teselagen BIOTECHNOLOGY

for Biological Product Optimization *Make Life Better™*

www.teselagen.com

The Artificial Intelligence enabled Operating System for Biotechnology. The TeselaGen[®] operating system connects biologists, lab technicians, and bioinformaticians so that they can collaboratively design and build experiments, organize and standardize data, test and continually learn. Our modern approach, coupled with artificial intelligence modeling, has opened the door for a radical transformation of biology and chemistry, enabling rapid expansion of potential applications.

TeselaGen's founding team met at Stanford while working on problems in computational and molecular biology. The team includes an elite group of engineers, biologists and physicists from Stanford, Cal, MIT and Harvard with wide experience in synthetic biology, molecular biology, automation, artificial intelligence, software development, and business development. TeselaGen has been now deployed by a number of small startups, Fortune 50 companies, as well as emerging innovators in biopharmaceuticals, agriculture, and specialty chemicals.

Reduce cost and time to market.

Our Artificial Intelligence-enabled operating system radically accelerates product development of therapeutics, high value chemicals, and agricultural products. TeselaGen has demonstrated that it can increase the design and build speed, as well as reduce the costs associated with research & development, by an order of magnitude.

Discover, generate and optimize biological products

TeselaGen's Discover module

> Therapeutics

Use our platform to design antibodies optimized for binding affinity, titer, specific productivity, immunogenicity, or other phenotypic variables of interest. Engineer viruses that specifically kill cancer cells or equip cells with multiple functions, granting them the ability to invade human cancer-derived cells.

Vaccine development

Enable a radically different strategy for vaccine development opening the door to attacking rapidly mutating viruses such as influenza, HCV, HIV, or coronaviruses. Use our platform to assist in the creation and optimization of different types of vaccines such as virus-like particles (VLPs), DNA, and RNA vaccines.



Predictive modeling

TeselaGen is powered by the Synthetic Evolution[®] machine learning engine.

Our proprietary artificial intelligence platform understands your data and helps you converge 10x faster.

Optimization of Productivity & Titer



- We implement predictive models that can be used to predict target values based of quantitative or qualitative inputs.
- TeselaGen's platform was recently used to optimize tryptophan production and titer in yeast, outperforming previously seen experimental strains [1].
- Teselagen's algorithm can be tuned for exploration vs exploitation, to attain sequence diversity that can help avoid local optima while optimizing through several DBTL optimization cycles.

[1] Zhang, Jie, et al. "Predictive engineering and optimization of tryptophan metabolism in yeast through a combination of mechanistic and machine learning models." BioRxiv (2019).



Antibody Optimization



- Generate and optimize mAb by training supervised models using experimental data.
- Different measurements for binding affinity, titer, specific productivity, immunogenicity, or other phenotypic variables of interest, could be used to optimize a single variable or to run our multi-target optimization algorithm
- Optimized sequences could be filtered to be close to antibodies contained in databases of known human mAbs.



Generation and optimization of peptides

← Return	letum		Select your o	Choose you	Choose your target and descriptors			
Targets. Three tables categorize your unas	ld like us to predict by cl are shown below with ti signed 'Column Names' i the left or the 'Targets'	te column na by moving et	imes of your sch row to eit	data. Please				
Descriptors			Unassigned			Targets		
Column Name	Type of values			Column Name			Column Name	Type of values
M32	categorical	+		CCK1[plC50] Line			CCK2(piC50)	numerical 😫
M33	categorical	•		Sequence				
M27->smiles	smiles	٠	« »		«	>>		
M26->smiles	smiles	\$						
M29->smiles	smiles	\$						
M32->smiles	smiles	٠						

- Peptides can be described by natural or unnatural amino acids. Unnatural amino acids can be described by its SMILES representation (molecular level description).
- Peptide sequences are associated with bioactivity target values.
- Peptides can then be **optimized** based on desired bioactivity target values.



Some Partners optimizing biological products with **TeselaGen**







"TeselaGen has developed one of the most advanced cloud-based solutions for designing, building, and optimizing complex biological workflows and products. We are enthusiastic about extending our collaboration with the TeselaGen team."

-Dr. Michael Köpke, Vice President Synthetic Biology, LanzaTech.

"In collaboration with TeselaGen, at DTU we have used machine learning models to generate new design recommendations, enabling us to successfully forward engineer the aromatic amino acid metabolism in yeast."

> -Michael Krogh Jensen, PhD, Co-Principal Investigator, The Novo Nordisk Foundation Center for Biosustainability.











Learn more about TeselaGen and request a demo today at:

www.teselagen.com