ShareYourCloning: an Open Source web application for cloning in the DBTL world

Manuel Lera-Ramirez[1], Jürg Bähler[1]
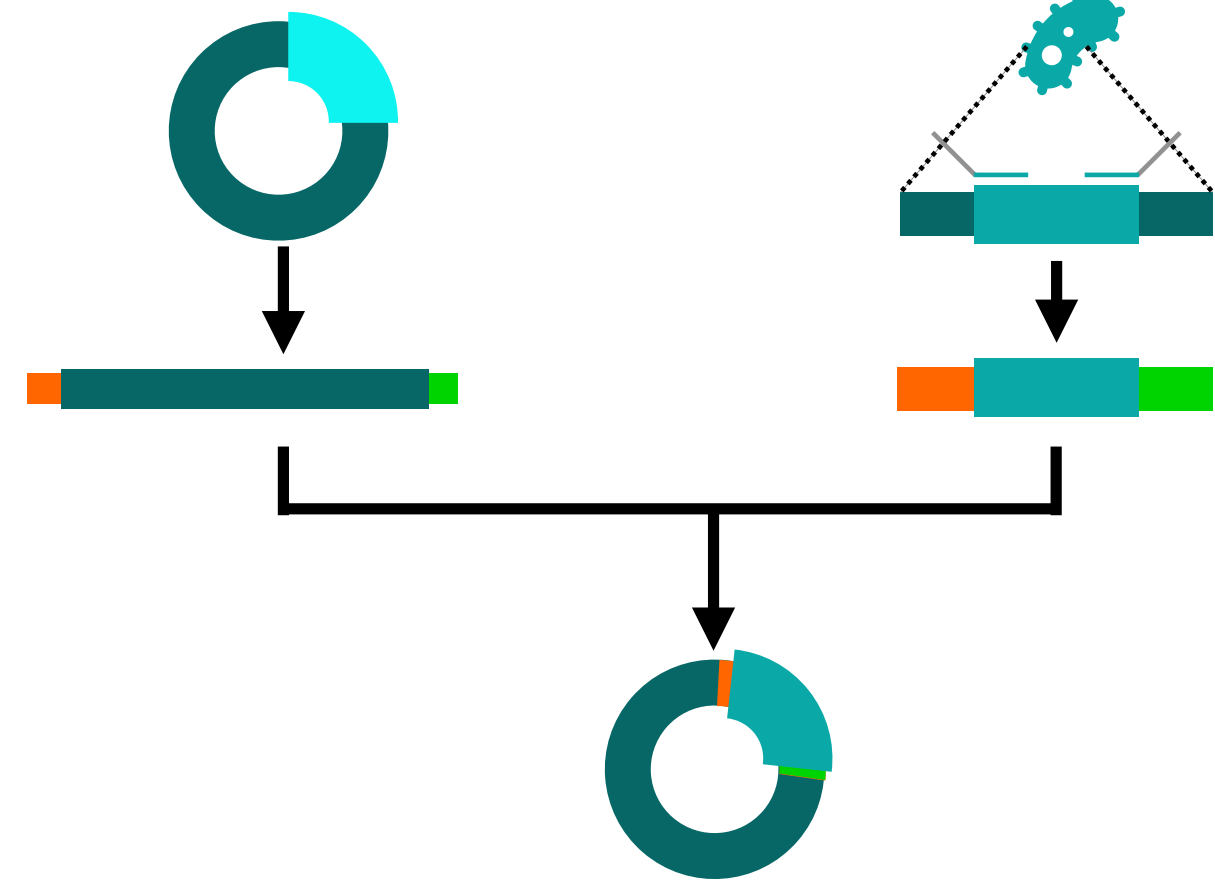
