CLAIMS

[Claim 1]

A polypeptide, which is any one of the following polypeptides:

(C-1) a polypeptide consisting of any one of the sequences of SEQ ID NOs: 4 to 7;

(C-2) a polypeptide consisting of any one of the sequences of SEQ ID NOs: 4 to 7 having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, and 34, having a cytosine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(C-3) a polypeptide having a sequence identity of at least 80% to any one of the sequences of SEQ ID NOs: 4 to 7, provided that the amino acids at positions 1, 4, 6, and 34 are unchanged, having a cytosine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(A-1) a polypeptide consisting of the sequence of SEQ ID NO: 8 having a substitution of the amino acid at position 6 with asparagine or aspartic acid;

(A-2) a polypeptide consisting of the sequence of (A-1) having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, and 34, having an adenine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(A-3) a polypeptide having a sequence identity of at least 80% to the sequence of (A-1), provided that the amino acids at positions 1, 4, 6, and 34 are unchanged, having an adenine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(G-1) a polypeptide consisting of the sequence of SEQ ID NO: 9 having a substitution of the amino acid at position 6 with asparagine or aspartic acid;

(G-2) a polypeptide consisting of the sequence of (G-1) having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, and 34, having a guanine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(G-3) a polypeptide having a sequence identity of at least 80% to the sequence of (G-1), provided that the amino acids at positions 1, 4, 6, and 34 are unchanged, having a guanine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(U-1) a polypeptide consisting of the sequence of SEQ ID NO: 10 having a substitution of the amino acid at position 6 with asparagine or aspartic acid;

(U-2) a polypeptide consisting of the sequence of (U-1) having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, and 34,

having a uracil-binding property, and being a PPR motif represented by the Formula 1 mentioned below; and

(U-3) a polypeptide having a sequence identity of at least 80% to the sequence of (U-1), provided that the amino acids at positions 1, 4, 6, and 34 are unchanged, having a uracil-binding property, and being a PPR motif represented by the Formula 1 mentioned below.

$$\text{(Helix A)-X-(Helix B)-L} \quad \text{(Formula 1)}$$

wherein, in the Formula 1:

Helix A is a moiety of 12-amino acid length capable of forming an α-helix structure, and is represented by the Formula 2;

$$A_1\text{-}A_2\text{-}A_3\text{-}A_4\text{-}A_5\text{-}A_6\text{-}A_7\text{-}A_8\text{-}A_9\text{-}A_{10}\text{-}A_{11}\text{-}A_{12} \quad \text{(Formula 2)}$$

wherein, in the Formula 2, A_1 to A_{12} independently represent an amino acid;

X does not exist, or is a moiety of 1- to 9-amino acid length;

Helix B is a moiety of 11- to 13-amino acid length capable of forming an α-helix structure; and

L is a moiety of 2- to 7-amino acid length represented by the Formula 3;

$$L_{vii}\text{-}L_{vi}\text{-}L_{v}\text{-}L_{iv}\text{-}L_{iii}\text{-}L_{ii}\text{-}L_{i} \quad \text{(Formula 3)}$$

wherein, in the Formula 3, the amino acids are numbered "i" (-1), "ii" (-2), and so on from the C-terminus side,

provided that L_{iii} to L_{vii} may not exist.

[Claim 2]

A polypeptide, which is any one of the following PPR motifs:

(C-1) a polypeptide consisting of any one of the sequences of SEQ ID NOs: 4 to 7;

(C-2) a polypeptide consisting of any one of the sequences of SEQ ID NOs: 4 to 7 having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, 9, and 34, having a cytosine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(C-3) a polypeptide having a sequence identity of at least 80% to any one of the sequences of SEQ ID NOs: 4 to 7, provided that the amino acids at positions 1, 4, 6, 9, and 34 are unchanged, having a cytosine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;

