THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An engineered Type I CRISPR Cas3 mutant protein ("mCas3 protein") capable of reduced movement along DNA relative to a wild-type Type I CRISPR Cas3 protein ("wtCas3 protein"), the mCas3 protein comprising:

   a nuclear localization signal is covalently connected at the amino terminus, carboxy terminus, or both the amino and carboxy termini, and

   wherein the DNA is double-stranded DNA (dsDNA) comprising a target region comprising a nucleic acid target sequence;

   wherein the mCas3 protein is a *Pseudomonas sp.* S-6-2 D448A mCas3 protein .

2. The mCas3 protein of claim 1, wherein coding sequences for the mCas3 protein are covalently connected to the amino terminus or carboxy terminus of coding sequences of a Cas protein of the Cascade NP complex.

3. The mCas3 protein of claim 1 or claim 2, wherein the DNA is within a cell.

4. The mCas3 protein of claim 3, wherein the cell is a eukaryotic cell.

5. A Type I CRISPR Cascade nucleoprotein complex comprising the mCas3 protein of any one of claims 1 to 4.

6. An engineered Type I CRISPR-Cas effector composition comprising:

   a Type I CRISPR-Cas subunit protein;

   a Type I guide polynucleotide; and

   an engineered Type I CRISPR mCas3 protein, which is a *Pseudomonas sp.* S-6-2 D448A mCas3.

7. The engineered Type I CRISPR-Cas effector composition of claim 6, wherein the *Pseudomonas sp.* S-6-2 mCas3 protein comprises SEQ ID NO:1919.

8. The engineered Type I CRISPR-Cas effector composition of claim 6, further comprising a linker polypeptide covalently connecting the engineered Type I CRISPR mCas3 protein and the Type I CRISPR-Cas subunit protein.

9. The engineered Type I CRISPR-Cas effector composition of claim 6, wherein the Type I CRISPR-Cas subunit protein is selected from the group consisting of a Cas8 protein, a Cas5 protein, and a Cas7 protein.

10. The engineered Type I CRISPR-Cas effector composition of claim 9 further comprising a Type I CRISPR Cas6 protein.

11. The engineered Type I CRISPR-Cas effector composition of claim 9 further comprising a Type I CRISPR Cse2 protein.

12. A cell comprising the engineered Type I CRISPR-Cas effector composition of any one of claims 6 to 11.

13. The cell of claim 12 further comprising:
a second engineered Type I CRISPR-Cas effector composition comprising:
a second Type I CRISPR-Cas subunit protein;
a second Type I guide polynucleotide; and
a second engineered Type I CRISPR mCas3 protein, which is a *Pseudomonas sp.* S-6-2 D448A mCas3.

14. The cell of claim 12 or claim 13 further comprising a donor polynucleotide.

15. The cell of claim 12 or claim 13, wherein the cell comprises a eukaryotic cell.

16. The eukaryotic cell of claim 15 comprising an induced pluripotent stem cell.

17. A method of nicking double-stranded DNA (dsDNA) comprising:
contacting a first nick site in a first target region in the dsDNA with a first engineered Type I CRISPR-Cas effector composition comprising:
a first Type I CRISPR-Cas subunit protein;
a first Type I guide polynucleotide; and
a first engineered Type I CRISPR mCas3 protein, wherein the first engineered Type I CRISPR mCas3 is a *Pseudomonas sp.* S-6-2 D448A mCas3;

thereby resulting in the first engineered Type I CRISPR-Cas effector composition binding the first target region and the first engineered Type I CRISPR mCas3 protein binding and nicking the dsDNA at the first nick site.

18. The method of claim 17 further comprising:

contacting a second nick site in a second target region in the dsDNA with a second engineered Type I CRISPR-Cas effector composition comprising:

a second Type I CRISPR-Cas subunit protein;

a second Type I guide polynucleotide; and

a second engineered Type I CRISPR mCas3 protein, wherein the second engineered Type I CRISPR mCas3 is a *Pseudomonas sp.* S-6-2 D448A mCas3;

thereby resulting in the second engineered Type I CRISPR-Cas effector composition binding the second target region and the second engineered Type I CRISPR mCas3 protein binding and nicking the dsDNA at the second nick site.

19. The method of claim 18, wherein the distance between the first nick site and the second nick site on the dsDNA is between 1 and 120 base pairs.

20. The method of any one of claims 17 to 19, wherein the method is performed *in vitro*.