1. University College London, Institute of Healthy Ageing and Department of Genetics, Evolution & Environment, London, U.K.
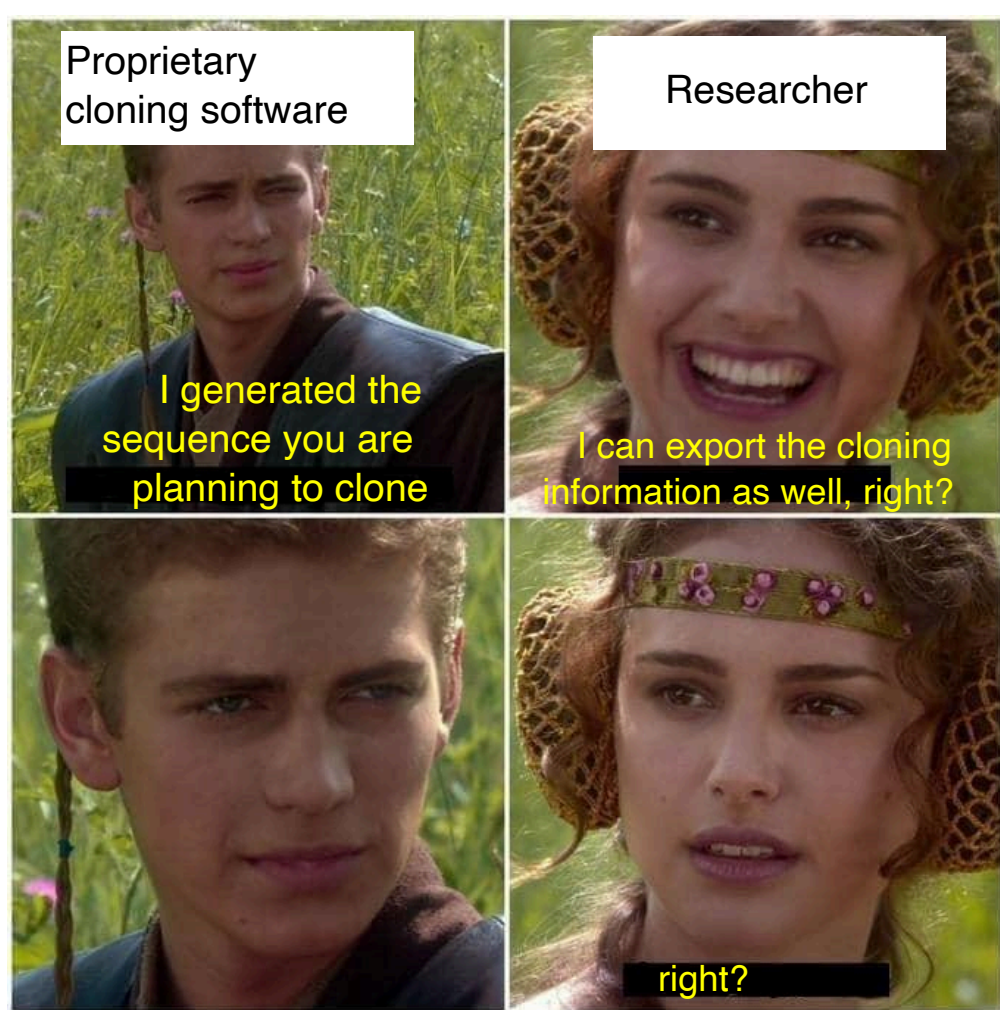
UCL

