teselagen
BIOTECHNOLOGY

for DNA and Protein Design

Make Life Better™

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.

TeselaGen as your Operating System for R&D.

➢ Why TeselaGen?

Large and small companies that participate in the bio-economy are replacing traditional methods with modern biotechnology and machine learning driven techniques. This is opening the door for a radical transformation of biology and a rapid expansion of potential applications. This increased demand requires a secure, scalable, interoperable, protocol-driven platform that can span multiple users working on multiple projects across large, geographically distributed organizations.

➢ The four pillars of our system

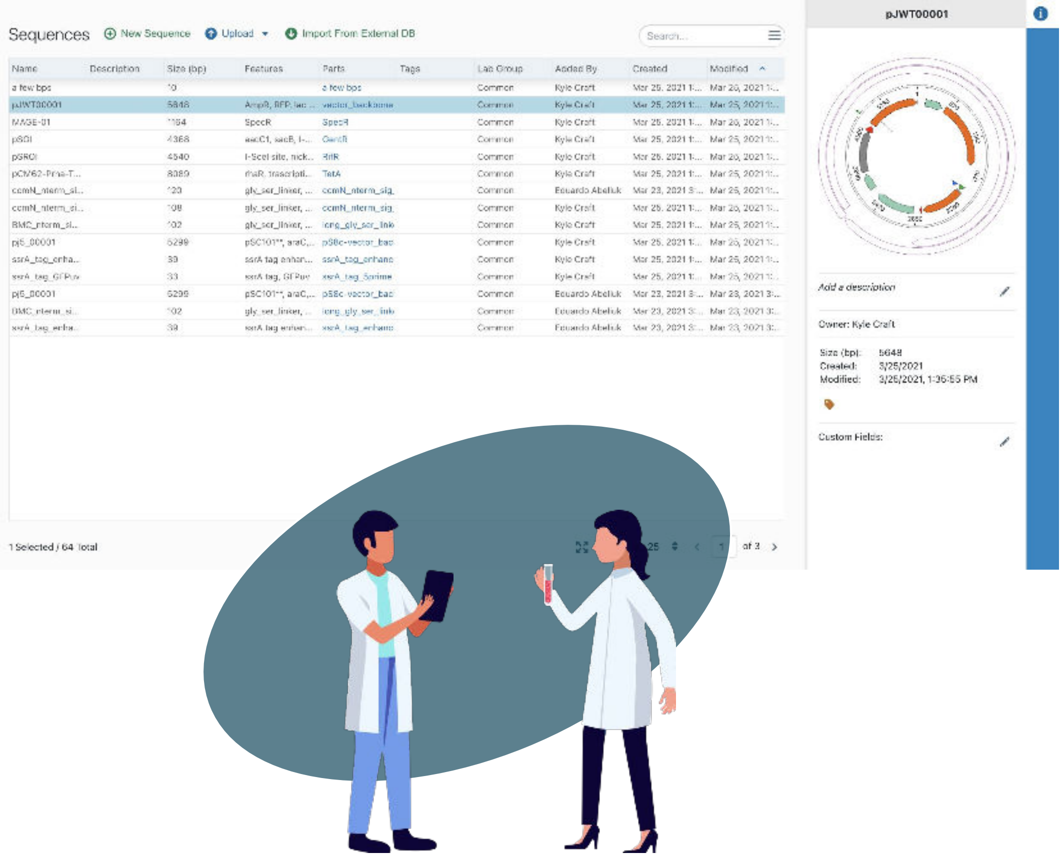
- **Design Management:** From DNA to protein design, to the most advanced large scale combinatorial and hierarchical designs that use state-of-art synthetic biology approaches for product development, our design tools help you design complex libraries that can get built quickly in the lab.

- **Lab Management:** A fully integrated laboratory management system that knows how to talk to you and your robots. Our system can orchestrate workflows, hands off to automation, manages samples, freezers and inventory, coordinates inventory and purchasing, guides quality control, and keeps track of everything you need to apply machine learning to optimizing your product.

- **Data Management:** All too often, data is scattered and isolated in places that make it hard to find and difficult to use. Our system provides a connected resource that acquires data from analytic and monitoring equipment and brings it together, links it to your design-build process, transforms it and makes it ready for analysis, predictive modeling, and machine learning.

