

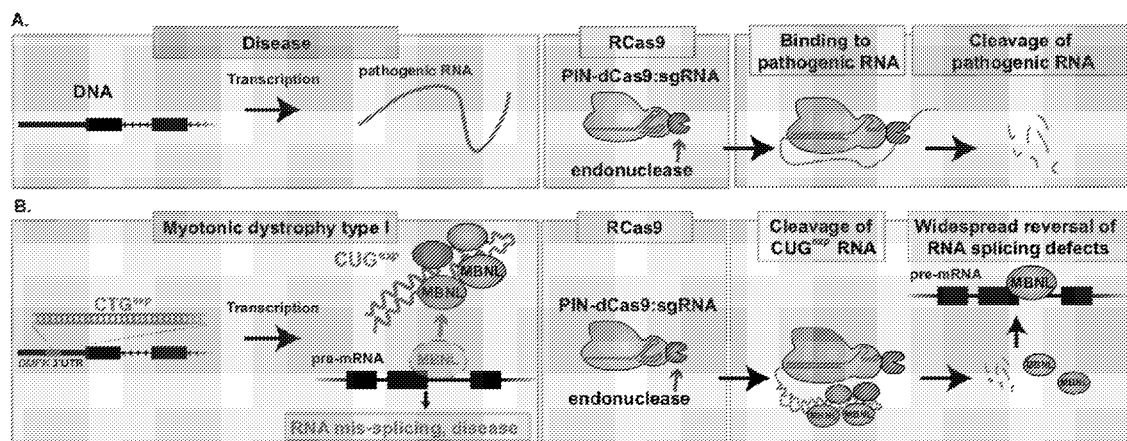


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(54) Title: RNA-TARGETING FUSION PROTEIN COMPOSITIONS AND METHODS FOR USE

FIGURE 1



(57) Abstract: Disclosed are compositions comprising: (a) a sequence comprising a guide RNA (gRNA) that specifically binds a target sequence within an RNA molecule and (b) a sequence encoding a fusion protein, the sequence comprising a sequence encoding a first RNA-binding polypeptide and a sequence encoding a second RNA-binding polypeptide, wherein neither the first RNA-binding polypeptide nor the second RNA-binding polypeptide comprises a significant DNA-nuclease activity, wherein the first RNA-binding polypeptide and the second RNA-binding polypeptide are not identical, and wherein the second RNA-binding polypeptide comprises an RNA-nuclease activity. Methods of making and methods of using compositions of the disclosure are also provided. For example, compositions of the disclosure may be used in the treatment of a disease or disorder in a subject. Exemplary disease or disorders of the disclosure include genetic and epigenetic diseases or disorders.



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RNA-TARGETING FUSION PROTEIN COMPOSITIONS AND METHODS FOR USE**FIELD OF THE DISCLOSURE**

[01] The disclosure is directed to molecular biology, and more, specifically, to compositions and methods for modifying expression and activity of RNA molecules.

RELATED APPLICATIONS

[02] This application claims priority to U.S. Patent Application No. 62/682,271, filed June 8, 2018, the contents of which are herein incorporated by reference in their entirety. The contents of U.S. Patent Application No. 62/682,276, filed June 8, 2018, are herein incorporated by reference in their entirety.

INCORPORATION OF SEQUENCE LISTING

[03] The contents of the text file named "LOCN_002_001WO_SeqList_ST25", which was created on June 6, 2019 and is 773 KB in size, are hereby incorporated by reference in their entirety.

BACKGROUND

[04] There has been a long-felt but unmet need in the art for a method of specifically binding target RNA molecules for modification of expression or activity of the RNA molecule or a protein encoded by the RNA molecule. The disclosure provides compositions and methods for specifically targeting RNA molecules in sequence-specific manner that further precludes modification of DNA sequences.

SUMMARY

[05] The disclosure provides a composition comprising (a) a sequence comprising a guide RNA (gRNA) that specifically binds a target sequence within an RNA molecule and (b) a sequence encoding a fusion protein, the sequence comprising a sequence encoding a first RNA-binding polypeptide and a sequence encoding a second RNA-binding polypeptide, wherein

neither the first RNA-binding polypeptide nor the second RNA-binding polypeptide comprises a significant DNA-nuclease activity, wherein the first RNA-binding polypeptide and the second RNA-binding polypeptide are not identical, and wherein the second RNA-binding polypeptide comprises an RNA-nuclease activity wherein the first RNA-binding polypeptide and the second RNA-binding polypeptide are not identical, and wherein the second RNA-binding polypeptide comprises an RNA-nuclease activity.

[006] The disclosure also provides a composition comprising a sequence encoding an RNA-guided target RNA-binding fusion protein comprising (a) a sequence encoding a first RNA-binding polypeptide or portion thereof; and (b) a sequence encoding a second RNA-binding polypeptide, wherein the first RNA-binding polypeptide binds a target RNA guided by a gRNA sequence, and wherein the second RNA-binding polypeptide comprises RNA-nuclease activity.

[007] The disclosure additionally provides a composition comprising a sequence encoding a target RNA-binding fusion protein comprising (a) a sequence encoding a first RNA-binding polypeptide or portion thereof; and (b) a sequence encoding a second RNA-binding polypeptide, wherein the first RNA-binding polypeptide binds a target RNA without a gRNA sequence, and wherein the second RNA-binding polypeptide comprises RNA-nuclease activity.

[008] In some embodiments of the compositions of the disclosure, the target sequence comprises at least one repeated sequence.

[009] In some embodiments of the compositions of the disclosure, the sequence comprising the gRNA further comprises a sequence encoding a promoter capable of expressing the gRNA in a eukaryotic cell.

[010] In some embodiments of the compositions of the disclosure, the eukaryotic cell is an animal cell. In some embodiments, the animal cell is a mammalian cell. In some embodiments, the animal cell is a human cell.

[011] In some embodiments of the compositions of the disclosure, the promoter is a constitutively active promoter. In some embodiments, the promoter sequence is isolated or derived from a promoter capable of driving expression of an RNA polymerase. In some embodiments, the promoter sequence is isolated or derived from a U6 promoter. In some embodiments, the promoter is a sequence isolated or derived from a promoter capable of driving expression of a transfer RNA (tRNA). In some embodiments, the promoter is isolated or derived

from an alanine tRNA promoter, an arginine tRNA promoter, an asparagine tRNA promoter, an aspartic acid tRNA promoter, a cysteine tRNA promoter, a glutamine tRNA promoter, a glutamic acid tRNA promoter, a glycine tRNA promoter, a histidine tRNA promoter, an isoleucine tRNA promoter, a leucine tRNA promoter, a lysine tRNA promoter, a methionine tRNA promoter, a phenylalanine tRNA promoter, a proline tRNA promoter, a serine tRNA promoter, a threonine tRNA promoter, a tryptophan tRNA promoter, a tyrosine tRNA promoter, or a valine tRNA promoter. In some embodiments, the promoter is isolated or derived from a valine tRNA promoter.

