WHAT IS CLAIMED IS:

1. An RNA sensor system comprising:

(a) a single-stranded RNA (ssRNA) sensor comprising a stop codon and a payload; optionally wherein the ssRNA sensor further comprises a normalizing gene; and

(b) an adenosine deaminase acting on RNA (ADAR) deaminase;

wherein the sensor is capable of binding to a ssRNA target to form a double-stranded RNA(dsRNA) duplex that becomes a substrate for the ADAR deaminase;

wherein the substrate comprises a mispairing within the stop codon;

wherein the mispairing is editable by the ADAR deaminase, which editing can effectively remove the stop codon so as to enable translation and expression of the payload.

2. A single-stranded RNA (ssRNA) sensor for expressing a protein in a target cell comprising:

(a) a first region comprising: (i) a nucleotide sequence configured to hybridize to a target RNA; and (ii) and a stem-loop sequence comprising one or more editable codons, and

(b) a second region comprising a sequence encoding said protein;

wherein said target RNA is present in said target cell.

3. The ssRNA sensor of claim 2, wherein said one or more editable codons further comprise a stop codon.

4. The ssRNA sensor of claim 2, wherein said nucleotide sequence configured to hybridize to said target RNA in (i) comprises an amount of sequence complementarity sufficient to permit hybridization to said target RNA.

5. A method for expressing a protein in a target cell, the method comprising combining said target cell with a sensor RNA comprising:

(a) a first region comprising: (i) a nucleotide sequence configured to hybridize to a target RNA; and (ii) a stem-loop sequence comprising one or more editable codons, and

(b) a second region comprising a sequence encoding said protein;

wherein said target RNA is present in said target cell.

6. The method of claim 5, wherein said one or more editable codons further comprises a stop codon.

7. The method of claim 5, wherein said one or more editable codons further comprises a plurality of stop codons.

8. The method of claim 6, wherein said stop codon further comprises any one of 5′-UGA-3′, 5′-UAA-3′, or 5′-UAG-3′.

9. The method of claim 5, wherein said one or more editable codons further comprises a start codon.

10. The method of claim 9, wherein said stem-loop sequence further comprises a Kozak sequence operably linked to said start codon.

11. The method of claim 5, wherein said one or more editable codons further comprises a non-stop, non-start codon that is edited to become a start codon by said target cell.

12. The method of claim 11, wherein said stem-loop sequence further comprises a Kozak sequence operably linked to said non-stop, non-start codon.

13. The method of claim 11, wherein said non-stop, non-start codon further comprises 5′-AUA -3′.

14. The method of claim 5, wherein said nucleotide sequence configured to hybridize to said target RNA in (i) is configured to hybridize to a 3′ untranslated region (UTR) of said target RNA or to a 5′ UTR of said target RNA.

15. The method of claim 5, wherein said protein comprises a toxin, killing factor, a T-cell receptor, or a chimeric antigen receptor.

16. The method of claim 5, wherein said protein comprises a fluorescent protein, a genomic modification protein, a transcription factor, an antigen, a therapeutic protein, or an enzyme.

17. The method of claim 5, wherein said combining said target cell with said sensor RNA comprises combining said target cell with a lipid nanoparticle comprising said sensor RNA.

18. The method of claim 5, wherein said combining said target cell with said sensor RNA comprises combining the target cell with an adeno-associated virus (AAV) encoding said sensor RNA.

19. The method of claim 5, wherein said target cell comprises an adenosine deaminase acting on RNA (ADAR) protein or a coding sequence encoding thereof.

20. The method of claim 5, wherein said target RNA is an mRNA, a long non-coding RNA (lncRNA), a transfer RNA (tRNA), a ribosomal RNA (rRNA), a microRNA (miRNA), or a small nucleolar RNA (snoRNA).

21. The method of claim 5, wherein said nucleotide sequence that is configured to hybridize to said target RNA in (i) and said stem-loop sequence comprising one or more editable codons in (ii) are non-overlapping.

22. The method of claim 5, wherein said one or more editable codons are in a stem sequence of said stem-loop sequence.

23. The method of claim 5, wherein said one or more editable codons comprise at least one base that is mismatched with a sequence within the stem-loop opposite said one or more editable codons.

24. The method of claim 5, wherein said protein is in frame with said one or more editable codons.

25. The method of claim 5, wherein said nucleotide sequence configured to hybridize to said target RNA in (i) comprises an amount of sequence complementarity sufficient to permit hybridization to said target RNA.

26. The method of claim 5, wherein said nucleotide sequence configured to hybridize to said target RNA in (i) comprises at least 60% complementarity to said target RNA.

27. The method of claim 5, wherein a stem of said stem-loop is at least 12 base pairs in length.

28. The method of claim 5, wherein said target RNA comprises an encoded gene fusion.

29. The method of claim 5, wherein said nucleotide sequence that is configured to hybridize to said target RNA in (i) is configured to hybridize to two or more non-contiguous sequences within said target RNA.

30. Use of a sensor RNA in the manufacture of a medicament for expressing a protein in a target cell, wherein said target cell is to be combined with said sensor RNA, wherein said sensor RNA is to be administered to a patient, wherein said sensor RNA comprises:

(a) a first region comprising: (i) a nucleotide sequence configured to hybridize to a target RNA; and (ii) and a stem-loop sequence comprising one or more editable codons, and

(b) a second region comprising a sequence encoding said protein;

wherein said target RNA is present in said target cell.