- **Intelligence:** teams can combine their knowledge and data with AI algorithms built to understand biology — leading to new, high performance bio based products faster than ever before. Our AI models allow you to converge on an optimal product ten times faster then using traditional approaches.

DNA and Protein Sequences Libraries



Sequences ⊕ New Sequence Upload Import From External DB Search...

Name	Description	Size (bp)	Features	Parts	Tags	Lab Group	Added By	Created	Modified
a few bps		10		a few bps		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
pJWT00001		5648	AmpR, RFP, lac ...	vector_backbone		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
MAGE-01		1164	SpecR	SpecR		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
pSOI		4368	aacC1, sacB, I-...	GentR		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
pSROI		4540	I-SceI site, nick...	RifR		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
pCM62-Prha-T...		8089	rhaR, trascripti...	TetA		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
ccmN_nterm_si...		120	gly_ser_linker, ...	ccmN_nterm_sig		Common	Eduardo Abeliuk	Mar 23, 2021 3:...	Mar 25, 2021 1:...
ccmN_nterm_si...		108	gly_ser_linker, ...	ccmN_nterm_sig		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
BMC_nterm_si...		102	gly_ser_linker, ...	long_gly_ser_link		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
pj5_00001		5299	pSC101**, araC,...	pS8c-vector_bac		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
ssrA_tag_enha...		39	ssrA tag enhan...	ssrA_tag_enhanc		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
ssrA_tag_GFPuv		33	ssrA tag, GFPuv	ssrA_tag_5prime		Common	Kyle Craft	Mar 25, 2021 1:...	Mar 25, 2021 1:...
pj5_00001		5299	pSC101**, araC,...	pS8c-vector_bac		Common	Eduardo Abeliuk	Mar 23, 2021 3:...	Mar 23, 2021 3:...
BMC_nterm_si...		102	gly_ser_linker, ...	long_gly_ser_link		Common	Eduardo Abeliuk	Mar 23, 2021 3:...	Mar 23, 2021 3:...
ssrA_tag_enha...		39	ssrA tag enhan...	ssrA_tag_enhanc		Common	Eduardo Abeliuk	Mar 23, 2021 3:...	Mar 23, 2021 3:...