😟 The problem 😟

We can describe sequence features in open formats (such as .gb), but not cloning strategies.

Let's imagine a typical strategy to clone a gene into a plasmid through Gibson assembly:

🤔 There must be an Open Standard to represent this, since it is routinely done in **hundreds of laboratories**.

Proprietary cloning software / Researcher

I generated the sequence you are planning to clone

I can export the cloning information as well, right?

right?

😔 No standards means no way to automate tasks or design tools 😔

🧙 The solution 🧙

🧁 A data model to represent cloning strategies

Every **Sequence** comes from a **Source** representing:

a) An external import
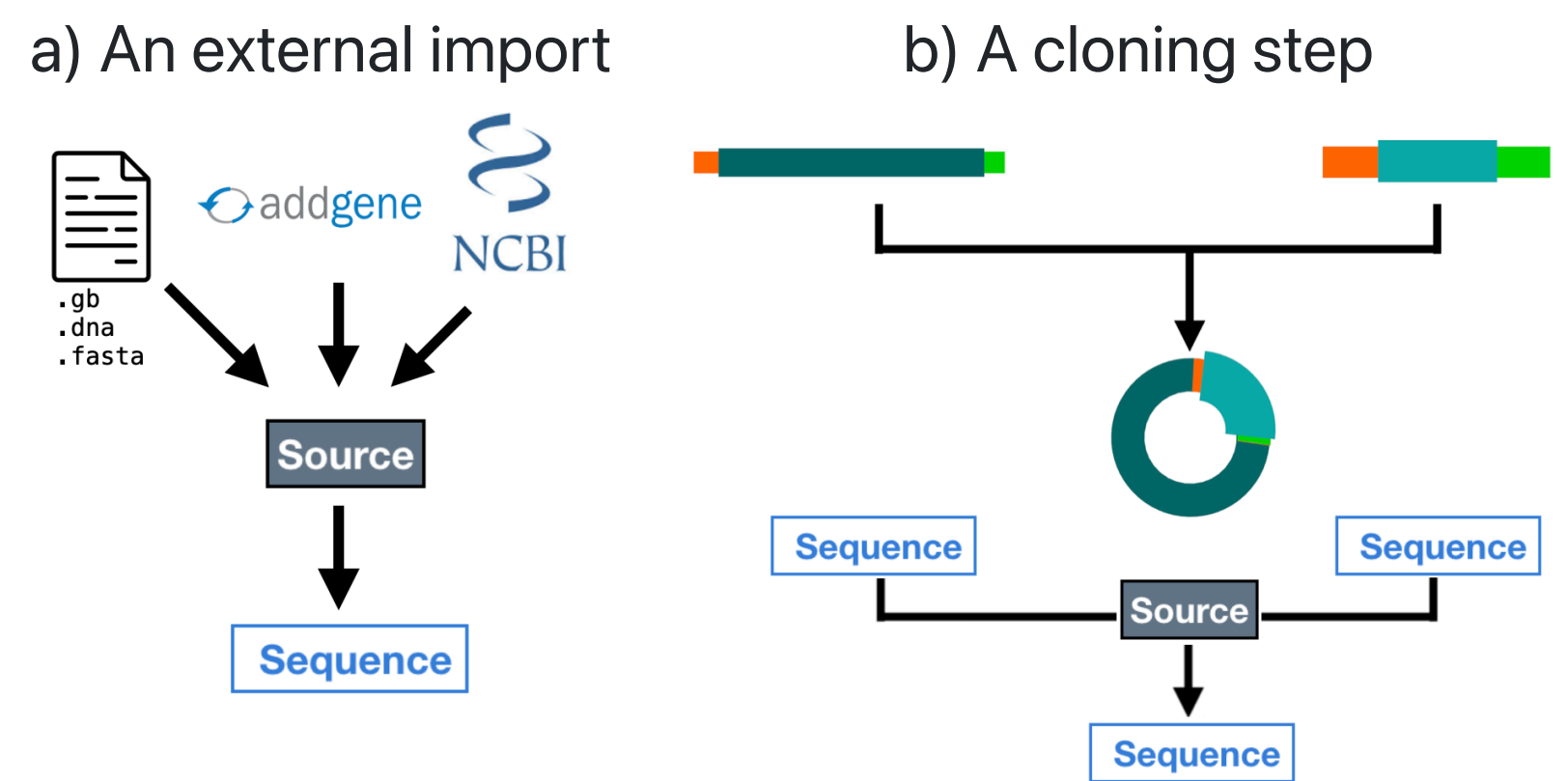
b) A cloning step

👑 An amazing Open Source web application

Enter 🔥🔥 **ShareYourCloning** 🔥🔥, a web application where you can simulate your cloning strategy and export it in this format to share with others or for publication.

