Claims

1. A complex comprising a nucleic acid sequence-recognizing module and a proteolysis tag, wherein the module is linked to the proteolysis tag, the module specifically binds to a target nucleotide sequence in a double stranded DNA, and the tag consists of a peptide containing 3 hydrophobic amino acid residues at the C-terminal, wherein the 3 amino acid residues are leucine-valine-alanine, leucine-alanine-alanine, or alanine-serine-valine.

2. The complex according to claim 1, wherein the complex is further bound with a nucleic acid altering enzyme, and converts one or more nucleotides in the targeted site to other one or more nucleotides or deletes them, or insert one or more nucleotides in the targeted site.

3. The complex according to claim 1 or 2, wherein the nucleic acid sequence-recognizing module is a CRISPR-Cas system in which only one of the two DNA cleavage abilities of Cas or both DNA cleavage abilities are inactivated.

4. The complex according to claim 1 or 2, wherein the complex is a complex in which the proteolysis tag is bound to a CRISPR-Cas system.

5. The complex according to claim 2, or claim 3 when dependent from claim 2, wherein the nucleic acid altering enzyme is a nucleic acid base converting enzyme or a DNA glycosylase.

6. The complex according to claim 5, wherein the nucleic acid base converting enzyme is deaminase.

7. The complex according to claim 5 or 6, wherein a base excision repair inhibitor is further bound to the complex.

8. A nucleic acid encoding the complex according to any one of claims 1 to 7.

9. A method for altering a targeted site of a double stranded DNA of a bacterium, or regulating an expression of a gene encoded by a double-stranded DNA near the site, comprising a step of bringing a complex comprising a nucleic acid sequence-recognizing module specifically binding to a target nucleotide sequence in a selected double stranded DNA and a proteolysis tag, wherein the proteolysis tag consists of a peptide containing 3 hydrophobic amino acid residues at the C-terminal, into contact with the double stranded DNA, wherein the 3 amino acid residues are leucine-valine-alanine, leucine-alanine-alanine, or alanine-serine-valine.

10. The method according to claim 9, comprising a step of converting one or more nucleotides in the targeted site to other one or more nucleotides or delete one or more nucleotides, or inserting one or more nucleotides into said targeted site, wherein the complex is further bound with a nucleic acid altering enzyme.

11. The method according to claim 9 or 10, wherein the nucleic acid sequence-recognizing module is a CRISPR-Cas system in which only one of the two DNA cleavage abilities of Cas or both DNA cleavage abilities are inactivated.

12. The method according to claim 9 or 10, wherein the complex is a complex in which the proteolysis tag is bound to a CRISPR-Cas system.

13. The method according to any one of claims 9 to 12, wherein two or more kinds of nucleic acid sequence-recognizing modules each specifically binding to a different target nucleotide

sequence are used.

14. The method according to claim 13, wherein the different target nucleotide sequence is present in a different gene.

15. The method according to claim 10, or claims 11, 13 and 14 when dependent from claim 10, wherein the nucleic acid altering enzyme is a nucleic acid base converting enzyme or a DNA glycosylase.

16. The method according to claim 15, wherein the nucleic acid base converting enzyme is deaminase.

17. The method according to claim 15 or 16, wherein the complex is further bound with a base excision repair inhibitor.

18. The method according to any one of claims 9 to 17, wherein the double stranded DNA is brought into contact with the complex by introduction the nucleic acid encoding the complex into the bacterium having the double stranded DNA.