1 Selected / 64 Total

25 of 3

pJWT00001

Add a description

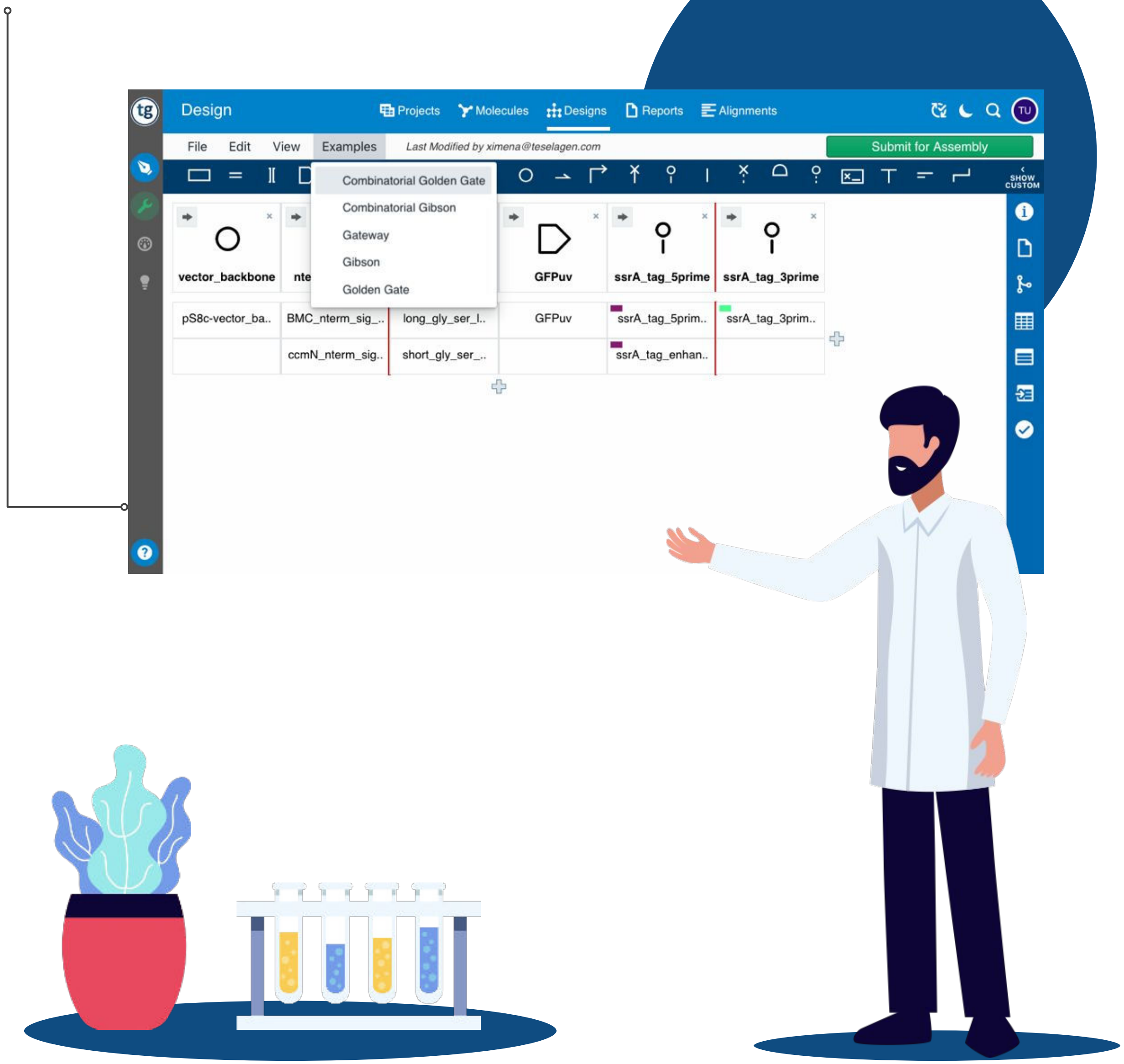
Owner: Kyle Craft

Size (bp): 5648
Created: 3/25/2021
Modified: 3/25/2021, 1:36:55 PM

Custom Fields:

- ➤ TeselaGen supports the **main file formats** that can easily be used to import and exported DNA and protein sequences and libraries: .gb, .gbk, .zip, .fasta, .csv, .xlsx and .json.
- ➤ Use custom fields so you can easily search, **sort** and **filter** your sequences. Additional fields can be used to group your sequences accordingly.
- ➤ **Auto-annotate features**: automatically create features that match on base pairs with a list of existing features that you select.

