CLAIMS

What is claimed is:

1. A fusion protein comprising:

a first fragment comprising a cytidine or adenosine deaminase or a catalytic domain thereof,

a second fragment inhibiting the first fragment, comprising:

i) an amino acid sequence selected from SEQ ID NO: 1-2 and 48-135, or

ii) amino acids residues AA128-AA223 of SEQ ID NO:1, and

a protease cleavage site between the first fragment and the second fragment, wherein protease cleavage site is a protease cleavage site of a protease selected from the group consisting of TEV protease, TuMV protease, PPV protease, PVY protease, ZIKV protease and WNV protease, or is a self-cleavage site.

2. The fusion protein of claim 1, wherein the adenosine deaminase is selected from the group consisting of tRNA-specific adenosine deaminase (TadA), adenosine deaminase tRNA specific 1 (ADAT1), adenosine deaminase tRNA specific 2 (ADAT2), adenosine deaminase tRNA specific 3 (ADAT3), adenosine deaminase RNA specific B1 (ADARB1), adenosine deaminase RNA specific B2 (ADARB2), adenosine monophosphate deaminase 1 (AMPD1), adenosine monophosphate deaminase 2 (AMPD2), adenosine monophosphate deaminase 3 (AMPD3), adenosine deaminase (ADA), adenosine deaminase 2 (ADA2), adenosine deaminase like (ADAL), adenosine deaminase domain containing 1 (ADAD1), adenosine deaminase domain containing 2 (ADAD2), adenosine deaminase RNA specific (ADAR) and adenosine deaminase RNA specific B1 (ADARB1).

3. The fusion protein of claim 1, wherein the cytidine deaminase is selected from the group consisting of APOBEC3B (A3B), APOBEC3C (A3C), APOBEC3D (A3D), APOBEC3F (A3F), APOBEC3G (A3G), APOBEC3H (A3H), APOBEC1 (A1), APOBEC3 (A3), APOBEC2 (A2), APOBEC4 (A4) and AICDA (AID).

4. The fusion protein of claim 3, wherein the catalytic domain is mouse A3 cytidine deaminase domain 1 (CDA1) or human A3B cytidine deaminase domain 2 (CDA2).

5. A fusion protein comprising:

a first fragment comprising a cytidine deaminase or a catalytic domain thereof,

a second fragment inhibiting the first fragment, comprising:

i) an amino acid sequence selected from SEQ ID NO: 1-2 and 48-135, or

ii) amino acids residues AA128-AA223 of SEQ ID NO:1,

a first RNA recognition peptide, and

a TEV protease cleavage site between the nucleobase deaminase or a catalytic domain thereof and the nucleobase deaminase inhibitor.

6. An *in vitro* method for conducting gene editing in a cell, comprising introducing to the cell:

(a) a first molecule comprising a Cas protein;

(b) a second molecule comprising the fusion protein of any one of claims 1-5 and a first RNA recognition peptide;

(c) a third molecule comprising an inactive portion of the TEV protease and a second RNA recognition peptide;

(d) a fourth molecule comprising another portion of the TEV protease which, in combination with the inactive portion of the TEV protease, can carry out the TEV protease activity to cleave the cleavage site in (b);

(e) a fifth molecule comprising a helper sgRNA that comprises a first RNA recognition site recognizable by the first RNA recognition peptide of (b); and

(f) a sixth molecule comprising a sgRNA that comprises a second RNA recognition site recognizable by the second RNA recognition peptide of (c).

7. One or more polynucleotides for conducting gene editing in a subject, wherein the one or more polynucleotides encode:

(a) a first molecule comprising a Cas protein;

(b) a second molecule comprising the fusion protein of any one of claims 1-5 and a first RNA recognition peptide;

(c) a third molecule comprising an inactive portion of the TEV protease and a second RNA recognition peptide;

(d) a fourth molecule comprising another portion of the TEV protease which, in combination with the inactive portion of the TEV protease, can carry out the TEV protease activity to cleave the cleavage site in (b);

(e) a fifth molecule comprising a helper sgRNA that comprises a first RNA recognition site recognizable by the first RNA recognition peptide of (b); and

(f) a sixth molecule comprising a sgRNA that comprises a second RNA recognition site recognizable by the second RNA recognition peptide of (c).