generated, the one or more biological sequences are synthesized. Further provided herein are computerized systems further comprising receiving instructions for changing the vector and the at least one of the plurality of insert sequences corresponding to at least 20% of the harmful biological sequence to remove the harmful biological sequence. Further provided herein are computerized systems for providing enhanced polynucleotide synthesis wherein the plurality of received design instructions are received at one or more time points. Further provided herein are computerized systems wherein the plurality of received design instructions are received from different sources. Further provided herein are computerized systems wherein the plurality of received design instructions are from 3 or more different sources. Further provided herein are computerized systems wherein the plurality of received design instructions are from 5 or more different sources. Further provided herein are computerized systems wherein the plurality of received design instructions are from 10 or more different sources. Further provided herein are computerized systems wherein the one or more biological sequences are each no more than 200 bases in length. Further provided herein are computerized systems wherein the one or more biological sequences are each no more than 100 bases in length. Further provided herein are computerized systems wherein the one or more biological sequences are each no more than 50 bases in length. Further provided herein are computerized systems wherein the one or more biological sequences are each no more than 20 bases in length.

**[0005a]** Provided herein are computerized systems suitable for providing enhanced polynucleotide synthesis: a) a server for hosting a database, wherein the database is adapted for representing a list of sequences; b) a network connection; and c) a computer readable medium comprising instructions for a general purpose computer, wherein said computerized system is configured for operating in a method of: i) providing a plurality of biological sequences, wherein each biological sequence of the plurality of biological sequences is no more than 500 bases in length; ii) combining at least two biological sequences of the plurality of biological sequences to generate a combined sequence; iii) automatically determining whether the combined sequence comprises a portion that corresponds to at least 20% of a harmful biological sequence contained in the database, wherein the portion corresponding to at least 20% of the harmful biological sequence is from more than one of the at least two biological sequences; iv) if the portion that corresponds to at least 20% of the harmful biological sequence is detected in step c) automatically generating an alert indicating the presence in the combined sequence of the portion that corresponds to at least 20% of the harmful

biological sequence, removing from the combined sequence the portion that corresponds to at least 20% of the harmful biological sequence.

**[0006]** Provided herein are methods for providing enhanced polynucleotide synthesis comprising: 1) receiving one or more design instructions, wherein the design instructions comprise a plurality of biological sequences, wherein the plurality of biological sequences is a vector sequence, and a plurality of additional insert sequences; 2) automatically determining whether the vector and at least one of the plurality of insert sequences collectively corresponds to at least 20% of a harmful biological sequence in the database; and

3) automatically generating an alert if at least 20% of the harmful biological sequence is detected. Further provided herein are methods wherein the biological sequences are obtained from sequencing a physical nucleic acid or protein sample. Further provided herein are methods further comprising wherein if no alert is generated, the one or more biological sequences are synthesized. Further provided herein are methods receiving instructions for changing the vector and the at least one of the plurality of insert sequences corresponding to at least 20% of the harmful biological sequence to remove the harmful biological sequence.

**[0006a]** Provided herein arecomputerized systems suitable for providing enhanced polynucleotide synthesis: a) a server for hosting a database, wherein the database is adapted for representing a list of sequences; b) a network connection; and c) a computer readable medium comprising instructions for a general purpose computer, wherein said computerized system is configured for operating in a method of: i) providing a plurality of biological sequences, wherein each biological sequence of the plurality of biological sequences is no more than 500 bases in length, and wherein the plurality of biological sequences comprises a vector sequence, and a plurality of additional insert sequences; ii) combining at least two biological sequences of the plurality of biological sequences to generate a combined sequence; iii) automatically determining whether the

combined sequence comprises a portion that corresponds to at least 20% of a harmful biological sequence contained in the database, wherein the portion corresponding to at least 20% of the harmful biological sequence is from more than one of the at least two biological sequences; iv) if the portion that corresponds to at least 20% of the harmful biological sequence is detected in step c) automatically generating an alert indicating the presence in the combined sequence of the portion that corresponds to at least 20% of the harmful biological sequence ; and v) receiving instructions for changing the vector and the at least one of the plurality of insert sequences corresponding to at least 20% of the harmful biological sequence to remove the harmful biological sequence.