Powerful Design Editor

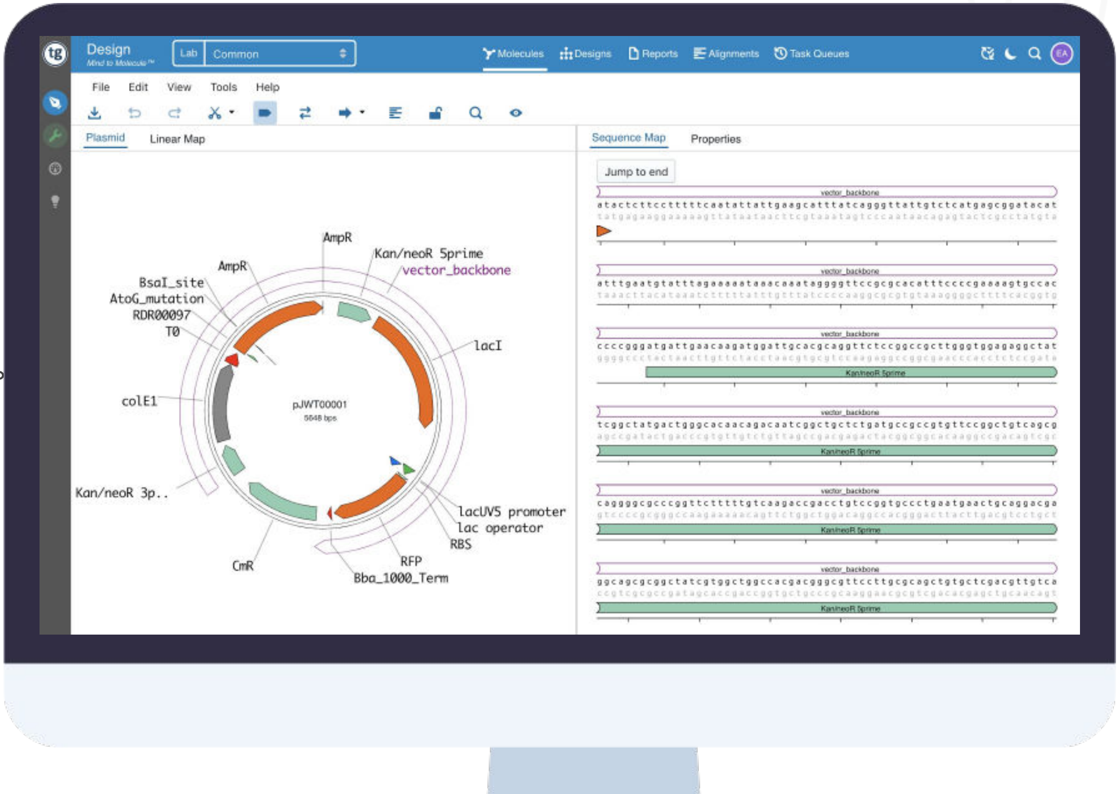


Last Modified by ximena@teselagen.com

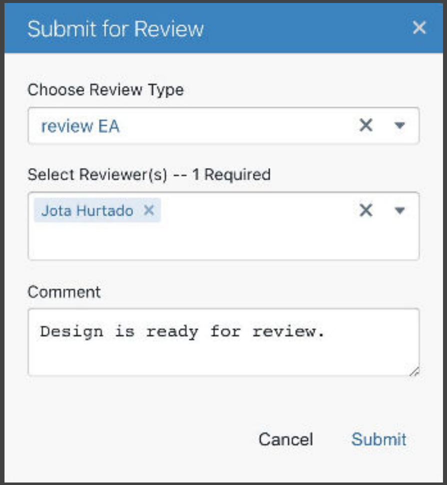
vector_backbone	nte		GFPuv	ssrA_tag_5prime	ssrA_tag_3prime
pS8c-vector_ba..	BMC_nterm_sig_..	long_gly_ser_l..	GFPuv	ssrA_tag_5prim..	ssrA_tag_3prim..
	ccmN_nterm_sig..	short_gly_ser_..		ssrA_tag_enhan..	

- Design simple constructs, **combinatorial** libraries, or **hierarchical** designs.
- The hierarchical capability is particularly useful for some DNA assembly strategies (such as **MoClo**)
- Users who build very long pieces of **scarless DNA** or construct gene stacks will find the streamlined interface a convenient and reproducible way to break down very long target designs into buildable submodules.
- **Share different entities** (e.g. parts, designs and projects) with colleagues.

Intuitive Vector Editor



- Visually **edit** and **annotate DNA** and **protein** sequences.
- Create **reusable design parts** based of sequences.
- Manage **restriction enzymes** and visualize their **cutsites**.