(A-1) a polypeptide consisting of the sequence of SEQ ID NO: 8 having such

substitutions of the amino acids at positions 6 and 9 that any one of the combinations defined below is satisfied;
(A-2) a polypeptide consisting of the sequence of (A-1) having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, 9, and 34, having an adenine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;
(A-3) a polypeptide having a sequence identity of at least 80% to the sequence of (A-1), provided that the amino acids at positions 1, 4, 6, 9, and 34 are unchanged, having an adenine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;
(G-1) a polypeptide consisting of the sequence of SEQ ID NO: 9 having such substitutions of the amino acids at positions 6 and 9 that any one of the combinations defined below is satisfied;
(G-2) a polypeptide consisting of the sequence of (G-1) having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, 9, and 34, having a guanine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;
(G-3) a polypeptide having a sequence identity of at least 80% to the sequence of (G-1), provided that the amino acids at positions 1, 4, 6, 9, and 34 are unchanged, having a guanine-binding property, and being a PPR motif represented by the Formula 1 mentioned below;
(U-1) a polypeptide consisting of the sequence of SEQ ID NO: 10 having such substitutions of the amino acids at positions 6 and 9 that any one of the combinations defined below is satisfied;
(U-2) a polypeptide consisting of the sequence of (U-1) having a substitution, deletion, or addition of 1 to 9 amino acids other than the amino acids at positions 1, 4, 6, 9, and 34, having a uracil-binding property, and being a PPR motif represented by the Formula 1 mentioned below; and
(U-3) a polypeptide having a sequence identity of at least 80% to the sequence of (U-1), provided that the amino acids at positions 1, 4, 6, 9, and 34 are unchanged, having a uracil-binding property, and being a PPR motif represented by the Formula 1 mentioned below;
- a combination of asparagine as the amino acid at position 6 and glutamic acid as the amino acid at position 9,
- a combination of asparagine as the amino acid at position 6 and glutamine as the amino acid at position 9,

- a combination of asparagine as the amino acid at position 6 and lysine as the amino acid at position 9, and
- a combination of aspartic acid as the amino acid at position 6 and glycine as the amino acid at position 9;

$$\text{(Helix A)-X-(Helix B)-L} \quad \text{(Formula 1)}$$

wherein, in the Formula 1:

Helix A is a moiety of 12-amino acid length capable of forming an α-helix structure, and is represented by the Formula 2;

$$A_1\text{-}A_2\text{-}A_3\text{-}A_4\text{-}A_5\text{-}A_6\text{-}A_7\text{-}A_8\text{-}A_9\text{-}A_{10}\text{-}A_{11}\text{-}A_{12} \quad \text{(Formula 2)}$$

wherein, in the Formula 2, A_1 to A_{12} independently represent an amino acid;

X does not exist, or is a moiety of 1- to 9-amino acid length;

Helix B is a moiety of 11- to 13-amino acid length capable of forming an α-helix structure; and

L is a moiety of 2- to 7-amino acid length represented by the Formula 3;

$$L_{vii}\text{-}L_{vi}\text{-}L_{v}\text{-}L_{iv}\text{-}L_{iii}\text{-}L_{ii}\text{-}L_{i} \quad \text{(Formula 3)}$$

wherein, in the Formula 3, the amino acids are numbered "i" (-1), "ii" (-2), and so on from the C-terminus side,

provided that L_{iii} to L_{vii} may not exist.

[Claim 3]

The polypeptide according to claim 1 or 2, which is any one of the following PPR motifs:

(C-4) a polypeptide consisting of the sequence of SEQ ID NO: 4;

(A-4) a polypeptide consisting of the sequence of SEQ ID NO: 58;

(G-4) a polypeptide consisting of the sequence of SEQ ID NO: 59; and

(U-4) a polypeptide consisting of the sequence of SEQ ID NO: 60.

[Claim 4]

Use of the polypeptide according to any one of claims 1 to 3 in a PPR protein as the first PPR motif from the N-terminus.

[Claim 5]

The use according to claim 4, which is for reducing aggregation of the PPR

protein.

[Claim 6]

A protein capable of binding to a target nucleic acid having a specific nucleotide sequence, which comprises 1 to 30 of PPR motifs represented by the Formula 1 mentioned below, and

wherein the A_6 amino acid of the first PPR motif (M_1) from the N-terminus is a hydrophilic amino acid; or

the polypeptide according to any one of claims 1 to 3:

$$\text{(Helix A)-X-(Helix B)-L} \quad \text{(Formula 1)}$$

wherein, in the Formula 1:

Helix A is a moiety of 12-amino acid length capable of forming an α-helix structure, and is represented by the Formula 2;

$$A_1\text{-}A_2\text{-}A_3\text{-}A_4\text{-}A_5\text{-}A_6\text{-}A_7\text{-}A_8\text{-}A_9\text{-}A_{10}\text{-}A_{11}\text{-}A_{12} \quad \text{(Formula 2)}$$

wherein, in the Formula 2, A_1 to A_{12} independently represent an amino acid;

X does not exist, or is a moiety of 1- to 9-amino acid length;

Helix B is a moiety of 11- to 13-amino acid length capable of forming an α-helix structure; and

L is a moiety of 2- to 7-amino acid length represented by the Formula 3;

$$L_{vii}\text{-}L_{vi}\text{-}L_{v}\text{-}L_{iv}\text{-}L_{iii}\text{-}L_{ii}\text{-}L_{i} \quad \text{(Formula 3)}$$

wherein, in the Formula 3, the amino acids are numbered "i" (-1), "ii" (-2), and so on from the C-terminus side,

provided that L_{iii} to L_{vii} may not exist.