[012] In some embodiments of the compositions of the disclosure, the sequence comprising the gRNA further comprises a spacer sequence that specifically binds to the target RNA sequence. In some embodiments, the spacer sequence has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 87%, 90%, 95%, 97%, 99% or any percentage in between of complementarity to the target RNA sequence. In some embodiments, the spacer sequence has 100% complementarity to the target RNA sequence. In some embodiments, the spacer sequence comprises or consists of 20 nucleotides. In some embodiments, the spacer sequence comprises or consists of 21 nucleotides. In some embodiments, the spacer sequence comprises or consists of the sequence UGGAGCGAGCAUCCCCAAA (SEQ ID NO: 1), GUUUGGGGGAUGCUCGCUCCA (SEQ ID NO: 2), CCCUCACUGCUGGGGAGUCC (SEQ ID NO: 3), GGACUCCCCAGCAGUGAGGG (SEQ ID NO: 4), GCAACUGGAUCAAUUUGCUG (SEQ ID NO: 5), GCAGCAAUUGAUCCAGUUGC (SEQ ID NO: 6), GCAUUCUUAUCUGGUCAGUGC (SEQ ID NO: 7), GCACUGACCAGAUAAAGAAUG (SEQ ID NO: 8), GAGCAGCAGCAGCAGCAGCAG (SEQ ID NO: 9), GCAGGCAGGCAGGCAGGCAGG (SEQ ID NO: 10), GCCCCGGCCCCGGCCCCGGC (SEQ ID NO: 11), or GCTGCTGCTGCTGCTGCTGC (SEQ ID NO: 12), GGGGCCGGGGCCGGGGCCGG (SEQ ID NO: 74), GGGCCGGGGCCGGGGCCGGG (SEQ ID NO: 75), GGCCGGGGCCGGGGCCGGGG (SEQ ID NO: 76), GCCGGGGCCGGGGCCGGGGC (SEQ ID NO: 77), CCGGGGCCGGGGCCGGGGCC (SEQ ID NO: 78), or CGGGGCCGGGGCCGGGGCCG (SEQ ID NO: 79).

[013] In some embodiments of the compositions of the disclosure, the sequence comprising the gRNA further comprises a spacer sequence that specifically binds to the target RNA

sequence. In some embodiments, the spacer sequence has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 87%, 90%, 95%, 97%, 99% or any percentage in between of complementarity to the target RNA sequence.

[014] In some embodiments, the spacer sequence has 100% complementarity to the target RNA sequence. In some embodiments, the spacer sequence comprises or consists of 20 nucleotides. In some embodiments, the spacer sequence comprises or consists of 21 nucleotides. In some embodiments, the spacer sequence comprises or consists of the sequence GUGAUAAGUGGAAUGCCAUG (SEQ ID NO: 14), CUGGUGAACUCCGAUAGUG (SEQ ID NO: 15), or GAGATATAGCCTGGTGGTTC (SEQ ID NO: 16).

[015] In some embodiments of the compositions of the disclosure, the sequence comprising the gRNA further comprises a spacer sequence that specifically binds to the target RNA sequence. In some embodiments, the spacer sequence has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 87%, 90%, 95%, 97%, 99% or any percentage in between of complementarity to the target RNA sequence. In some embodiments, the spacer sequence has 100% complementarity to the target RNA sequence. In some embodiments, the spacer sequence comprises or consists of 20 nucleotides. In some embodiments, the spacer sequence comprises or consists of 21 nucleotides. In some embodiments, the spacer sequence comprises or consists of a sequence comprising at least 1, 2, 3, 4, 5, 6, or 7 repeats of the sequence CUG (SEQ ID NO: 18), CCUG (SEQ ID NO: 19), CAG (SEQ ID NO: 80), GGGGCC (SEQ ID NO: 81) or any combination thereof.

[016] In some embodiments of the compositions of the disclosure, the sequence comprising the gRNA further comprises a scaffold sequence that specifically binds to the first RNA binding protein. In some embodiments, the scaffold sequence comprises a stem-loop structure. In some embodiments, the scaffold sequence comprises or consists of 90 nucleotides. In some embodiments, the scaffold sequence comprises or consists of 93 nucleotides. In some embodiments, the scaffold sequence comprises or consists of the sequence GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUU AUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUUUU (SEQ ID NO: 13). In some embodiments, the scaffold sequence comprises or consists of the sequence GGACAGCAUAGCAAGUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUU (SEQ ID NO: 17). In some embodiments, the scaffold

sequence comprises or consists of the sequence

GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUU
AUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 82) or
GUUUUAGAGCUAGAAAUAGCAAGUUAAAUAAGGCUAGUCCGUUAUCAACUUGA
AAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 83).

[017] In some embodiments of the compositions of the disclosure, the gRNA does not bind or does not selectively bind to a second sequence within the RNA molecule.

[018] In some embodiments of the compositions of the disclosure, an RNA genome or an RNA transcriptome comprises the RNA molecule.

[019] In some embodiments of the compositions of the disclosure, the first RNA binding protein comprises a CRISPR-Cas protein. In some embodiments, the CRISPR-Cas protein is a Type II CRISPR-Cas protein. In some embodiments, the first RNA binding protein comprises a Cas9 polypeptide or an RNA-binding portion thereof. In some embodiments, the CRISPR-Cas protein comprises a native RNA nuclease activity. In some embodiments, the native RNA nuclease activity is reduced or inhibited. In some embodiments, the native RNA nuclease activity is increased or induced. In some embodiments, the CRISPR-Cas protein comprises a native DNA nuclease activity and the native DNA nuclease activity is inhibited. In some embodiments, the CRISPR-Cas protein comprises a mutation. In some embodiments, a nuclease domain of the CRISPR-Cas protein comprises the mutation. In some embodiments, the mutation occurs in a nucleic acid encoding the CRISPR-Cas protein. In some embodiments, the mutation occurs in an amino acid encoding the CRISPR-Cas protein. In some embodiments, the mutation comprises a substitution, an insertion, a deletion, a frameshift, an inversion, or a transposition. In some embodiments, the mutation comprises a deletion of a nuclease domain, a binding site within the nuclease domain, an active site within the nuclease domain, or at least one essential amino acid residue within the nuclease domain.

[020] In some embodiments of the compositions of the disclosure, the first RNA binding protein comprises a CRISPR-Cas protein. In some embodiments, the CRISPR-Cas protein is a Type V CRISPR-Cas protein. In some embodiments, the first RNA binding protein comprises a Cpf1 polypeptide or an RNA-binding portion thereof. In some embodiments, the CRISPR-Cas protein comprises a native RNA nuclease activity. In some embodiments, the native RNA

nuclease activity is reduced or inhibited. In some embodiments, the native RNA nuclease activity is increased or induced. In some embodiments, the CRISPR-Cas protein comprises a native DNA nuclease activity and the native DNA nuclease activity is inhibited. In some embodiments, the CRISPR-Cas protein comprises a mutation. In some embodiments, a nuclease domain of the CRISPR-Cas protein comprises the mutation. In some embodiments, the mutation occurs in a nucleic acid encoding the CRISPR-Cas protein. In some embodiments, the mutation occurs in an amino acid encoding the CRISPR-Cas protein. In some embodiments, the mutation comprises a substitution, an insertion, a deletion, a frameshift, an inversion, or a transposition. In some embodiments, the mutation comprises a deletion of a nuclease domain, a binding site within the nuclease domain, an active site within the nuclease domain, or at least one essential amino acid residue within the nuclease domain.