Submit for Review

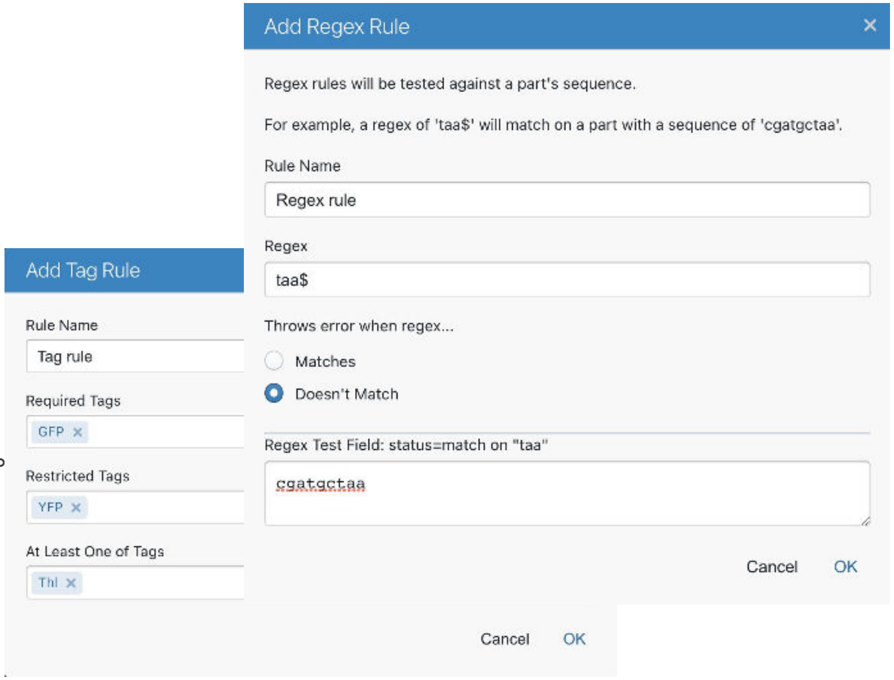
Choose Review Type: review EA

Select Reviewer(s) -- 1 Required: Jota Hurtado

Comment: Design is ready for review.

Be an individual contributor or collaborator, helping and reviewing your team's designs and workflows.

Design rulesets and design templates



Add Regex Rule

Regex rules will be tested against a part's sequence.

For example, a regex of 'taa$' will match on a part with a sequence of 'cgatgctaa'.

Rule Name: Regex rule

Regex: taa$

Throws error when regex...

○ Matches

● Doesn't Match

Regex Test Field: status=match on "taa"

cgatgctaa

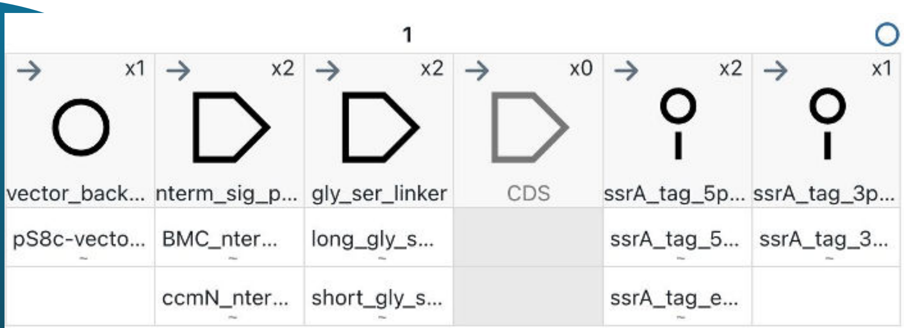
Add Tag Rule

Rule Name: Tag rule

Required Tags: GFP ×

Restricted Tags: YFP ×

At Least One of Tags: Thl ×



1

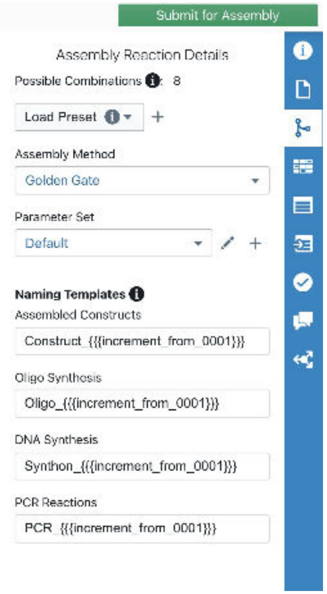
x1	x2	x2	x0	x2	x1
vector_back...	nterm_sig_p...	gly_ser_linker	CDS	ssrA_tag_5p...	ssrA_tag_3p...
pS8c-vecto...	BMC_nter...	long_gly_s...		ssrA_tag_5...	ssrA_tag_3...
	ccmN_nter...	short_gly_s...		ssrA_tag_e...	

- Create rules to **constrain** the complexity of your combinatorial designs.
- Easily define rules with **validation logic** based on either part tags (e.g. all parts in the first column need to have the “backbone” tag) or a part’s base pairs (e.g. all parts in the cds column need to begin with “ATG”).
- Create and reuse **design templates** to aid the design process.
  - Any aspect of the design editor can be stored in a **template for reuse**, including specifications for DNA parts, overhang validation and assembly reactions.

