

## WHAT IS CLAIMED:

1. A method for amplifying a target double-stranded nucleic acid comprising:
  - (a) providing a system having:
    - a clustered regularly interspaced short palindromic repeats (CRISPR) RNA (crRNA), and
    - a CRISPR-associated (Cas) protein,wherein the crRNA contains a target-specific nucleotide region complementary to a region of a first strand of the target double-stranded nucleic acid;
  - (b) contacting the target double-stranded nucleic acid with the system to form a complex;
  - (c) hybridizing a primer to a second strand of the target double-stranded nucleic acid, the primer containing a sequence complementary to a region of the second strand of the target double-stranded nucleic acid, and
  - (d) extending a nucleic acid complementary to the second strand of the target double-stranded nucleic acid from the primer using a polymerase.
2. The method of claim 1,
  - i) wherein the target double-stranded nucleic acid is linearly amplified; or
  - ii) wherein the target double-stranded nucleic acid is exponentially amplified, or
  - iii) wherein the target nucleic acid is a double-stranded DNA (dsDNA), or
  - iv) wherein the target nucleic acid is a double-stranded RNA (dsRNA), or
  - v) wherein the system is a Type I CRISPR-Cas system, or
  - vi) wherein the system is a Type II CRISPR-Cas system, or
  - vii) wherein the system is a Type III CRISPR-Cas system, or
  - viii) wherein the system further comprises a trans-activating crRNA (tracrRNA), or

ix) wherein the crRNA is a polynucleotide comprising a crRNA polynucleotide fused to a tracrRNA polynucleotide,

x) wherein the first strand of the target double-stranded nucleic acid contains a sequence complementary to a 5'-NGG protospacer-adjacent motif (PAM), or

xi) wherein the first strand of the target double-stranded nucleic acid contains a universal sequence, and wherein the crRNA contains a sequence complementary to a region of the universal sequence, or

xii) further comprising repeating step (a) to step (d) for one or more times.

3. The method of claim 2 wherein the first strand of the target double-stranded nucleic acid contains a universal sequence, and wherein the crRNA contains a sequence complementary to a region of the universal sequence,

wherein

i) the primer contains a sequence of a region of the universal sequence, or

ii) the universal sequence has a sequence of SEQ ID No. 3,

optionally wherein the crRNA contains a sequence of SEQ ID No.7,

optionally wherein the primer contains a sequence of SEQ ID No. 5, or

iii) wherein the universal sequence has a sequence of SEQ ID No. 4, optionally

wherein the crRNA contains a sequence of SEQ ID No.8, optionally

wherein the primer contains a sequence of SEQ ID No. 6.

4. The method of claim 1, wherein the Cas protein is a Cas9 protein optionally

wherein the Cas9 protein contains two inactivated nuclease domains, optionally

wherein the two inactivated nuclease domains comprise a first mutation in the domain that cleaves the strand complementary to the crRNA and a second mutation in the domain that cleaves the strand non-complementary to the crRNA, optionally

wherein the first mutation is D10A and the second mutation is H840A.

5. The method of claim 1, wherein

(i) the Cas protein is a Cascade protein, or

ii) the Cas protein is a Cas3 protein, or

iii) the polymerase is a strand-displacing polymerase, optionally

wherein the polymerase is selected from a group consisting of Bst, Bsu, and Phi29.

6. The method of claim 1, further comprising:

applying at least one transposase and at least one transposon end composition containing a transferred strand to a sample containing a target nucleic acid under conditions where the target nucleic acid and the transposon end composition undergo a transposition reaction to generate a mixture, wherein the target nucleic acid is fragmented to generate a plurality of target nucleic acid fragments, and

incorporating a universal primer sequence into each of the plurality of target nucleic acid fragments,

wherein the crRNA contains a target-specific nucleotide region complementary to a region of the universal primer, optionally

wherein the universal primer is incorporated into the plurality of target nucleic acid fragments by a PCR reaction, optionally

wherein a) the universal primer has sequence complementary to a 5'-NGG protospacer-adjacent motif (PAM), or

b) the universal sequence has a sequence of SEQ ID No. 3, optionally

wherein the crRNA contains a sequence of SEQ ID No.7, optionally

wherein the primer contains a sequence of SEQ ID No.5, or

c) the universal primer has a sequence of SEQ ID No. 4, optionally

wherein the crRNA contains a sequence of SEQ ID No.8, optionally

wherein the primer contains a sequence of SEQ ID No. 6.