[021] In some embodiments of the compositions of the disclosure, the first RNA binding protein comprises a CRISPR-Cas protein. In some embodiments, the CRISPR-Cas protein is a Type VI CRISPR-Cas protein. In some embodiments, the first RNA binding protein comprises a Cas13 polypeptide or an RNA-binding portion thereof. In some embodiments, the first RNA binding protein comprises a CasRx/Cas13d polypeptide or an RNA-binding portion thereof. In some embodiments, the CRISPR-Cas protein comprises a native RNA nuclease activity. In some embodiments, the native RNA nuclease activity is reduced or inhibited. In some embodiments, the native RNA nuclease activity is increased or induced. In some embodiments, the CRISPR-Cas protein comprises a native DNA nuclease activity and the native DNA nuclease activity is inhibited. In some embodiments, the CRISPR-Cas protein comprises a mutation. In some embodiments, a nuclease domain of the CRISPR-Cas protein comprises the mutation. In some embodiments, the mutation occurs in a nucleic acid encoding the CRISPR-Cas protein. In some embodiments, the mutation occurs in an amino acid encoding the CRISPR-Cas protein. In some embodiments, the mutation comprises a substitution, an insertion, a deletion, a frameshift, an inversion, or a transposition. In some embodiments, the mutation comprises a deletion of a nuclease domain, a binding site within the nuclease domain, an active site within the nuclease domain, or at least one essential amino acid residue within the nuclease domain.

[022] In some embodiments of the compositions of the disclosure, the first RNA binding protein comprises a Pumilio and FBF (PUF) protein or an RNA binding portion thereof. In some

embodiments, the first RNA binding protein comprises a Pumilio-based assembly (PUMBY) protein or an RNA binding portion thereof.

[023] In some embodiments of the compositions of the disclosure, the first RNA binding protein does not require multimerization for RNA-binding activity. In some embodiments, the first RNA binding protein is not a monomer of a multimer complex. In some embodiments, a multimer protein complex does not comprise the first RNA binding protein.

[024] In some embodiments of the compositions of the disclosure, the first RNA binding protein selectively binds to a target sequence within the RNA molecule. In some embodiments, the first RNA binding protein does not comprise an affinity for a second sequence within the RNA molecule. In some embodiments, the first RNA binding protein does not comprise a high affinity for or selectively bind a second sequence within the RNA molecule.

[025] In some embodiments of the compositions of the disclosure, an RNA genome or an RNA transcriptome comprises the RNA molecule.

[026] In some embodiments of the compositions of the disclosure, the first RNA binding protein comprises between 2 and 1300 amino acids, inclusive of the endpoints.

[027] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein further comprises a sequence encoding a nuclear localization signal (NLS), a nuclear export signal (NES) or tag. In some embodiments, the sequence encoding a nuclear localization signal (NLS) is positioned 3' to the sequence encoding the first RNA binding protein. In some embodiments, the first RNA binding protein comprises an NLS at a C-terminus of the protein.

[028] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein further comprises a first sequence encoding a first NLS and a second sequence encoding a second NLS. In some embodiments, the sequence encoding the first NLS or the second NLS is positioned 3' to the sequence encoding the first RNA binding protein. In some embodiments, the first RNA binding protein comprises the first NLS or the second NLS at a C-terminus of the protein.

[029] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a nuclease domain. In some embodiments, the second RNA

binding protein binds RNA in a manner in which it associates with RNA. In some embodiments, the second RNA binding protein associates with RNA in a manner in which it cleaves RNA.

[030] In some embodiments of the compositions of the disclosure, the sequence encoding the second RNA binding protein comprises or consists of an RNase. In some embodiments, the second RNA binding protein comprises or consists of an RNase1. In some embodiments, the RNase1 comprises or consists of SEQ ID NO: 20. In some embodiments, the second RNA binding protein comprises or consists of an RNase4. In some embodiments, the RNase4 comprises or consists of SEQ ID NO: 21. In some embodiments, the second RNA binding protein comprises or consists of an RNase6. In some embodiments, the RNase6 comprises or consists of SEQ ID NO: 22. In some embodiments, the second RNA binding protein comprises or consists of an RNase7. In some embodiments, the RNase7 comprises or consists of SEQ ID NO: 23. In some embodiments, the second RNA binding protein comprises or consists of an RNase8. In some embodiments, the RNase8 protein comprises or consists of SEQ ID NO: 24. In some embodiments, the second RNA binding protein comprises or consists of an RNase2. In some embodiments, the RNase2 protein comprises or consists of SEQ ID NO: 25. In some embodiments, the second RNA binding protein comprises or consists of an RNase6PL. In some embodiments, the RNase6PL protein comprises or consists of SEQ ID NO: 26. In some embodiments, the second RNA binding protein comprises or consists of an RNaseL. In some embodiments the RNaseL protein comprises or consists of SEQ ID NO: 27. In some embodiments, the second RNA binding protein comprises or consists of an RNaseT2. In some embodiments, the RNaseT2 protein comprises or consists of SEQ ID NO: 28. In some embodiments, the second RNA binding protein comprises or consists of an RNase11. In some embodiments, the RNase11 protein comprises or consists of SEQ ID NO: 29. In some embodiments, the second RNA binding protein comprises or consists of an RNaseT2-like. In some embodiments, the RNaseT2-like protein comprises or consists of SEQ ID NO: 30.

[031] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a mutated RNase. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R)) polypeptide. In some embodiments, the Rnase1 (K41R) polypeptide comprises or consists of SEQ ID NO: 116. In some embodiments, the second RNA binding protein comprises or consists of a mutated

Rnase1 (Rnase1(K41R, D121E)) polypeptide. In some embodiments, the Rnase1 (Rnase1(K41R, D121E)) polypeptide comprises or consists of SEQ ID NO: 66. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R, D121E, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(K41R, D121E, H119N)) polypeptide comprises or consists of SEQ ID NO: 118. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(H119N)) polypeptide comprises or consists SEQ ID NO: 119. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide comprises or consists of SEQ ID NO: 120. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N, K41R, D121E)) polypeptide comprises or consists of SEQ ID NO: 121. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D)) polypeptide comprises or consists of SEQ ID NO: 122.

[032] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a NOB1 polypeptide. In some embodiments, the NOB1 polypeptide comprises or consists of SEQ ID NO: 31.

[033] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an endonuclease. In some embodiments, the second RNA binding protein comprises or consists of an endonuclease V (ENDOV). In some embodiments, the ENDOV protein comprises or consists of SEQ ID NO: 32. In some embodiments, the second RNA binding protein comprises or consists of an endonuclease G (ENDOG). In some embodiments, the ENDOG protein comprises or consists of SEQ ID NO: 33. In some embodiments, the second RNA binding protein comprises or consists of an endonuclease D1 (ENDOD1). In some embodiments, the ENDOD1 protein comprises or consists of SEQ ID NO:

34. In some embodiments, the second RNA binding protein comprises or consists of a Human flap endonuclease-1 (hFEN1). In some embodiments, the hFEN1 protein comprises or consists of SEQ ID NO: 35. In some embodiments, the second RNA binding protein comprises or consists of a DNA repair endonuclease XPF (ERCC4) polypeptide. In some embodiments, the ERCC4 protein comprises or consists of SEQ ID NO: 64.

[034] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an Endonuclease III-like protein 1 (NTHL) polypeptide. In some embodiments, the NTHL polypeptide comprises or consists of SEQ ID NO: 123.

[035] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a human Schlafen 14 (hSLFN14) polypeptide. In some embodiments, the hSLFN14 polypeptide comprises or consists of SEQ ID NO: 36.

