Loom Documentation

What does Loom do?

Loom is Ginkgo's platform for designing and ordering DNA libraries. It allows users to create designs from a curated and searchable library of genetic parts and easily group calculated constructs into transactions that can be ordered from synthesis vendors with the click of a button.

The vision of Loom is **Democratize and scale the DNA library design and ordering process.** We aim to do this with the following strategic focuses:

- A curated parts library
- Intuitive design interface for combinatorial library design
- Streamlined DNA ordering and tracking
- Enable cross-team knowledge sharing and collaboration
- Efficient part discovery

Meet the Team!

Loom is built by the Terminators Software team. Please don't hesitate to find us to chat about DNA design and ordering!

See the crew here :

Access the Environments

- **Training environment** - https://portal-training.ginkgobioworks.com/ - please use this for testing out new features or workflows or for getting up to familiar with the software.
- **Production environment** - https://portal.ginkgobioworks.com/ - please use this for all production workflows and data

Python Client: dna_tools_client_examples

New to Loom?

Check out the Quick Start to learn the basics and find links to more in depth documentation for the main functionality in Loom.

Docs and Training

Search

- Loom Basics
- Loom Advanced

Best Practices

Design Unit upload and selection

- DUs should represent the smallest possible, labelled part of the DNA design. This builds out a more functional DU library where parts can more easily be referenced and reused.
- Miscellaneous should be used as a last resort when nothing else in the part library is representative. The miscellaneous part type is being overused for DUs that represent concatenated parts, resulting in a

Designing in the Loom UI

- Use a representative block for the DU type so the design annotations are logical.
- When using reverse complement in DNA design, make sure the block is reverse complemented rather than a DU with a reversed complemented sequence.

large part of the DU library being unusable in future applications.

- The traditional definition of an Open Reading Frame (ORF) is a coding sequence made up of multiple of 3 bp, from start to stop codon. The Loom definition is slightly different; ORFs represent the coding sequence of one gene. The ORF part is incomplete by biological definition and should be flanked by separate start and stop codon parts.
- Backbones should be annotated with origin of replication and antibiotic resistance at a bare minimum. If they contain an origin of transfer or other part types, such as promoter, RBS, start and stop codons, then those should be annotated too. This would prevent replicate parts and make it easier to manually review designs.
- The DU metadata and annotations should be filled out as honestly and fully as possible. Standards can be developed around what “correct” metadata and annotations entails on a project-by-project base from literature, user expertise, previous use cases, and/or positive experimental result.

Why do we need these?

As the number of Loom users grows, there needs to be a core set of best practices to unify users across all teams. This would help create an accessible DU Library with reusable parts, and all DNA Designs would be understood easily by users across the board. Centralized best practices brings Loom a step closer to fulfill its vision to democratize and scale DNA design and transactions.