Frontend — inputs: [1, 2] experiment: cool_experiment — **Backend**

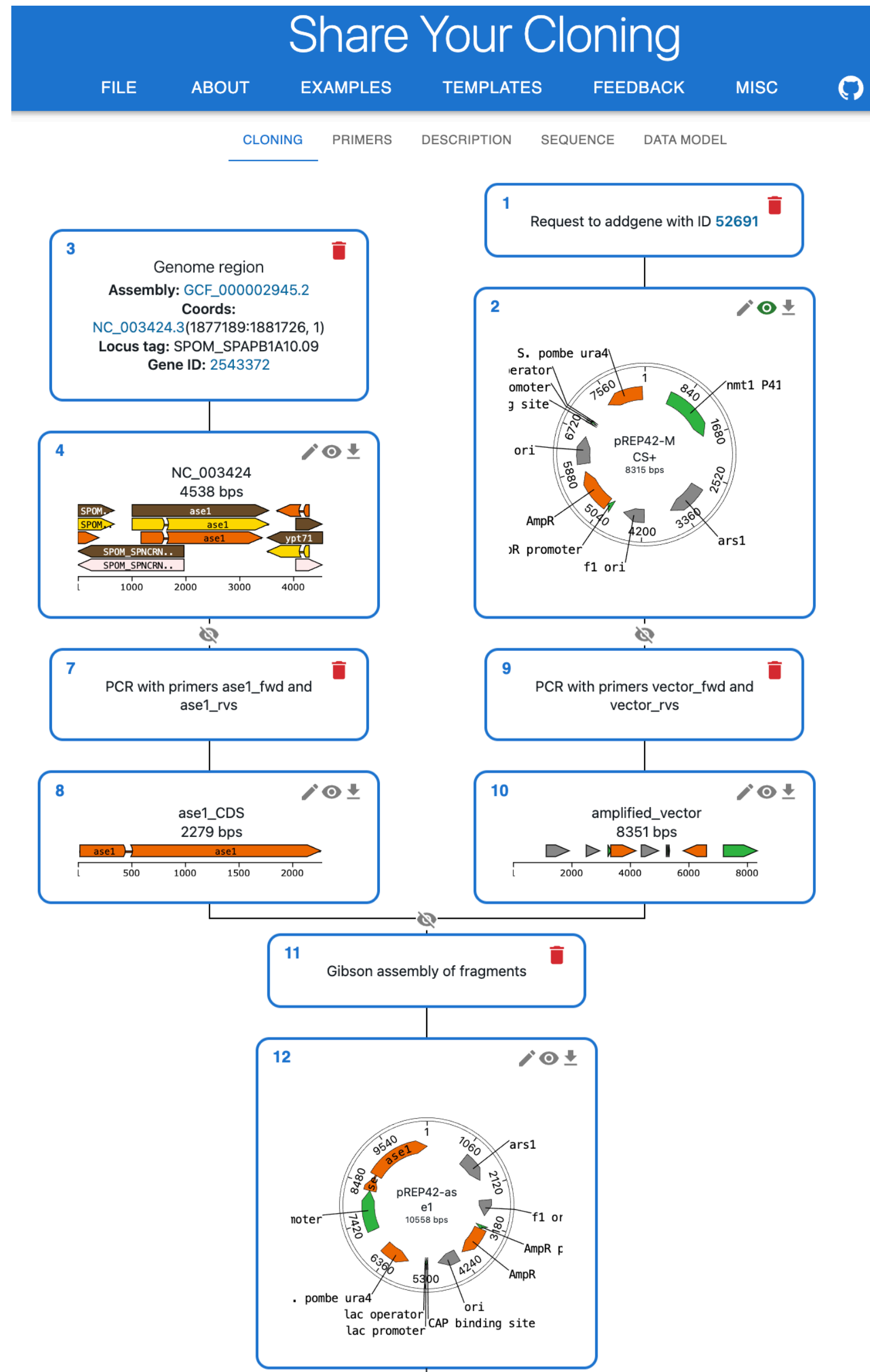output: cool_output 😎

🐍 FastAPI
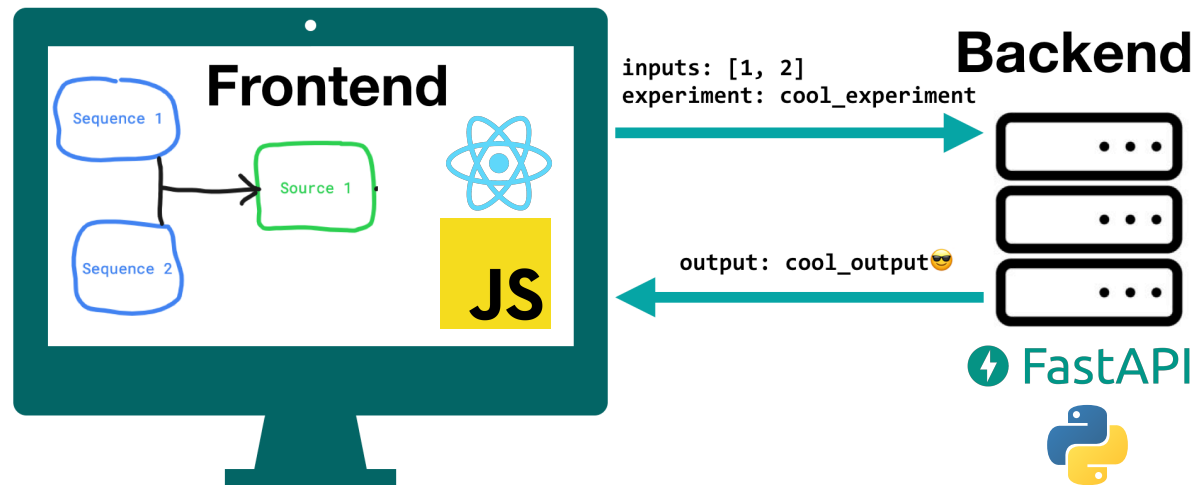
🐍 Extending and maintaining cloning libraries

As part of the project I maintain, use and extend **pydna**, a BioPython-based library to simulate cloning.