[036] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a human beta-lactamase-like protein 2 (hLACTB2) polypeptide. In some embodiments, the hLACTB2 polypeptide comprises or consists of SEQ ID NO: 37.

[037] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an apurinic/aprimidinic (AP) endodeoxyribonuclease (APEX) polypeptide. In some embodiments, the second RNA binding protein comprises or consists of an apurinic/aprimidinic (AP) endodeoxyribonuclease (APEX2) polypeptide. In some embodiments, the APEX2 polypeptide comprises or consists of SEQ ID NO: 38. In some embodiments, the APEX2 polypeptide comprises or consists of SEQ ID NO: 39. In some embodiments, the second RNA binding protein comprises or consists of an apurinic or apyrimidinic site lyase (APEX1) polypeptide. In some embodiments, the APEX1 polypeptide comprises or consists of SEQ ID NO: 125.

[038] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an angiogenin (ANG) polypeptide. In some embodiments, the ANG polypeptide comprises or consists SEQ ID NO: 40.

[039] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a heat responsive protein 12 (HRSP12) polypeptide. In some embodiments, the HRSP12 polypeptide comprises or consists of SEQ ID NO: 41.

[040] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Zinc Finger CCCH-Type Containing 12A (ZC3H12A) polypeptide. In some embodiments, the ZC3H12A polypeptide comprises or consists of SEQ ID NO: 42. In some embodiments, the ZC3H12A polypeptide comprises or consists of SEQ ID NO: 43.

[041] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Reactive Intermediate Imine Deaminase A (RIDA) polypeptide. In some embodiments, the RIDA polypeptide comprises or consists of SEQ ID NO: 44.

[042] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Phospholipase D Family Member 6 (PDL6) polypeptide. In some embodiments, the PDL6 polypeptide comprises or consists of SEQ ID NO: 126.

[043] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a mitochondrial ribonuclease P catalytic subunit (KIAA0391) polypeptide. In some embodiments, the KIAA0391 polypeptide comprises or consists of SEQ ID NO: 127.

[044] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an argonaute 2 (AGO2) polypeptide. In some embodiments of the compositions of the disclosure, the AGO2 polypeptide comprises or consists of SEQ ID NO: 128.

[045] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a mitochondrial nuclease EXOG (EXOG) polypeptide. In some embodiments, the EXOG polypeptide comprises or consists of SEQ ID NO: 129.

[046] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Zinc Finger CCCH-Type Containing 12D (ZC3H12D) polypeptide. In some embodiments, the ZC3H12D polypeptide comprises or consists of SEQ ID NO: 130.

[047] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an endoplasmic reticulum to nucleus signaling 2 (ERN2)

polypeptide. In some embodiments, the ERN2 polypeptide comprises or consists of SEQ ID NO: 131.

[048] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a pelota mRNA surveillance and ribosome rescue factor (PELO) polypeptide. In some embodiments, the PELO polypeptide comprises or consists of SEQ ID NO: 132.

[049] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a YBEY metalloproteinase (YBEY) polypeptide. In some embodiments, the YBEY polypeptide comprises or consists of SEQ ID NO: 133.

[050] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a cleavage and polyadenylation specific factor 4 like (CPSF4L) polypeptide. In some embodiments, the CPSF4L polypeptide comprises or consists of SEQ ID NO: 134.

[051] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an hCG_2002731 polypeptide. In some embodiments, the hCG_2002731 comprises or consists of SEQ ID NO: 135. In some embodiments, the hCG_2002731 polypeptide comprises or consists of SEQ ID NO: 136.

[052] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an Excision Repair Cross-Complementation Group 1 (ERCC1) polypeptide. In some embodiments, the ERCC1 polypeptide comprises or consists of SEQ ID NO: 137.

[053] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a ras-related C3 botulinum toxin substrate 1 isoform (RAC1) polypeptide. In some embodiments, the RAC1 polypeptide comprises or consists of SEQ ID NO: 138.

[054] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Ribonuclease A A1 (RAA1) polypeptide. In some embodiments, the RAA1 polypeptide comprises or consists of SEQ ID NO: 139.

[055] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Ras Related Protein (RAB1) polypeptide. In some embodiments, the RAB1 polypeptide comprises or consists of SEQ ID NO: 140.

[056] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a DNA Replication Helicase/Nuclease 2 (DNA2) polypeptide. In some embodiments, the DNA2 polypeptide comprises or consists of SEQ ID NO: 141.

[057] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a FLJ35220 polypeptide. In some embodiments, the FLJ35220 polypeptide comprises or consists of SEQ ID NO: 142.

[058] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a FLJ13173 polypeptide. In some embodiments, the FLJ13173 polypeptide comprises or consists of SEQ ID NO: 143.

[059] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein (TENM) polypeptide. In some embodiments, the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein 1 (TENM1) polypeptide. In some embodiments, the TENM1 polypeptide comprises or consists of SEQ ID NO: 144. In some embodiments, the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein 2 (TENM2) polypeptide. In some embodiments, the TENM2 polypeptide comprises or consists of SEQ ID NO: 145.

[060] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Ribonuclease Kappa (RNaseK) polypeptide. In some embodiments, the RNaseK polypeptide comprises or consists of SEQ ID NO: 204.

[061] In some embodiments, the fusion proteins of the disclosure are used in methods for treating a subject in need thereof, the methods comprising contacting a target RNA with a fusion protein or the sequence encoding the fusion protein.

BRIEF DESCRIPTION OF THE DRAWINGS

[062] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[063] Figure 1A-B is a schematic diagram of an exemplary embodiment of a composition of the disclosure. (A) An RNA-targeting Cas9 system fused to an endonuclease targets and cleaves a disease-causing RNA. (B) Depicts an application of (A) in the context of myotonic dystrophy type 1, wherein an RNA-targeting Cas9 system fused to an endonuclease targets and cleaves a repetitive RNA composed of repeating CUG units. In the absence of the RNA-targeting Cas9 system, the repetitive RNA composed of repeating CUG units binds to a splicing factor MBLN and causes pathology via dysfunctional RNA splicing. Cleavage of this repetitive RNA ameliorates disease.

[064] Figure 2 is a schematic diagram depicting an exemplary modular therapeutic platform for treating genetic disease by targeting RNA molecules.

[065] Figure 3A-B is a pair of schematic diagrams depicting (A) a “high expression” control system (also referred to as “pos control”) comprising a two plasmid system comprising a cytomegalovirus promoter driving expression of the RNA endonuclease/Cas9 fusion and (B) a “low expression” control system (also referred to as “P13”) comprising a single plasmid system comprising a lower-expression promoter (pEFS) driving expression of the RNA endonuclease/Cas9 fusion.

[066] Figure 4A is a pair of schematic diagrams depicting an exemplary RNA Endonuclease-*C. jejuni* Cas9 fusion protein (left) and a vector comprising an exemplary RNA Endonuclease-*S. pyogenes* Cas9 fusion protein (right)

[067] Figure 4B is a graph depicting the ability of a variety of fusion proteins comprising either *C. jejuni* Cas9 or *S. pyogenes* Cas9, as shown in Figure 4A, to cleave repetitive RNA molecules.

