

CLAIMS

What is claimed as new and desired to be protected by Letters Patent of the United States is:

1. A computer-implemented method of designing a DNA construct, comprising:
 - at an electronic device with a display,
 - receiving an input selecting a vector backbone, wherein the vector backbone comprises a plurality of functional parts;
 - in response to receiving the input selecting the vector backbone, displaying a graphical representation of the vector backbone;
 - receiving an input selecting one or more functional parts of the plurality of functional parts of the vector backbone;
 - after receiving the input selecting one or more functional parts on the vector backbone, receiving a drag-and-drop input comprising an indication of a functional part;
 - in response to receiving the drag-and-drop input, updating the vector backbone based on the functional part indicated in the drag-and-drop input and the selected one or more functional parts of the plurality of functional parts of the vector backbone; and
 - displaying a graphical representation of the updated vector backbone.
2. The method of claim 1, wherein the drag-and-drop input comprises a click and drag input made with a mouse.
3. The method of claim 1, wherein the drag-and-drop input comprises a tap and drag input made with a finger on a touch-sensitive display.
4. The method of any of claims 1-3, wherein the graphical representation of the selected vector backbone includes a plasmid map, or a sequence map, or a combination thereof.

5. The method of any of claims 1-4,
 - wherein the one or more functional parts includes an existing gene on the vector backbone, and
 - wherein updating the vector backbone comprises replacing the exiting gene with the functional part indicated in the drag-and-drop input.
6. The method of any of claims 1-5,
 - wherein the one or more functional parts includes one or more cloning sites on the vector backbone, and
 - wherein updating the vector backbone comprises inserting the functional part indicated in the drag-and-drop input at a cloning site of the one or more cloning sites on the vector backbone.
7. The method of any of claims 1-6, further comprising:
 - receiving an input including a search term corresponding to a functional part;
 - identifying one or more search results based on a plurality of databases.
8. The method of claim 7, wherein the plurality of databases includes a user-specific database, a system-specific database, a public database, or any combination thereof.
9. The method of any of claims 1-8, further comprising:
 - while displaying the graphical representation of the updated vector backbone,
 - receiving an input indicative of an error-checking request;
 - in response to receiving the input indicative of the error-checking request, identifying an error with the updated vector backbone; and
 - providing an output indicative of the identified error.
10. The method of any of claims 1-9, further comprising:

in response to receiving the drag-and-drop input, automatically identifying the functional part indicated in the drag-and-drop input based on a plurality of databases; and based on the identifying, displaying a graphical representation of the functional part indicated in the drag-and-drop input in accordance with one or more visual characteristics associated with the functional part.

11. The method of any of claims 1-10, wherein the plurality of functional parts include:

- a promoter;
- a gene of interest;
- a terminator;
- a tag;
- an antibiotic resistance;
- a cloning site;
- an origin;
- a reporter gene;
- a coding sequence (“CDS”);
- an activator;
- an enhancer;
- an intron;
- an repressor;
- a signal sequence;
- a terminal repeat sequence;
- a linker; or
- any combination thereof.

12. An electronic device, comprising:

- a display;
- one or more processors;

a memory; and

one or more programs, wherein the one or more programs are stored in the memory and configured to be executed by the one or more processors, the one or more programs including instructions for:

receiving an input selecting a vector backbone, wherein the vector backbone comprises a plurality of functional parts;

in response to receiving the input selecting the vector backbone, displaying a graphical representation of the vector backbone;

receiving an input selecting one or more functional parts of the plurality of functional parts of the vector backbone;

after receiving the input selecting one or more functional parts on the vector backbone, receiving a drag-and-drop input comprising an indication of a functional part;

in response to receiving the drag-and-drop input, updating the vector backbone based on the functional part indicated in the drag-and-drop input and the selected one or more functional parts of the plurality of functional parts of the vector backbone; and displaying a graphical representation of the updated vector backbone.

13. A non-transitory computer-readable storage medium storing one or more programs, the one or more programs comprising instructions, which when executed by one or more processors of an electronic device having a display, cause the electronic device to:

receive an input selecting a vector backbone, wherein the vector backbone comprises a plurality of functional parts;

in response to receiving the input selecting the vector backbone, display a graphical representation of the vector backbone;

receive an input selecting one or more functional parts of the plurality of functional parts of the vector backbone;

after receiving the input selecting one or more functional parts on the vector backbone, receive a drag-and-drop input comprising an indication of a functional part;

in response to receiving the drag-and-drop input, update the vector backbone based on the functional part indicated in the drag-and-drop input and the selected one or more functional parts of the plurality of functional parts of the vector backbone; and display a graphical representation of the updated vector backbone.

