CLAIMS

WHAT IS CLAIMED IS:

1. A computerized system 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) receiving one or more design instructions, wherein the design instructions comprise a plurality of biological sequences, wherein each of the biological sequences is no more than 500 bases in length, and wherein the plurality of biological sequences comprise a nucleic acid or amino acid sequence;

        ii) automatically determining whether at least two biological sequences of the plurality of biological sequences collectively correspond to at least 20% of a harmful biological sequence in the database; and

        iii) automatically generating an alert if at least 20% of the harmful biological sequence is detected.

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 method for providing enhanced polynucleotide synthesis comprising:
    a) receiving one or more design instructions, wherein the design instructions comprise a plurality of biological sequences, wherein each of the biological sequences is no more than 500 bases in length, and wherein the plurality of biological sequences comprise a nucleic acid or amino acid sequence;
    b) automatically determining whether at least two biological sequences of the plurality of biological sequences collectively correspond to at least 20% of a harmful biological sequence in a database; and
    c) automatically generating an alert if at least 20% of the harmful biological sequence is detected.

13. The method of claim 12, 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.

14. The method of claim 12, 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.

15. A computerized system 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) receiving one or more design instructions, wherein the design instructions comprise a plurality of biological sequences, wherein the plurality of biological

sequences comprises a vector sequence, and a plurality of additional insert sequences;

ii) 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

iii) automatically generating an alert if at least 20% of the harmful biological sequence is detected.

16. The system of claim 15, 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.

17. The system of claim 15, 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.

18. The system of claim 15, wherein the one or more design instructions are received at one or more time points.

19. The system of claim 15, wherein the one or more design instructions are received from different sources.

20. The system of claim 15, wherein the plurality of received design instructions are from 3 or more different sources.

21. The system of claim 15, wherein the plurality of received design instructions are from 10 or more different sources.

22. The system of claim 15, wherein the plurality of biological sequences are no more than 200 bases in length.

23. A method for providing enhanced polynucleotide synthesis comprising:

a) receiving one or more design instructions, wherein the design instructions comprise a plurality of biological sequences, wherein the plurality of biological sequences comprises a vector sequence, and a plurality of additional insert sequences;

b) 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

c) automatically generating an alert if at least 20% of the harmful biological sequence is detected.

24. The method of claim 23, wherein the biological sequences are obtained from sequencing a physical nucleic acid or protein sample.
25. The method of claim 23, 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.
26. The method of claim 23, 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.
27. 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.
28. The computerized system of claim 27, wherein the gene is from a bacterial or a viral genome.
29. The method of claim 12, wherein the harmful biological sequence encodes for a gene or gene fragment that, when translated or transcribed, results in a pathogenic product.
30. The method of claim 29, wherein the gene is from a bacterial or a viral genome.