[068] Figure 5A is a pair of schematic diagrams depicting an exemplary RNA Endonuclease-*C. jejuni* Cas9 fusion protein (left) and a vector comprising an exemplary RNA Endonuclease-*S. pyogenes* Cas9 fusion protein (right)

[069] Figure 5B is a graph depicting the ability of a variety of fusion proteins comprising either *C. jejuni* Cas9 or *S. pyogenes* Cas9, as shown in Figure 5A, to cleave mRNA molecules encoding a luciferase protein.

[070] Figure 6 is a table providing a key to the endonucleases shown in Figures 4B, 5B, and 9.

[071] Figure 7A is a schematic diagram depicting an exemplary RNA Endonuclease-*C. jejuni* Cas9 fusion protein.

[072] Figure 7B is a graph depicting changes in expression levels of Zika NS5 in the presence of both E43 and E67 CjeCas9-endonuclease fusions with sgRNAs containing the various NS5-targeting spacer sequences as indicated in Table 2. Zika NS5 expression is displayed as fold change relative to the endonuclease loaded with an sgRNA containing a control (Lambda) spacer sequence.

[073] Figure 8A is a fluorescence microscopy image of cells transfected with CjeCas9-endonuclease fusions loaded with an sgRNA containing a Zika NS5-targeting spacer sequence.

[074] Figure 8B is a graph depicting changes of expression of Zika NS5 in the presence of CjeCas9-endonuclease fusions loaded with the appropriate Zika NS5-targeting sgRNA as compared to a CjeCas9-endonuclease fusions loaded with a non-Zika NS5 targeting sgRNA.

[075] Figure 9 is a graph depicting the cleavage efficiencies of a variety of exemplary fusion proteins (SpyCas9 fused to the annotated endonuclease).

DETAILED DESCRIPTION

[076] The disclosure provides an RNA-guided fusion protein that selectively binds and, optionally, cleaves RNA molecules. The disclosure provides vectors, compositions and cells comprising the RNA-guided fusion protein. The disclosure provides methods of using the RNA-guided fusion protein, vectors, compositions and cells of the disclosure to treat a disease or disorder.

Guide RNA

[077] The terms guide RNA (gRNA) and single guide RNA (sgRNA) are used interchangeably throughout the disclosure.

[078] Guide RNAs (gRNAs) of the disclosure may comprise of a spacer sequence and a scaffolding sequence. In some embodiments, a guide RNA is a single guide RNA (sgRNA)

comprising a contiguous spacer sequence and scaffolding sequence. In some embodiments, the spacer sequence and the scaffolding sequence are not contiguous. In some embodiments, a scaffold sequence comprises a “direct repeat” (DR) sequence. DR sequences refer to the repetitive sequences in the CRISPR locus (naturally-occurring in a bacterial genome or plasmid) that are interspersed with the spacer sequences. It is well known that one would be able to infer the DR sequence of a corresponding Cas protein if the sequence of the associated CRISPR locus is known. In some embodiments, a sequence encoding a guide RNA or single guide RNA of the disclosure comprises or consists of a spacer sequence and a scaffolding sequence, that are separated by a linker sequence. In some embodiments, the linker sequence may comprise or consist of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or any number of nucleotides in between. In some embodiments, the linker sequence may comprise at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50 or any number of nucleotides in between.

[079] Guide RNAs (gRNAs) of the disclosure may comprise non-naturally occurring nucleotides. In some embodiments, a guide RNA of the disclosure or a sequence encoding the guide RNA comprises or consists of modified or synthetic RNA nucleotides. Exemplary modified RNA nucleotides include, but are not limited to, pseudouridine (Ψ), dihydrouridine (D), inosine (I), and 7-methylguanosine (m7G), hypoxanthine, xanthine, xanthosine, 7-methylguanine, 5, 6-Dihydrouracil, 5-methylcytosine, 5-methylcytidine, 5-hydroxymethylcytosine, isoguanine, and isocytosine.

[080] Guide RNAs (gRNAs) of the disclosure may bind modified RNA within a target sequence. Within a target sequence, guide RNAs (gRNAs) of the disclosure may bind modified RNA. Exemplary epigenetically or post-transcriptionally modified RNA include, but are not limited to, 2'-O-Methylation (2'-OMe) (2'-O-methylation occurs on the oxygen of the free 2'-OH of the ribose moiety), N6-methyladenosine (m6A), and 5-methylcytosine (m5C).

[081] In some embodiments of the compositions of the disclosure, a guide RNA of the disclosure comprises at least one sequence encoding a non-coding C/D box small nucleolar RNA (snoRNA) sequence. In some embodiments, the snoRNA sequence comprises at least one sequence that is complementary to the target RNA, wherein the target sequence of the RNA molecule comprises at least one 2'-OMe. In some embodiments, the snoRNA sequence comprises at least one sequence that is complementary to the target RNA, wherein the at least

one sequence that is complementary to the target RNA comprises a box C motif (RUGAUGA) and a box D motif (CUGA).

[082] Spacer sequences of the disclosure bind to the target sequence of an RNA molecule. Spacer sequences of the disclosure may comprise a CRISPR RNA (crRNA). Spacer sequences of the disclosure comprise or consist of a sequence having sufficient complementarity to a target sequence of an RNA molecule to bind selectively to the target sequence. Upon binding to a target sequence of an RNA molecule, the spacer sequence may guide one or more of a scaffolding sequence and a fusion protein to the RNA molecule. In some embodiments, a sequence having sufficient complementarity to a target sequence of an RNA molecule to bind selectively to the target sequence has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96, 97%, 98%, 99%, or any percentage identity in between to the target sequence. In some embodiments, a sequence having sufficient complementarity to a target sequence of an RNA molecule to bind selectively to the target sequence has 100% identity the target sequence.

[083] Scaffolding sequences of the disclosure bind the first RNA-binding polypeptide of the disclosure. Scaffolding sequences of the disclosure may comprise a trans acting RNA (tracrRNA). Scaffolding sequences of the disclosure comprise or consist of a sequence having sufficient complementarity to a target sequence of an RNA molecule to bind selectively to the target sequence. Upon binding to a target sequence of an RNA molecule, the scaffolding sequence may guide a fusion protein to the RNA molecule. In some embodiments, a sequence having sufficient complementarity to a target sequence of an RNA molecule to bind selectively to the target sequence has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96, 97%, 98%, 99%, or any percentage identity in between to the target sequence. In some embodiments, a sequence having sufficient complementarity to a target sequence of an RNA molecule to bind selectively to the target sequence has 100% identity the target sequence. Alternatively, or in addition, in some embodiments, scaffolding sequences of the disclosure comprise or consist of a sequence that binds to a first RNA binding protein or a second RNA binding protein of a fusion protein of the disclosure. In some embodiments, scaffolding sequences of the disclosure comprise a secondary structure or a tertiary structure. Exemplary secondary structures include, but are not limited to, a helix, a stem loop, a bulge, a tetraloop and a pseudoknot. Exemplary tertiary structures include, but are not limited to, an A-form of a helix,

a B-form of a helix, and a Z-form of a helix. Exemplary tertiary structures include, but are not limited to, a twisted or helicized stem loop. Exemplary tertiary structures include, but are not limited to, a twisted or helicized pseudoknot. In some embodiments, scaffolding sequences of the disclosure comprise at least one secondary structure or at least one tertiary structure. In some embodiments, scaffolding sequences of the disclosure comprise one or more secondary structure(s) or one or more tertiary structure(s).

