

Optimer Biotech/Optimally engineered biopolymers

Industry

Biotech

Key Features

Optimer is developing a general biopolymer engineering platform for applications in drug discovery and diagnostics

Financing Sought, Funding Strategy and Use of Proceeds:

Available upon request

Total External Capital Invested

50k pilot grant from the Columbia TRx accelerator. Dr. Bussemaker is Principal Investigator on two R01 grants from NIH. He has received over 8M in external funding for his research on computational genomics methods since 2001.

Scientific Advisors

Harmen Bussemaker, Ph.D.

Professor and Chair, Dept. of Biological Sciences; Professor, Dept. of Systems Biology

Neel Shah, Ph.D.

Assistant Professor
Department of Chemistry

H. Tomas Rube, Ph.D.

Research Scientist & Co-inventor

Company Lead Contact

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Business/Technology Description: Researchers are increasingly looking at biopolymers for numerous applications due to their superior specificity and efficacy. However, their large size and complexity has prevented the development of effective computational and experimental engineering methods, thus forcing developers to settle for suboptimal molecules. Nowhere is this more prevalent than in drug discovery and diagnostics: patients routinely develop strong immunogenic reactions to biologics. For example, many SARS-CoV-2 IgG tests have issues with specificity and affinity, leading to dubious positive predictive values. Optimer intends to change the status quo through its hybrid computational and experimental biopolymer engineering platform capable of designing DNA, RNA and proteins with superior properties - especially target activity and specificity - for a broad range of biotechnology solutions. Optimer is currently rigorously testing and aggressively pursuing patent protection for its methodology at Columbia University and was accepted to and won a pilot grant in the 2020 cohort of Columbia's Translational Therapeutics (TRx) Lab-to-Market accelerator program, which provides funding and industry mentorship.

Technology: Optimer uses Metric-seq, a highly flexible, assumption-free approach to accurately and comprehensively search molecular space for optimal biopolymers. It does so using machine learning algorithms trained on high throughput screening (HTS) data, making it versatile. The tool works on any biopolymer class (DNA, RNA, proteins, and their synthetic variants); is structure- and scaffold-agnostic (can optimize peptides, cyclic polypeptides, TCR complexes, nanobodies, Fabs); is target-agnostic (proteins, small molecules, cells/tissues, undruggable targets); and can simultaneously optimize across wide range of molecular attributes probed using HT sequencing (plasma stability, binding affinity, enzymatic activity). Metric-seq has already been used to analyze the specificity of thousands of DNA/RNA binding proteins, discover the binding preferences of pMHC:TCR complexes and capture the enzymatic activity of tyrosine kinases. Additional target classes and phenomena are being assayed to demonstrate the platform's breadth.

Market size and growth: Optimer's platform makes it ideally suited to augment research efforts spanning nearly all areas of biotechnology, from *in vitro* diagnostics to vaccines, agriculture, and industrial enzymes. While the sector as a whole is growing rapidly, protein-based biologics are of particular interest: with an approximately \$200B market size and 12% CAGR in 2020, roughly \$35B will be spent on the R&D for hundreds of drugs and diagnostics, including cutting-edge therapeutic modalities such as targeted degraders, PROTACs, and ADCs. Optimer's structure and scaffold independent approach enables participation in nearly all aspects of this market, from monoclonal antibodies to CAR-T therapeutics.

Comparables: Established companies offering biologic drug discovery services include Schrödinger, ATUM, Peptidream, and Adimab. Startups include AbCellera (105M Series B), LabGenius (10M Series A), Molcure, ProteinQure (4M Seed), Peptone.

Intellectual Property: A PCT covering the computational inference methods has been filed.

Scientific Expertise: Dr. Bussemaker is an internationally known leader in computational genomics. His research group at Columbia University has pioneered many topics related to the DNA binding specificity of transcription factors and the structure and function of gene regulatory networks based on integrative analysis of functional genomics data of different types. Dr. Shah has expertise in protein chemistry and biochemistry. His research group at Columbia University uses a variety of chemical and biological approaches, including deep sequencing-based high-throughput biochemical assays, to probe the structures and functions of eukaryotic signaling enzymes. Dr. Rube is an expert in biophysically informed machine learning and genomics.

Awards/Recognition: Dr. Bussemaker was the recipient of a John Simon Guggenheim Foundation Fellowship, a Lenfest Distinguished Columbia Faculty Award, and a Royal Netherlands Academy of Sciences Visiting Professor Fellowship. Dr. Shah received a postdoctoral fellowship and the Damon Runyon-Dale F. Frey Award for Breakthrough Scientists from the Damon Runyon Cancer Research Foundation.