[Claim 7]

The protein according to claim 6, wherein the A_9 amino acid of M_1 is a hydrophilic amino acid or glycine.

[Claim 8]

The protein according to claim 6 or 7, wherein the A_6 amino acid of M_1 is asparagine or aspartic acid.

[Claim 9]

The protein according to any one of claims 6 to 8, wherein the A_9 amino acid of M_1 is glutamine, glutamic acid, lysine, or glycine.

[Claim 10]

The protein according to any one of claims 6 to 9, wherein the A_6 amino acid of M_1 and the A_9 amino acid of M_1 correspond to any of the following combinations:
- combination of asparagine as the A_6 amino acid and glutamic acid as the A_9 amino acid,
- combination of asparagine as the A_6 amino acid and glutamine as the A_9 amino acid,
- combination of asparagine as the A_6 amino acid and lysine as the A_9 amino acid, and
- combination of aspartic acid as the A_6 amino acid and glycine as the A_9 amino acid.

[Claim 11]

A fusion protein of

at least one selected from the group consisting of a fluorescent protein, a nuclear localization signal peptide, and a tag protein, and

a PPR protein containing the polypeptide according to any one of claims 1 to 3 as the first PPR motif from the N-terminus, or the protein according to any one of claims 6 to 10.

[Claim 12]

A method for reducing aggregation of a PPR protein containing the PPR motif represented by the Formula 1 mentioned below and capable of binding to a target nucleic acid having a specific nucleotide sequence, which comprises making the A_6 and A_9 amino acids of the first PPR motif (M_1) from the N-terminus according to any one of the combinations defined below:
- a combination of asparagine as the amino acid at position 6 and glutamic acid as the amino acid at position 9,
- a combination of asparagine as the amino acid at position 6 and glutamine as the amino acid at position 9,
- a combination of asparagine as the amino acid at position 6 and lysine as the amino acid at position 9, and
- a combination of aspartic acid as the amino acid at position 6 and glycine as the amino acid at position 9;

(Helix A)-X-(Helix B)-L (Formula 1)

wherein, in the Formula 1:

Helix A is a moiety of 12-amino acid length capable of forming an α-helix structure, and is represented by the Formula 2;

A_1-A_2-A_3-A_4-A_5-A_6-A_7-A_8-A_9-A_{10}-A_{11}-A_{12} (Formula 2)

wherein, in the Formula 2, A_1 to A_{12} independently represent an amino acid;

X does not exist, or is a moiety of 1- to 9-amino acid length;

Helix B is a moiety of 11- to 13-amino acid length capable of forming an α-helix structure; and

L is a moiety of 2- to 7-amino acid length represented by the Formula 3;

L_{vii}-L_{vi}-L_v-L_{iv}-L_{iii}-L_{ii}-L_i (Formula 3)

wherein, in the Formula 3, the amino acids are numbered "i" (-1), "ii" (-2), and so on from the C-terminus side,

provided that L_{iii} to L_{vii} may not exist.

[Claim 13]

A method for detecting a nucleic acid, which uses the protein according to any one of claims 6 to 10, or the fusion protein according to claim 11.

[Claim 14]

A nucleic acid encoding the polypeptide according to any one of claims 1 to 3, or the protein according to any one of claims 6 to 10.

[Claim 15]

A vector comprising the nucleic acid according to claim 14.

[Claim 16]

A cell containing the vector according to claim 15.

[Claim 17]

A method for manipulating a nucleic acid excluding a method of treatment of the human or animal body by surgery or therapy or of diagnosis practiced on the human or animal body, which uses the polypeptide according to any one of claims 1 to

3, the protein according to any one of claims 6 to 10, or the vector according to claim 15.

[Claim 18]

A method for producing an organism excluding human, which comprises the manipulation method according to claim 17.