[084] In some embodiments of the compositions of the disclosure, a guide RNA or a portion thereof selectively binds to a tetraloop motif in an RNA molecule of the disclosure. In some embodiments, a target sequence of an RNA molecule comprises a tetraloop motif. In some embodiments, the tetraloop motif is a “GRNA” motif comprising or consisting of one or more of the sequences of GAAA, GUGA, GCAA or GAGA.

[085] In some embodiments of the compositions of the disclosure, a guide RNA or a portion thereof that binds to a target sequence of an RNA molecule hybridizes to the target sequence of the RNA molecule. In some embodiments, a guide RNA or a portion thereof that binds to a first RNA binding protein or to a second RNA binding protein covalently binds to the first RNA binding protein or to the second RNA binding protein. In some embodiments, a guide RNA or a portion thereof that binds to a first RNA binding protein or to a second RNA binding protein non-covalently binds to the first RNA binding protein or to the second RNA binding protein.

[086] In some embodiments of the compositions of the disclosure, a guide RNA or a portion thereof comprises or consists of between 10 and 100 nucleotides, inclusive of the endpoints. In some embodiments, a spacer sequence of the disclosure comprises or consists of between 10 and 30 nucleotides, inclusive of the endpoints. In some embodiments, a spacer sequence of the disclosure comprises or consists of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 nucleotides. In some embodiments, the spacer sequence of the disclosure comprises or consists of 20 nucleotides. In some embodiments, the spacer sequence of the disclosure comprises or consists of 21 nucleotides. In some embodiments, a scaffold sequence of the disclosure comprises or consists of between 10 and 100 nucleotides, inclusive of the endpoints. In some embodiments, a scaffold sequence of the disclosure comprises or consists of 30, 35, 40, 45, 50, 55, 60, 65, 70, 76, 80, 87, 90, 95, 100 or any number of nucleotides in between. In some embodiments, the scaffold sequence of the disclosure comprises or consists of between 85 and

95 nucleotides, inclusive of the endpoints. In some embodiments, the scaffold sequence of the disclosure comprises or consists of 85 nucleotides. In some embodiments, the scaffold sequence of the disclosure comprises or consists of 90 nucleotides. In some embodiments, the scaffold sequence of the disclosure comprises or consists of 93 nucleotides.

[087] In some embodiments of the compositions of the disclosure, a guide RNA or a portion thereof does not comprise a nuclear localization sequence (NLS).

[088] In some embodiments of the compositions of the disclosure, a guide RNA or a portion thereof does not comprise a sequence complementary to a protospacer adjacent motif (PAM).

[089] Therapeutic or pharmaceutical compositions of the disclosure do not comprise a PAMmer oligonucleotide. In other embodiments, optionally, non-therapeutic or non-pharmaceutical compositions may comprise a PAMmer oligonucleotide. The term “PAMmer” refers to an oligonucleotide comprising a PAM sequence that is capable of interacting with a guide nucleotide sequence-programmable RNA binding protein. Non-limiting examples of PAMmers are described in O’Connell *et al. Nature* 516, pages 263–266 (2014), incorporated herein by reference. A PAM sequence refers to a protospacer adjacent motif comprising about 2 to about 10 nucleotides. PAM sequences are specific to the guide nucleotide sequence-programmable RNA binding protein with which they interact and are known in the art. For example, *Streptococcus pyogenes* PAM has the sequence 5’-NGG-3’, where “N” is any nucleobase followed by two guanine (“G”) nucleobases. Cas9 of *Francisella novicida* recognizes the canonical PAM sequence 5’-NGG-3’, but has been engineered to recognize the PAM 5’-YG-3’ (where “Y” is a pyrimidine), thus adding to the range of possible Cas9 targets. The Cpf1 nuclease of *Francisella novicida* recognizes the PAM 5’-TTTN-3’ or 5’-YTN-3’.

[090] In some embodiments of the compositions of the disclosure, a guide RNA or a portion thereof comprises a sequence complementary to a protospacer flanking sequence (PFS). In some embodiments, including those wherein a guide RNA or a portion thereof comprises a sequence complementary to a PFS, the first RNA binding protein may comprise a sequence isolated or derived from a Cas13 protein. In some embodiments, including those wherein a guide RNA or a portion thereof comprises a sequence complementary to a PFS, the first RNA binding protein may comprise a sequence encoding a Cas13 protein or an RNA-binding portion thereof. In some

embodiments, the guide RNA or a portion thereof does not comprise a sequence complementary to a PFS.

[091] In some embodiments of the compositions of the disclosure, guide RNA sequence of the disclosure comprises a promoter sequence to drive expression of the guide RNA. In some embodiments, a vector comprising a guide RNA sequence of the disclosure comprises a promoter sequence to drive expression of the guide RNA. In some embodiments, the promoter to drive expression of the guide RNA is a constitutive promoter. In some embodiments, the promoter sequence is an inducible promoter. In some embodiments, the promoter is a sequence is a tissue-specific and/or cell-type specific promoter. In some embodiments, the promoter is a hybrid or a recombinant promoter. In some embodiments, the promoter is a promoter capable of expressing the guide RNA in a mammalian cell. In some embodiments, the promoter is a promoter capable of expressing the guide RNA in a human cell. In some embodiments, the promoter is a promoter capable of expressing the guide RNA and restricting the guide RNA to the nucleus of the cell. In some embodiments, the promoter is a human RNA polymerase promoter or a sequence isolated or derived from a sequence encoding a human RNA polymerase promoter. In some embodiments, the promoter is a U6 promoter or a sequence isolated or derived from a sequence encoding a U6 promoter. In some embodiments, the promoter is a human tRNA promoter or a sequence isolated or derived from a sequence encoding a human tRNA promoter. In some embodiments, the promoter is a human valine tRNA promoter or a sequence isolated or derived from a sequence encoding a human valine tRNA promoter.

[092] In some embodiments of the compositions of the disclosure, a promoter to drive expression of the guide RNA further comprises a regulatory element. In some embodiments, a vector comprising a promoter sequence to drive expression of the guide RNA further comprises a regulatory element. In some embodiments, a regulatory element enhances expression of the guide RNA. Exemplary regulatory elements include, but are not limited to, an enhancer element, an intron, an exon, or a combination thereof.

[093] In some embodiments of the compositions of the disclosure, a vector of the disclosure comprises one or more of a sequence encoding a guide RNA, a promoter sequence to drive expression of the guide RNA and a sequence encoding a regulatory element. In some

embodiments of the compositions of the disclosure, the vector further comprises a sequence encoding a fusion protein of the disclosure.

Fusion Proteins

[094] Fusion proteins of the disclosure comprise a first RNA binding protein and a second RNA binding protein. In some embodiments, along a sequence encoding the fusion protein, the sequence encoding the first RNA binding protein is positioned 5' of the sequence encoding the second RNA binding protein. In some embodiments, along a sequence encoding the fusion protein, the sequence encoding the first RNA binding protein is positioned 3' of the sequence encoding the second RNA binding protein.

[095] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein capable of binding an RNA molecule. In some embodiments, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein capable of selectively binding an RNA molecule and not binding a DNA molecule, a mammalian DNA molecule or any DNA molecule. In some embodiments, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein capable of binding an RNA molecule and inducing a break in the RNA molecule. In some embodiments, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein capable of binding an RNA molecule, inducing a break in the RNA molecule, and not binding a DNA molecule, a mammalian DNA molecule or any DNA molecule. In some embodiments, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein capable of binding an RNA molecule, inducing a break in the RNA molecule, and neither binding nor inducing a break in a DNA molecule, a mammalian DNA molecule or any DNA molecule.