If you are into scripting and want to automate your cloning, you might want to try it.

```
> pip install pydna
```

🙆 Try it yourself! 🙆

Share Your Cloning

FILE ABOUT EXAMPLES TEMPLATES FEEDBACK MISC

CLONING PRIMERS DESCRIPTION SEQUENCE DATA MODEL

Web application | GitHub repository
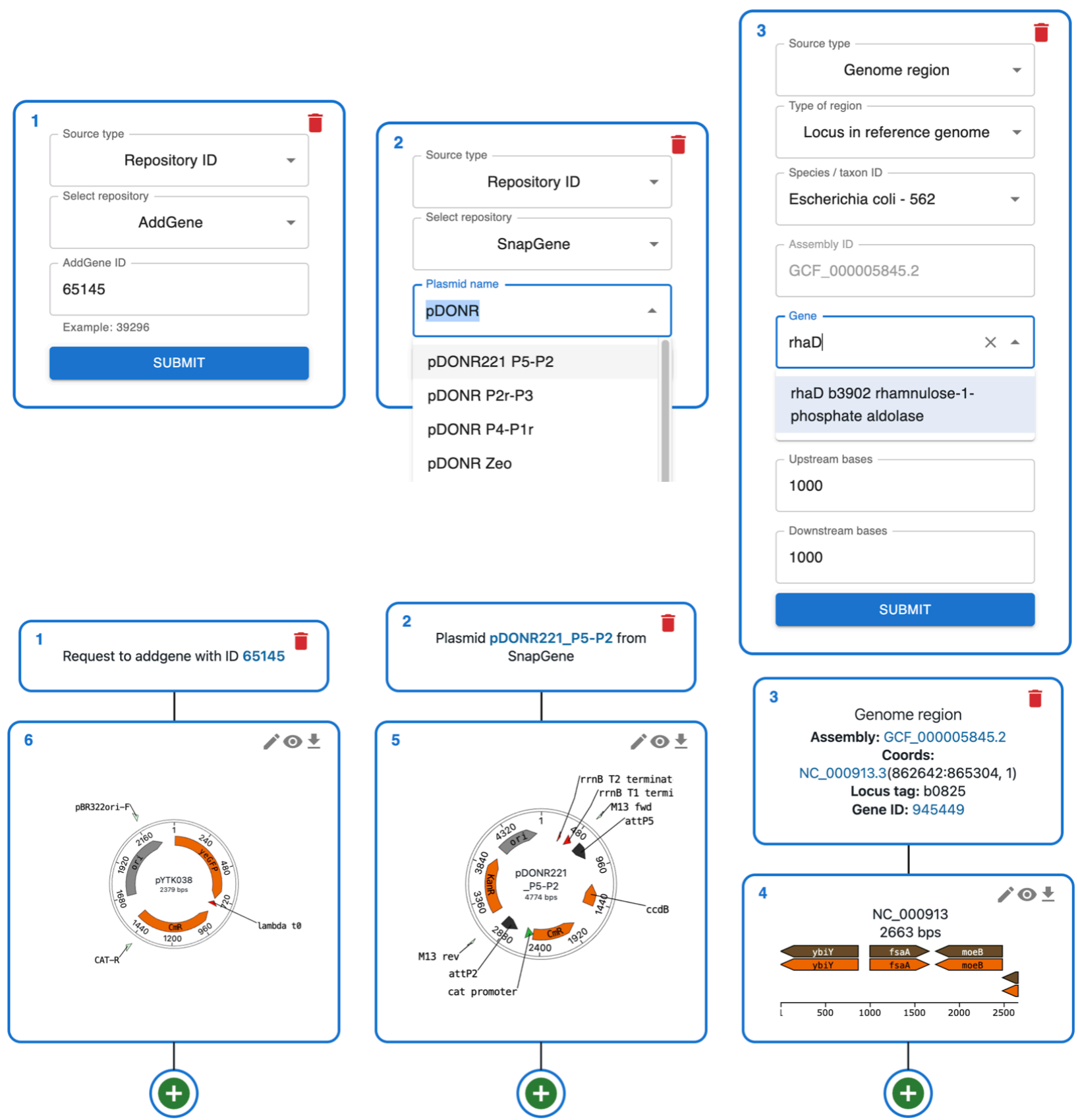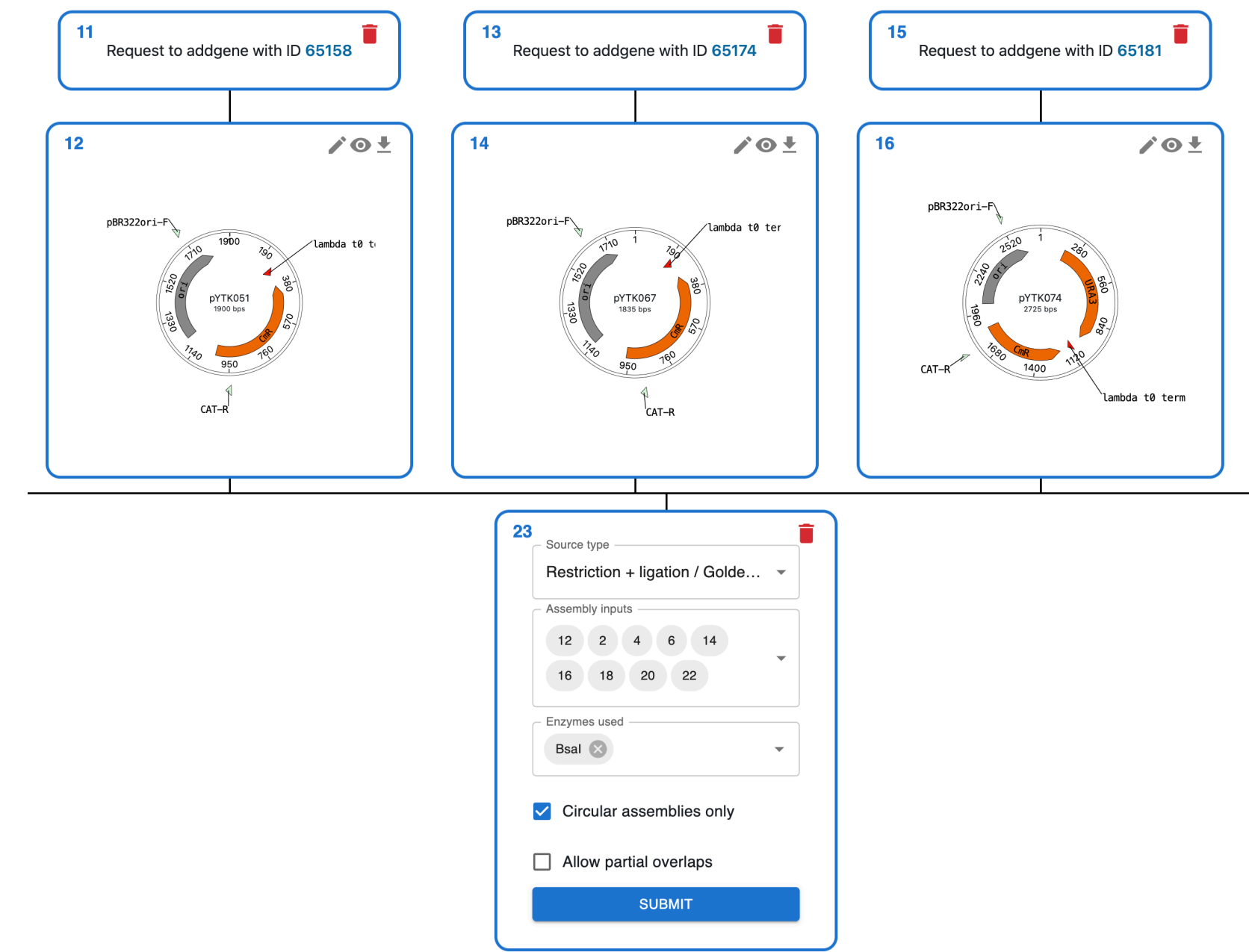
https://shareyourcloning.org/