14. A computer-implemented method of error-checking a user-edited DNA construct, wherein the user-edited DNA construct is edited based on an original DNA construct, the method comprising:
 - receiving an error-checking request on the user-edited DNA construct;
 - in response to receiving the input, identifying a set of sequences in the user-edited DNA construct, wherein the set of sequences is not present in the original DNA construct;
 - identifying a presence of one or more coding sequences by comparing the set of sequences with a plurality of databases;
 - identifying one or more errors in the identified one or more coding sequences based on a plurality of predefined rules; and
 - displaying an output indicative of the one or more errors.
15. The method of claim 14, wherein the output comprises: a textual output; a graphical output; an auditory output; or any combination thereof.
16. The method of any of claims 14-15, wherein identifying one or more errors comprises:
 - identifying one or more invalid characters in the set of sequences.
17. The method of any of claims 14-16, wherein the plurality of databases includes a user-specific database, a system-specific database, a public database, or any combination thereof.
18. The method of any of claims 14-17, wherein identifying the set of sequences in the user-edited DNA construct comprises:

identifying a first sequence not present in the original DNA construct;
identifying a second sequence not present in the original DNA construct, wherein the second sequence is within a predetermined distance from the first sequence in the user-edited DNA construct;
merging the first sequence and the second sequence to obtain a third sequence, wherein the third sequence is part of the set of sequences.

19. The method of any of claims 14-18, wherein identifying one or more errors comprises:
determining whether a stop codon is present within a coding sequence of the one or more coding sequences.
20. The method of any of claims 14-19, wherein identifying one or more errors comprises:
determining whether a start codon is present before a coding sequence of the one or more coding sequences.
21. The method of any of claims 14-20, wherein identifying one or more errors comprises:
determining whether two coding sequences of the one or more coding sequences are within a predefined distance in the user-edited DNA construct and whether the two coding sequences are of a same direction.
22. The method of claim 21, further comprising:
in accordance with a determination that two coding sequences of the one or more coding sequences are within a predefined distance in the user-edited DNA construct and that the two coding sequences are of a same direction: determining the two coding sequences are in-frame.
23. The method of claim 21, further comprising:

in accordance with a determination that two coding sequences of the one or more coding sequences are within a predefined distance in the user-edited DNA construct and that the two coding sequences are of a same direction: determining a stop codon is present between the two coding sequences.

24. The method of any of claims 14-23, wherein identifying one or more errors comprises:
- determining whether a promoter is present within a predefined distance with a coding sequence of the one or more coding sequences.
25. The method of claim 24, further comprising:
- in accordance with a determination that a promoter is present within a predefined distance with a coding sequence of the one or more coding sequences: determining whether the promoter is of a same direction as the coding sequence.
26. An electronic device, comprising:
- one or more processors;
- a memory; and
- one or more programs, wherein the one or more programs are stored in the memory and configured to be executed by the one or more processors, the one or more programs including instructions for:
- receiving an error-checking request on a user-edited DNA construct, wherein the user-edited DNA construct is edited based on an original DNA construct;
- in response to receiving the input, identifying a set of sequences in the user-edited DNA construct, wherein the set of sequences is not present in the original DNA construct;
- identifying a presence of one or more coding sequences by comparing the set of sequences with a plurality of databases;

identifying one or more errors in the identified one or more coding sequences based on a plurality of predefined rules; and
displaying an output indicative of the one or more errors.

27. A non-transitory computer-readable storage medium storing one or more programs, the one or more programs comprising instructions, which when executed by one or more processors of an electronic device having a display, cause the electronic device to:

receive an error-checking request on a user-edited DNA construct, wherein the user-edited DNA construct is edited based on an original DNA construct;

in response to receiving the input, identify a set of sequences in the user-edited DNA construct, wherein the set of sequences is not present in the original DNA construct;

identify a presence of one or more coding sequences by comparing the set of sequences with a plurality of databases;

identify one or more errors in the identified one or more coding sequences based on a plurality of predefined rules; and

display an output indicative of the one or more errors.