[096] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein with no DNA nuclease activity.

[097] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein having DNA nuclease activity, wherein the DNA nuclease activity does not induce a break in a DNA

molecule, a mammalian DNA molecule or any DNA molecule when a composition of the disclosure is contacted to an RNA molecule or introduced into a cell or into a subject of the disclosure.

[098] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a protein having DNA nuclease activity, wherein the DNA nuclease activity is inactivated and wherein the DNA nuclease activity does not induce a break in a DNA molecule, a mammalian DNA molecule or any DNA molecule when a composition of the disclosure is contacted to an RNA molecule or introduced into a cell or into a subject of the disclosure. In some embodiments, the sequence encoding the first RNA binding protein comprises a mutation that inactivates or decreases the DNA nuclease activity to a level at which the DNA nuclease activity does not induce a break in a DNA molecule, a mammalian DNA molecule or any DNA molecule when a composition of the disclosure is contacted to an RNA molecule or introduced into a cell or into a subject of the disclosure. In some embodiments, the sequence encoding the first RNA binding protein comprises a mutation that inactivates or decreases the DNA nuclease activity and the mutation comprises one or more of a substitution, inversion, transposition, insertion, deletion, or any combination thereof to a nucleic acid sequence or amino acid sequence encoding the first RNA binding protein or a nuclease domain thereof.

[099] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein of an RNA-guided fusion protein disclosed herein comprises a sequence isolated or derived from a CRISPR Cas protein. In some embodiments, the CRISPR Cas protein comprises a Type II CRISPR Cas protein. In some embodiments, the Type II CRISPR Cas protein comprises a Cas9 protein. Exemplary Cas9 proteins of the disclosure may be isolated or derived from any species, including, but not limited to, a bacteria or an archaea. Exemplary Cas9 proteins of the disclosure may be isolated or derived from any species, including, but not limited to, *Streptococcus pyogenes*, *Haloferax mediteranii*, *Mycobacterium tuberculosis*, *Francisella tularensis subsp. novicida*, *Pasteurella multocida*, *Neisseria meningitidis*, *Campylobacter jejune*, *Streptococcus thermophilus*, *Campylobacter lari* CF89-12, *Mycoplasma gallisepticum str. F*, *Nitratifactor salsuginis str. DSM 16511*, *Parvibaculum lavamentivorans*, *Roseburia intestinalis*, *Neisseria cinerea*, a *Gluconacetobacter diazotrophicus*,

an Azospirillum B510, a Sphaerochaeta globus str. Buddy, Flavobacterium columnare, Fluviicola taffensis, Bacteroides coprophilus, Mycoplasma mobile, Lactobacillus farciminis, Streptococcus pasteurianus, Lactobacillus johnsonii, Staphylococcus pseudintermedius, Filifactor alocis, Treponema denticola, Legionella pneumophila str. Paris, Sutterella wadsworthensis, Corynebacter diphtherias, Streptococcus aureus, and Francisella novicida.

[0100] Exemplary wild type *S. pyogenes* Cas9 proteins of the disclosure may comprise or consist of the amino acid sequence:

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1 MDKKYSIGLD IGTNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSGETAE
61 ATRLKRTARR RYTRRKNRIC YLQEIFSNEM AKVDDSFHR LEESFLVEED KKHERHPIFG
121 NIVDEVAYHE KYPTIYHLRK KLV DSTKAD LRLIYLALAH MIKFRGHFLI EGD LNPDNSD
181 VDKLFIQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN
241 LIALSLGLTP NFKSNFDLAE DAKLQLSKDT YDDDLNLLA QIGDQYADLF LAAKNLSDAI
301 LLSDILRVNT EITKAPLSAS MIKRYDEHHQ DLTKLLKALVR QQLPEKYKEI FFDQSKNGYA
361 GYIDGGASQE EFYKFIKPIL EKMDGTEELL VKLNREDLLR KQRTFDNGSI PHQIHLGELH
421 AILRRQEDFY PFLKDNREKI EKILTRIPY YVGPLARGNS RFAWMTRKSE ETITPWNFEE
481 VVDKGASAQS FIERMTNFDK NLPNEKVLPK HSLLYEYFTV YNELTKVKYV TEGMRKPAFL
541 SGEQKKAIVD LLFKTNRKVT VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLKI
601 IKDKDFLDNE ENEDILEDIV LTLTLFEDRE MIEERLKTYA HLFDDKVMKQ LKRRRYTGWG
661 RLSRKLINGI RDKQSGKTIL DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AQVSGQGD SL
721 HEHIANLAGS PAIKKGILQT VKVDELVKV MGRHKPENIV IEMARENQTT QKGQKNSRER
781 MKRIEEGIKE LGSQILKEHP VENTQLQNEK LYLYYLQNGR DMYVDQELDI NRLSDYDVDH
841 IVPQSFLKDD SIDNKVLT RS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDNL
901 TKAERGGLSE LDKAGFIKRQ LVETRQITKH VAQILD SRMN TKYDENDKLI REVKVITLKS
961 KLVSDFRKDF QFYKREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK
1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANG EIRKR PLIETNGETG EIVWDKGRDF
1081 ATVRKVL SMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWD PPK YGGFDSPTVA
1141 YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKD LI IKLPK
1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLGKSPE DNEQKQLFVE
1261 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRDK PIREQAENII HLFTLTNLGA
1321 PAAFKYFDTT IDRKRYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD (SEQ ID NO: 147).

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[0101] Nuclease inactivated *S. pyogenes* Cas9 proteins may comprise a substitution of an Alanine (A) for an Aspartic Acid (D) at position 10 and an alanine (A) for a Histidine (H) at position 840. Exemplary nuclease inactivated *S. pyogenes* Cas9 proteins of the disclosure may comprise or consist of the amino acid sequence (D10A and H840A bolded and underlined):