## INCORPORATION BY REFERENCE

**[0007]** All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent

## CLAIMS

**WHAT IS CLAIMED IS:**

1. A computerized system suitable for providing enhanced polynucleotide synthesis:

    a) a server for hosting a database, wherein the database is adapted for representing a list of harmful biological sequences;

    b) a network connection; and

    c) a computer readable medium comprising instructions for a general purpose computer, wherein said computerized system is configured for operating in a method of:

        i) providing a plurality of biological sequences, wherein each biological sequence of the plurality of biological sequences is no more than 500 bases in length;

        ii) combining at least two biological sequences of the plurality of biological sequences to generate a combined sequence;

        iii) automatically determining whether the combined sequence comprises a portion that corresponds to at least 20% of a harmful biological sequence contained in the database, wherein the portion corresponding to at least 20% of the harmful biological sequence is from more than one of the at least two biological sequences; and

        iv) if the portion that corresponds to at least 20% of the harmful biological sequence is detected in step c) automatically generating an alert indicating the presence in the combined sequence of the portion that corresponds to at least 20% of the harmful biological sequence, removing from the combined sequence the portion that corresponds to at least 20% of the harmful biological sequence .

2. The system of claim 1, further comprising wherein if no alert is generated, then one or more polynucleotides are synthesized, wherein the one or more polynucleotides encode for the plurality of biological sequences.

3. The system of claim 1, further comprising receiving instructions for changing the at least two biological sequences of the plurality of biological sequences corresponding to at least 20% of the harmful biological sequence to remove the harmful biological sequence.

4. The system of claim 1, wherein the one or more design instructions are received at one or more time points.

5. The system of claim 1, wherein the one or more design instructions are from different sources.
6. The system of claim 5, wherein the plurality of received design instructions are from 3 or more different sources.
7. The system of claim 5, wherein the plurality of received design instructions are from 10 or more different sources.
8. The system of claim 1, wherein the plurality of biological sequences are each no more than 200 bases in length.
9. The system of claim 8, wherein the one or more biological sequences are each no more than 100 bases in length.
10. The system of claim 8, wherein the one or more biological sequences are each no more than 50 bases in length.
11. The system of claim 8, wherein the plurality of biological sequences are each no more than 20 bases in length.
12. A computerized system suitable for providing enhanced polynucleotide synthesis:
    a) a server for hosting a database, wherein the database is adapted for representing a list of sequences;
    b) a network connection; and
    c) a computer readable medium comprising instructions for a general purpose computer, wherein said computerized system is configured for operating in a method of:
        i) providing a plurality of biological sequences, wherein each biological sequence of the plurality of biological sequences is no more than 500 bases in length, and wherein the plurality of biological sequences comprises a vector sequence, and a plurality of additional insert sequences;
        ii) combining at least two biological sequences of the plurality of biological sequences to generate a combined sequence;
        iii) automatically determining whether the combined sequence comprises a portion that corresponds to at least 20% of a harmful biological sequence contained in the database, wherein the portion corresponding to at least 20% of the harmful biological sequence is from more than one of the at least two biological sequences;
        iv) if the portion that corresponds to at least 20% of the harmful biological sequence is detected in step c) automatically generating an alert indicating

the presence in the combined sequence of the portion that corresponds to at least 20% of the harmful biological sequence ; and

v) receiving instructions for changing the vector and the at least one of the plurality of insert sequences corresponding to at least 20% of the harmful biological sequence to remove the harmful biological sequence.

13. The system of claim 12, wherein if no alert is generated, then one or more polynucleotides are synthesized, wherein the one or more polynucleotides encode for the plurality of biological sequences.
14. The system of claim 12, wherein the one or more design instructions are received at one or more time points.
15. The system of claim 12, wherein the one or more design instructions are received from different sources.
16. The system of claim 12, wherein the plurality of received design instructions are from 3 or more different sources.
17. The system of claim 12, wherein the plurality of received design instructions are from 10 or more different sources.
18. The system of claim 12, wherein the plurality of biological sequences are no more than 200 bases in length.
19. The computerized system of claim 1, wherein the harmful biological sequence encodes for a gene or gene fragment that, when translated or transcribed, results in a pathogenic product.
20. The computerized system of claim 19, wherein the gene is from a bacterial or a viral genome.