Features

⬇️ Import from anywhere ⬇️

- 🗄️ Local files
- 🔄 AddGene
- 💰 GenBank
- 🧬 NCBI genomes (by gene or region)
- ✏️ SnapGene website
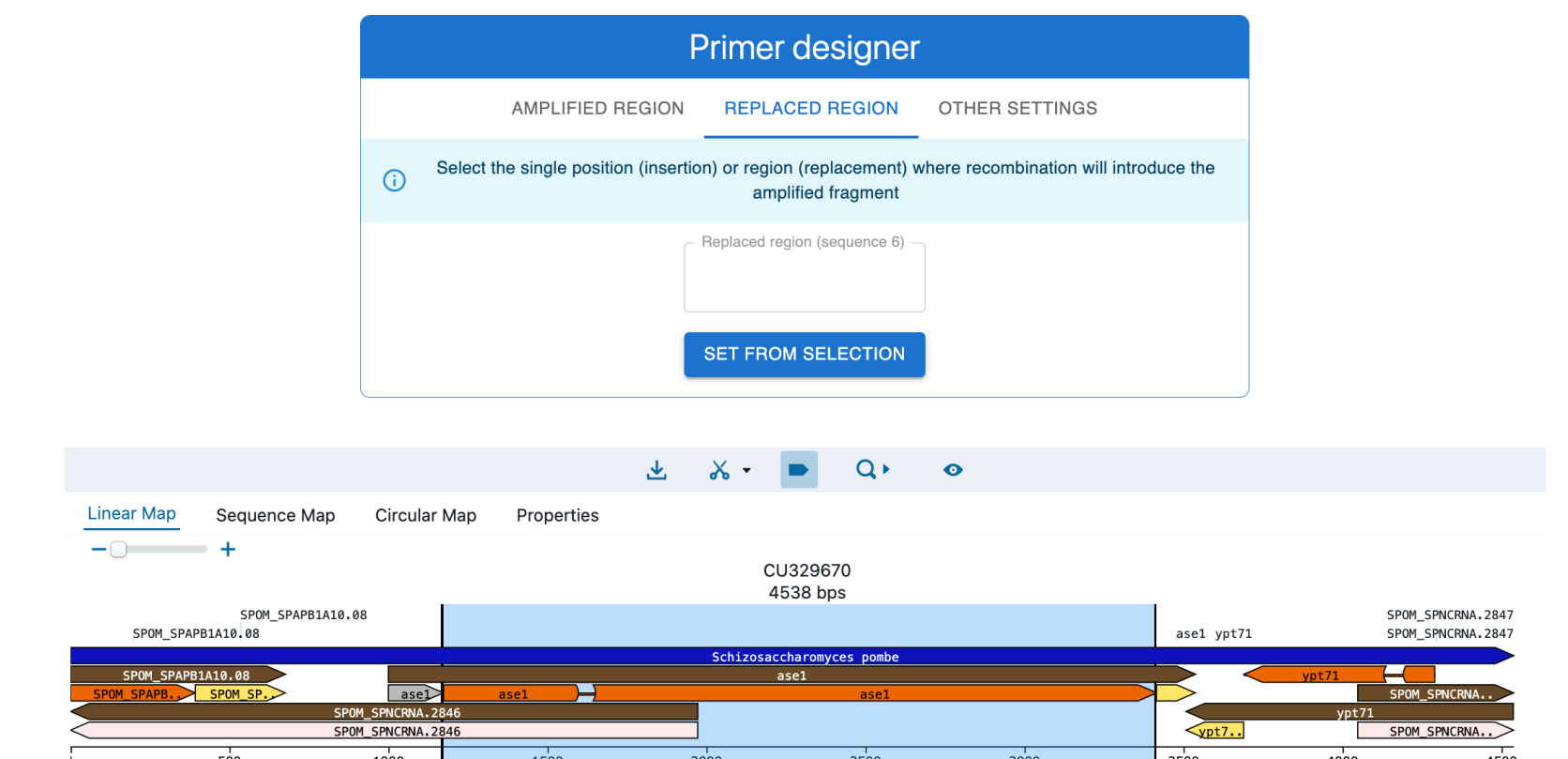- 🧫 Benchling link
- 🪼 EuroScarf

