.

Offering: An opportunity to invest in a leading *neo* biotechnology company that is accelerating and improving drug discovery. Our partnership / JV model, together with relationships with big pharma, will usher in a wave of R&D productivity and improve patient's lives across all disease areas.

CYCLICA

Pharma is changing, and we have the platform.

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