Modern DNA Assembly Protocols

- Our platform supports **modern DNA assembly protocols** such as Gibson, Golden Gate, MoClo, USER, PCR, and others.
- The interface automatically adds validation to ensure that parts are sourced with the appropriate flanking digest sites, if necessary.
- Automatically generate build instructions **optimized for cost and speed.**
- Get automated DNA assembly **warnings** and errors.

- Users are able to rapidly design complex hierarchical builds while maximizing part reuse and minimizing cost.
- Part reuse is important when the size of the built library is large and cost is a constraint. Without part reuse the cost of a library can grow linearly with the number of parts, while with part reuse it can grow logarithmically.
- Export build instructions directly into our Lab Information Management System.



Assembly Reaction Details

Possible Combinations: 8

Assembly Method: Golden Gate

Parameter Set: Default

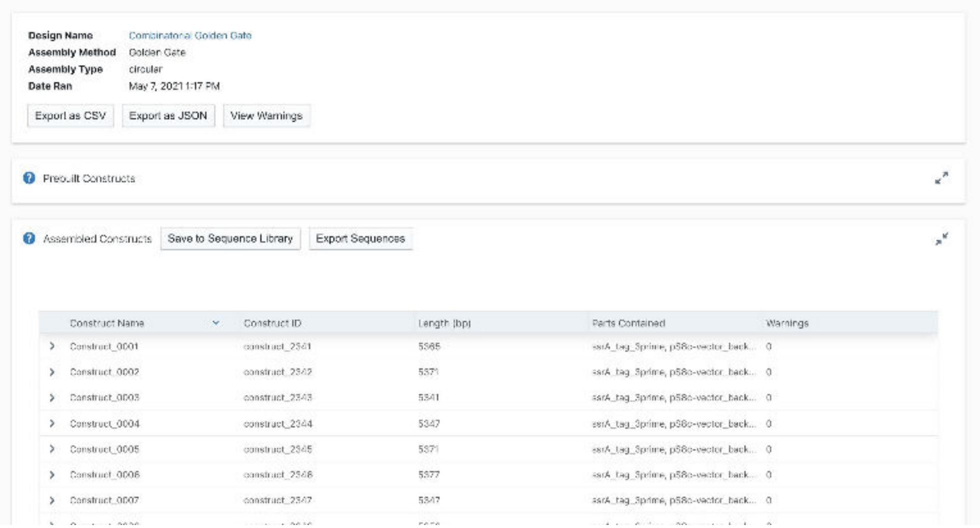
Naming Templates

Assembled Constructs: Construct_{{{increment_from_0001}}}

Oligo Synthesis: Oligo_{{{increment_from_0001}}}

DNA Synthesis: Synthon_{{{increment_from_0001}}}

PCR Reactions: PCR_{{{increment_from_0001}}}

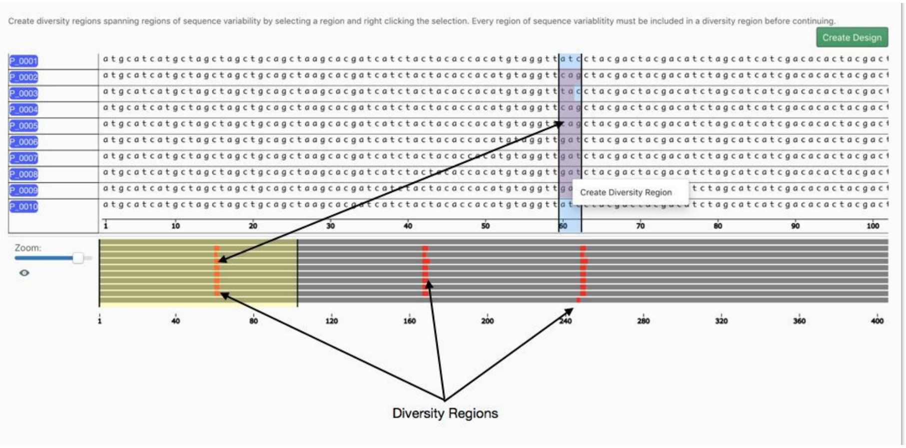


Design Name Combinatorial Golden Gate
Assembly Method Golden Gate
Assembly Type circular
Date Ran May 7, 2021 1:17 PM