🦐 Techniques supported 🦐

- 🔒 Golden Gate
- 🧩 Gibson Assembly
- ✂️ Restriction - ligation
- 🧬 PCR
- 🔄 Hom. Recombination
- 🦠 CRISPR-HDR
- 🔄 Overlap extension PCR
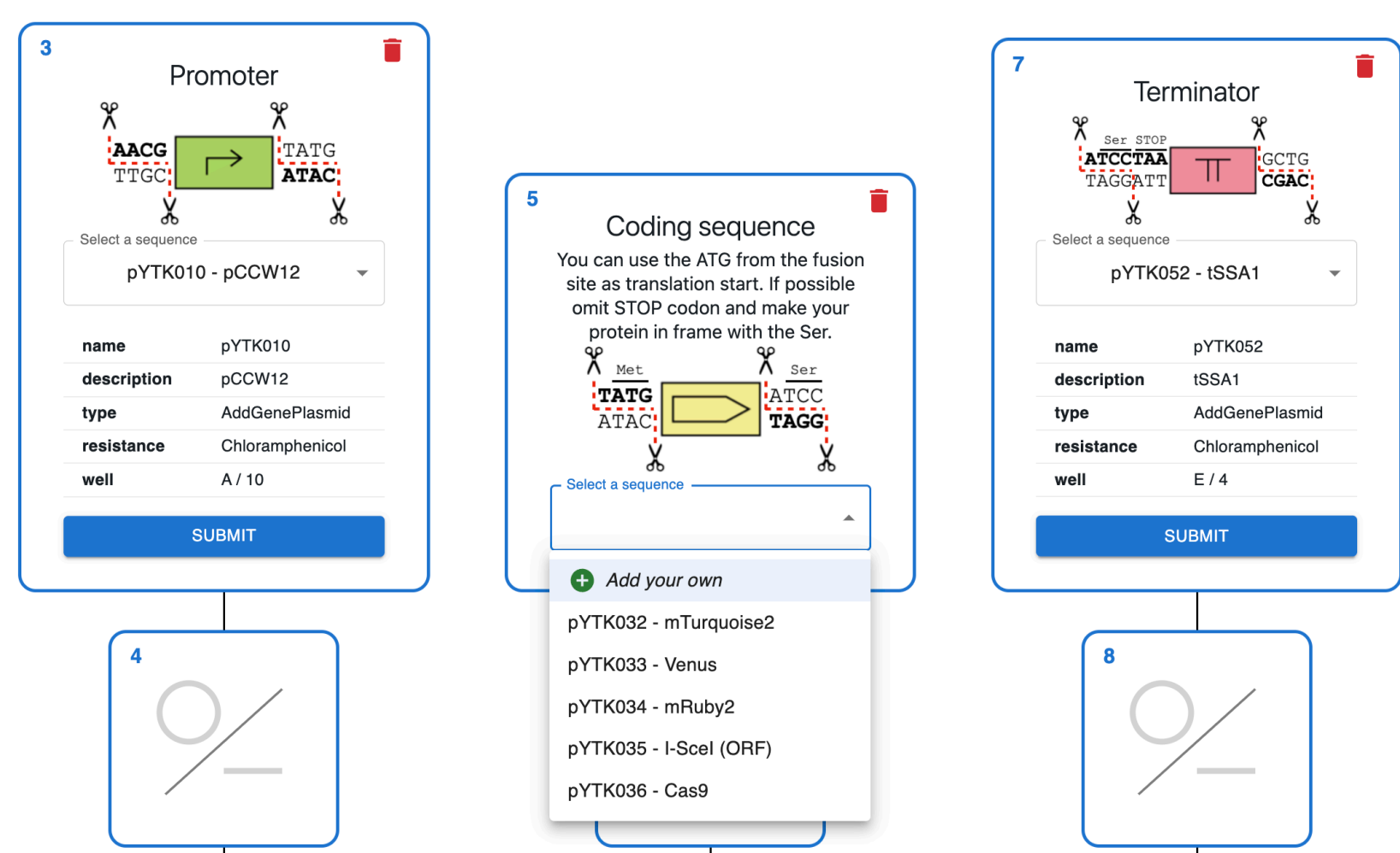- ⛩️ Gateway™
- ▶️ Polymerase extension
- 🧬 Oligo hybridization

🧰 Cloning kit templates 🧰

Promoter | Coding sequence | Terminator

Coding sequence: You can use the ATG from the fusion site as translation start. If possible omit STOP codon and make your protein in frame with the Set.

pYTK032 - mTurquoise2
pYTK033 - Venus
pYTK034 - mRuby2
pYTK035 - I-SceI (ORF)
pYTK036 - Cas9

It's very easy to create your own templates in Excel!

🧪 Primer design 🧪

- 🧩 Gibson Assembly
- 🔄 Hom. Recombination
- 🦠 CRISPR-HDR
- ✂️ Restriction - ligation
- 🔄 Checking PCR

Primer designer

AMPLIFIED REGION REPLACED REGION OTHER SETTINGS

Select the single position (insertion) or region (replacement) where recombination will introduce the amplified fragment

SET FROM SELECTION

👁️ Rich feature viewer 👁️

Linear Map Sequence Map Circular Map Properties

🔮 Coming soon 🔮

- 🔍 **Private sequence database for your lab** 🔍
  - Ancestry and progeny of all resources.
  - Rich queries (e.g., alleles of a certain gene, plasmids with a given marker)
- 🧫 **Strain and cell line support** 🧫
  - Genotypes as arrays of alleles.
  - Alleles as cloning strategies starting from wt locus.
- 🤖 **Better automation support** 🤖
  - Generate the same output using a pydna script.
- 📓⚙️ **Integration with e-lab notebooks** ⚙️📓
  - eLabFTW and LabID (EMBL).
- 🔗 **Attach supporting evidence** 🔗
  - Gel images
  - Sequencing data (auto-aligned).
- 📧 **One Click Export/Report/Share/Publish** 📧
  - Generate "Materials and Methods" text and files.
  - Generate publisher-specific tables (e.g., STAR).
  - Submit to repositories and generate unique IDs.