7. The method of claim 6, wherein two universal primers are incorporated into two ends of each of the plurality of target nucleic acid fragments, optionally

wherein the two universal primers have sequences of SEQ ID No.3 and SEQ ID No.4.

8. A method for amplifying a target double-stranded nucleic acid comprising:

(a) providing a first system having:

a first clustered regularly interspaced short palindromic repeats (CRISPR) RNA (crRNA), and

a first CRISPR-associated (Cas) protein, wherein the first crRNA contains a target-specific nucleotide region complementary to a region of a first strand of the target double-stranded nucleic acid;

(b) providing second system having:

a second clustered regularly interspaced short palindromic repeats (CRISPR) RNA (crRNA), and

a second CRISPR-associated (Cas) protein,

wherein the second crRNA contains a target-specific nucleotide region complementary to a region of a second strand of the target double-stranded nucleic acid;

(c) contacting the target double-stranded nucleic acid with the first system and the second system;

(d) hybridizing a first primer to a second strand of the target double-stranded nucleic acid, the first primer containing a sequence complementary to a region of the second strand of the target double-stranded nucleic acid, and hybridizing a second primer to a first strand of the target double-stranded nucleic acid, the second primer containing a sequence complementary to a region of the first strand of the target double-stranded nucleic acid, and

(e) extending the 3' end of the first primer and the second primer with one or more polymerases to generate a first and a second double stranded target nucleic acid.

9. The method of claim 8 wherein

a) the target nucleic acid is a double-stranded DNA (dsDNA), or

- b) the target nucleic acid is a double-stranded RNA (dsRNA), or
- c) the first system or the second system is a Type I CRISPR-Cas system, or
- d) the first system or the second system is a Type II CRISPR-Cas system, or
- e) the first system or a second system is a Type III CRISPR-Cas system, or
- f) the first system or the second system further comprises a trans-activating crRNA (tracrRNA), or
- g) the crRNA of the first system or the second system is a polynucleotide comprising a crRNA polynucleotide fused to a tracrRNA polynucleotide, or
- h) the first strand and the second strand of the target double-stranded nucleic acid contain a sequence complementary to a 5'-NGG protospacer-adjacent motif (PAM), or
- i) the method further comprises repeating step (a) to (e) for one or more times.

10. The method of claim 8, wherein:

the first strand of the target double-stranded nucleic acid contains a first universal sequence, and wherein the crRNA of the first system contains a sequence complementary to a region of the first universal sequence, and

the second strand of the target double-stranded nucleic acid contains a second universal sequence, and wherein the crRNA of the second system contains a sequence complementary to a region of the second universal sequence, optionally

wherein the first primer contains a sequence of a region of the first universal sequence, and the second primer contains a sequence of a region of the second universal sequence, optionally

wherein:

the first universal sequence has a sequence of SEQ ID No. 3, the crRNA of the first system contains a sequence of SEQ ID No.7, and the first primer contains a sequence of SEQ ID No. 5, and

the second universal sequence has a sequence of SEQ ID No. 4, the crRNA of the second system contains a sequence of SEQ ID No.8, and the second primer contains a sequence of SEQ ID No. 6.

11. The method of claim 8, wherein the Cas protein of the first system or the second system is a Cas9 protein, optionally

wherein the Cas9 protein contains two inactivated nuclease domains, optionally

wherein the two inactivated nuclease domains comprise a first mutation in the domain that cleaves the strand complementary to the crRNA and a second mutation in the domain that cleaves the strand non-complementary to the crRNA, optionally

wherein the first mutation is D10A and the second mutation is H840A.

12. The method of claim 8, wherein a) the Cas protein of the first system or the second system is a Cascade protein, or

b) the Cas protein of the first system or the second system is a Cas3 protein, or

c) the polymerase is a strand-displacing polymerase, optionally

wherein the polymerase is selected from a group consisting of Bst, Bsu, and Phi29.

13. The method of any one of claims 1-12, wherein the target nucleic acid is genomic DNA.

14. The method of any one of claims 1-12, wherein the target nucleic acid contains chromosomal DNA.

15. The method of any one of claims 1-12, wherein the target nucleic acid comprises a genome or a partial genome, optionally

further comprising sequencing the target nucleic acid or target nucleic acid fragments, optionally

wherein the sequencing comprises use of one or more of sequencing by synthesis, bridge PCR, chain termination sequencing, sequencing by hybridization, nanopore sequencing, and sequencing by ligation.