Construct Name	Construct ID	Length (bp)	Parts Contained	Warnings
Construct_0001	construct_2341	5365	sarA_tag_5prime, p58c-vector_back...	0
Construct_0002	construct_2342	5371	sarA_tag_5prime, p58c-vector_back...	0
Construct_0003	construct_2343	5341	sarA_tag_5prime, p58c-vector_back...	0
Construct_0004	construct_2344	5347	sarA_tag_5prime, p58c-vector_back...	0
Construct_0005	construct_2345	5371	sarA_tag_5prime, p58c-vector_back...	0
Construct_0006	construct_2346	5377	sarA_tag_5prime, p58c-vector_back...	0
Construct_0007	construct_2347	5347	sarA_tag_5prime, p58c-vector_back...	0

Bioinformatic Tools

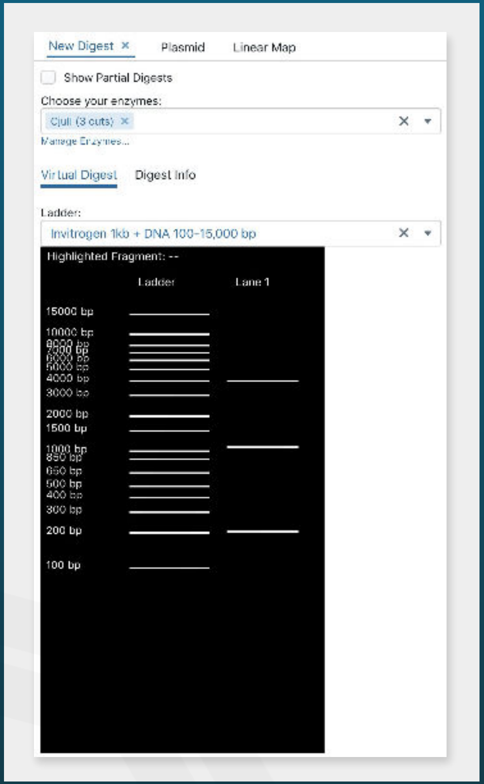
- Run sequence alignments of various types:
    - Pairwise Alignment tool:
        - Align one or more **pair of sequences**
    - Multiple Sequence Alignment tool
        - Align **multiple sequences** with homologous regions
    - Reads Mapping tool:
        - Align short **NGS reads** to a long reference sequence
    - Sanger Sequencing tool:
        - Visualize **sequencing chromatograms**
    - DAPPER tool:
        - Run an an alignment of Parallel Parts that Expose **Regions of Diversity**.



Create diversity regions spanning regions of sequence variability by selecting a region and right clicking the selection. Every region of sequence variability must be included in a diversity region before continuing.

Diversity Regions

- **Backtranslate** amino acid sequences to DNA based con customized codon maps.
- Simulate **digestions**



☐ Show Partial Digests

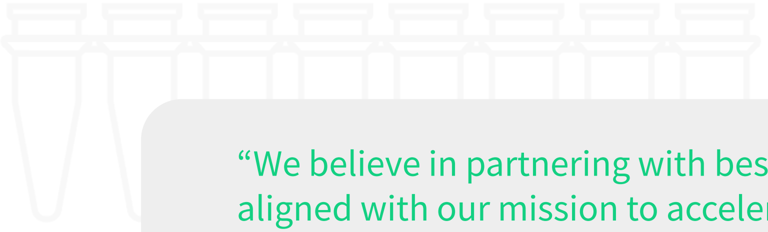
Choose your enzymes: CjuI (3 cuts)

Ladder: Invitrogen 1kb + DNA 100-15,000 bp

Highlighted Fragment: --

Some Partners designing with **TeselaGen**

LanzaTech JBEI MicroByre Ansa Biotechnologies



“We believe in partnering with best-in-class service providers that are aligned with our mission to accelerate biotech research and development.”

-Daniel Arlow, CEO at Ansa Biotechnologies

“Automated biological design is an essential foundation for our carbon recycling technology and TeselaGen has a reliable platform for modern industrial DNA design and cloning.”

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

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Learn more about TeselaGen and request a demo today at:

www.teselagen.com