Claims

1. A deaminase-recruiting RNA (dRNA) of 60-200 nucleotides, wherein:
   a) the dRNA comprises a complementary RNA sequence capable of hybridizing to a target RNA;
   b) the dRNA is capable of recruiting a deaminase or a construct comprising a deaminase or a construct comprising a catalytic domain of a deaminase to deaminate a target adenosine in the target RNA; and
   c) the dRNA comprises one or more chemical modifications.
2. The dRNA of claim 1, wherein the dRNA is longer than about any of 60nt, 65nt, 70nt, 80nt, 90nt, 100nt, or 110nt.
3. The dRNA of claim 1 or claim 2, comprising one or more mismatches, wobbles and/or bulges with the complementary target RNA region, particularly, the complementary RNA sequence comprises a cytidine, adenosine or uridine directly opposite to a target adenosine in the target RNA.
4. The dRNA of claim 3, wherein the cytidine, adenosine or uridine directly opposite to the target adenosine locates at least about 7 nucleotides away from the 3' end, for example at least about 8, 9, or 10 nucleotides from the 3' end, and/or wherein the cytidine, adenosine or uridine directly opposite to the target adenosinelocates at least about 25 nucleotides away from the 5' end, for example at least about 30, 35, 40, 45, 50 or 55 nucleotides from the 5' end.
5. The dRNA of any of claims 3-4, wherein the lengths of the 5' and 3' sequences flanking the cytidine, adenosine or uridine directly opposite to the target adenosine are unequal, alternatively, the length of the 5' sequence flanking the cytidine, adenosine or uridine directly opposite to the target adenosine is longer than the 3' sequence.
6. The dRNA of any one of claims 1-5, comprising a cytidine directly opposite to the target adenosine in the target RNA, and/or wherein the complementary RNA sequence comprises one or more guanosines each opposite to a non-target adenosine in the target RNA.
7. The dRNA of any one of claims 1-6, wherein the complementary sequence comprises two or more consecutive mismatch nucleotides opposite to a non-target adenosine in the target RNA.
8. The dRNA of any one of claims 1-7, wherein the target adenosine is in a three-base motif selected from the group consisting of UAG, UAC, UAA, UAU, CAG, CAC, CAA, CAU, AAG, AAC, AAA, AAU, GAG, GAC, GAA and GAU in the target RNA, particularly, the three-base motif is UAG, more particularly, the dRNA comprises an A directly opposite to the uridine in the three-base motif, a cytidine directly opposite to the target adenosine, and a cytidine, guanosine or uridine directly opposite the guanosine in the three-base motif, further more particularly, the dRNA comprises a 5'-CCA-3' directly opposite to the three-base motif of UAG.
9. The dRNA of any one of claims 1-8, wherein the chemical modification comprises methylation and/or phosphorothioation, particularly, the chemical modification comprises 2'-O-methylation and/or internucleotide phosphorothioate linkage, more particularly, the chemical modification comprises a 2'-O-methylationin the first and last 1-5, 2-5, 3-5, 4-5 nucleotides and/or phosphorothioations in the first and last 1-5, 2-5, 3-5, 4-5 internucleotide linkages, further more particularly, the chemical modification comprisesa 2'-O-methylation and/or a 3'-phosphorothioation in the nucleotide opposite to the target adenosine and/or its 5' and/or 3' most adjacent nucleotides.

10. The dRNA of any one of claims 1-9, the chemical modification is selected from a group consisting of:

1) 2’-O-methylations in the first and last 3 nucleotides and/or phosphorothiations in the first and last 3 internucleotide linkages;
2) 2’-O-methylations in the first and last 3 nucleotides and/or phosphorothiations in the first and last 3 internucleotide linkages, and 2’-O-methylations in a single or multiple or all uridines;
3) 2’-O-methylations in the first and last 3 nucleotides, phosphorothiations in the first and last 3 internucleotide linkages, 2’-O-methylations in a single or multiple or all uridines, and a modification in the nucleotide opposite to the target adenosine, and/or its 5’ and/or 3’ most adjacent nucleotides;
4) 2’-O-methylations in the first and last 3 nucleotides, phosphorothiations in the first and last 3 internucleotide linkages, 2’-O-methylations in a single or multiple or all uridines, and 2’-O-methylation in the nucleotide most adjacent to the 3’ terminus and/or 5’ terminus of the nucleotide opposite to the target adenosine;
5) 2’-O-methylations in the first and last 3 nucleotides, phosphorothiations in the first and last 3 internucleotide linkages, 2’-O-methylations in a single or multiple or all uridines, and phosphorothiation linkage in the nucleotide opposite to the target adenosine and/or its 5’ and/or 3’ most adjacent nucleotides;
6) 2’-O-methylations in the first and last 1-5 nucleotides and/or phosphorothiations in the first and last 1-5 internucleotide linkages,

particularly, the modification in the nucleotide opposite to the target adenosine, and/or one or two nucleotides most adjacent to the nucleotide opposite to the target adenosine is 2’-O-methylation and/or phosphorothiation linkage.

11. The dRNA of any one of claims 1-10, which does not comprise an ADAR-recruiting domain capable of forming an intramolecular stem loop structure for binding an ADAR enzyme.
12. A construct comprising or encoding a dRNA of any one of claims 1-11.
13. A method for editing a target RNA in a host cell, comprising introducing a dRNA of any one of claims 1-11 into host cells, particularly, introducing a plurality of the dRNAs each targeting a different target RNA, optionally, further introducing an inhibitor of ADAR3 and/or a stimulator of interferon to the host cell.
14. The method of claim13, further comprises introducing an exogenous ADAR to the host cell, particularly the ADAR is an ADAR1 comprising an E1008 mutation.
15. A construction, composition, cell, library or kit comprising the dRNAs of any one of claims 1-11.