1 MDKKYSIGL**A** IGTVNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSGETAE
 61 ATRLKRTARR RYTRRKNRIC YLQEIFSNEM AKVDDSFHRL EESFLVEED KKHERHPIFG
 121 NIVDEVAYHE KYPTIYHLRK KLVDSTDKAD LRLIYLALAH MIKFRGHFLI EGDLPDNDSD
 181 VDKLFIQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN
 241 LIALSLGLTP NFKSNFDLAE DAKLQLSKDT YDDDLNLLA QIGDQYADLF LAAKNLSDAI
 301 LLSDILRVNT EITKAPLSAS MIKRYDEHHQ DLTKLLKALVR QQLPEKYKEI FFDQSKNGYA
 361 GYIDGGASQE EFKYFIKPIL EKMDGTEELL VKLNREDLLR KQRTFDNGSI PHQIHLGELH
 421 AILRRQEDFY PFLKDNREKI EKILTRIFRIPY YVGPLARGNS RFAWMTRKSE ETITPWNFEE
 481 VVDKGASAQS FIERMTNFDK NLPNEKVLPK HSLLYEYFTV YNELTKVKYV TEGMRKPAFL
 541 SGEQKKAIVD LLFKTNRKVT VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLKI
 601 IKDKDFLDNE ENEDILEDIV LTLTLFEDRE MIEERLKTYA HLFDDKVMKQ LKRRRYTGWG
 661 RLSRKLINGI RDKQSGKTIL DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AOVSGQGDLSL
 721 HEHIANLAGS PAIKKGILQT VKVDELVKV MGRHKPENIV IEMARENQTT QKGQKNSRER
 781 MKRIEEGIKE LGSQILKEHP VENTQLQNEK LYLYYLQNGR DMYVDQELDI NRLSDYD**VDA**
 841 IVPQSFLKDD SIDNKVLTNS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDNL
 901 TKAERGGLSE LDKAGFIKQK LVETRQITKH VAQILDSTRM TKYDENDKLI REVKVITLKS
 961 KLVSDFRKDF QFYKREINN YHHAHDAYLN AVVGTALIKK YPKLESEFVY GDYKVYDVRK
 1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNGETG EIVWDKGRDF
 1081 ATVRKVLVSM QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA
 1141 YSVLVVAKVE KGKSKKLKSV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDIIKLPK
 1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFYLLAS HYEKLGKGSPE DNEQKQLFVE
 1261 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRDK PIREQAENII HLFTLTNLGA
 1321 PAAFKYFDTT IDRKRYTSTK EVLDATLIHQ SITGLYETRI DLSQLGGD (SEQ ID NO: 148).

[0102] Nuclease inactivated *S. pyogenes* Cas9 proteins may comprise deletion of a RuvC nuclease domain or a portion thereof, an HNH domain, a DNase active site, a $\beta\beta$ -metal fold or a portion thereof comprising a DNase active site or any combination thereof.

[0103] Other exemplary Cas9 proteins or portions thereof may comprise or consist of the following amino acid sequences.

[0104] In some embodiments the Cas9 protein can be *S. pyogenes* Cas9 and may comprise or consist of the amino acid sequence:

MDKKYSIGLDIGTVNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRR
 YTRRKNRICYLQEIFSNEMAKVDDSFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLV
 DSTDKADLRLIYLALAHMIKFRGHFLIEGDLPDNDSDVDKLFILVQTYNQLFEENPINASGVDAKAILSAR
 LSKSRLENLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAE DAKLQLSKDTYDDDLNLLAQIGDQY
 ADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTKLLKALVRQQLPEKYKEIFFDQSKNG

YAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYF
 FLKDNREKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLP
 NEKVLPKHSLLEYEFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIE
 CFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDK
 VMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQ
 GDSLHEHIANLAGSPAIIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIE
 IKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLT
 RSDKNRKGSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGSELDKAGFIKRQLVETRQIT
 KHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKREINNYHHAHDAYLNAVVGTA
 LKKYPKLESEFVYGDYKVDVVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNG
 ETGEIVWDKGRDFATVRKVLSPQVNIKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVA
 YSVLVVAKVEKGGSKKLSVKELGITIMERSSEKPNIDFLEAKGYKEVKKDLIILPKYSLFELENGRKR
 MLASAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHGHYLDIIEQISEFSKRVILAD
 ANLDKVL SAYNKHDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ
 SITGLYE TRIDLSQLGGD (SEQ ID NO: 149)

[0105] In some embodiments the Cas9 protein can be *S. aureus* Cas9 and may comprise or consist of the amino acid sequence:

MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQRVKKLLF
 DYNLLTDHSELGINPYEARVKGLSQKLSSEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSK
 ALEEKYVAELQLERLKKDGEVRSINRFKTSYVKEAKQLLVQKAYHQLDQSFIDTYIDLLETRRTYIEG
 PGEKSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYEKFQII
 ENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIENAEALDQIAKIL
 TIY QSSEDIQEELTNLNSLQEEIEQISNLKGYTGTHNLSLKAJNLILDELWHTNDNQIAIFNRLKLVKQV
 DLS QQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPNDIIELAREKNSKDAQKMINEMQKRN
 RQTNERIE EIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFYEVVDHIIPRSVSF
 DNSFNKVLVKQEE NSKKGNRTPFQYLSSSDSKISYETFKKHILNLAGKGRISKTKKEYLLEERDINRFS
 VQKDFINRNLVDTRYA TRGLMNLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHAED
 ALIANADFIKWKKLD KAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYS
 HRVDKKNRELINDTLYSTRKD DKGNLIVNNLNGLYDKDNDKLLKLINKSPEKLLMYHHD
 PQTYQKLLKIMEQYGDENPLYKYEETGN YLTKYSKKNPVIKKIKYYGNKLNALHDITDDYPNSR
 NKVVKLSLKPYPYRFDVYLDNGVYKFFVTVKNL DVIKKENYEVNSKCYEEAKKLLKISNQA
 EFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVMIDITYREYL ENMNDKRPPRIKIASKTQSIK
 KYSTDILGNLYEVKSKKHPQIIKKG (SEQ ID NO: 150)

[0106] In some embodiments the Cas9 protein can be *S. thermophiles* CRISPR1 Cas9 and may comprise or consist of the amino acid sequence:

MSDLVLGLDIGIGSVGVGILNKVVTGEIIHKNSRIFPAAQAENNLVRRTNRQGRRLARRKKHRRVRLNRLFEE

SGLITDFTKISINLNPYQLRVKGLTDELSNEELFIALKNMVKHRGISYLDDASDDGNSSVGDY AQIVKENS
 QLETKTPGQIQLERYQTYGQLRGDFTVEKDGGKHRLINVFPTSA YRSEALRILQTQQEFNPQITDEFINRYLE
 ILTGKRKYHGPNGEKSRDYGRTSGETLDNIFILIGKCTFY PDEFRAAKASYTAQEFNLLNDLNNLTV
 PTETKLSKEQKNQIINYVKNEKAMGPAKLFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLE
 TLDIEQMDRETLDKLAYVLTNTEREIQEAEHEFADGSFSQKQVDEL VQFRKANSSIFGKGWHNFSVKL
 MMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEIYNP VVAKSVRQAIKIVNAAIKEYGDFD
 NIVIEMARETNEDDEKKAIQKIQKANKDEKDAAMLK AANQYNGKAELPHSVFHGHKQLATKIRLWHQQG
 ERCLYTGKTISIHDLNNSNQFEVDHILPLSITFDDSLANK VL VYATANQEKGQRTPYQALDSMDDAWSFRE
 LKAFVRESKTL SNKKKEYLLTEEDISKFDVRKKFIERNLVDTRYASRVVLNALQEHFRAHKIDTKVS VVRG
 QFTSQLRRHWGIEKTRD TYHHHAVDALIIAASSQLNLWKKQKNTLVS YSEDQLLDIETGELISDDEYKESVF
 KAPYQHFVDTLKSKEFEDSILFSYQVDSKFN RKISDATIYATRQAKVGKDKADETYVLGKIKDIYTQDGYD
 AFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPNKQINDKGKEVPCNPFLKYKEEHGYIRKYSKKGNGP
 EIKSLKYYDSKLG NHIDITPKDSNNKVV LQSVSPWRADVFNKTTGKYEILGLKYADLQFDKGTGTYKISQ
 EKYNDIKKKEGVSDSEFKFTLYKNDLLL VKDTETKEQQLFRFLSRTMPKQKHVELKPYDKQKFEGGEA
 LIKVLGNVANSQGCKKGLGKSNISYKVRTDVLGNQHIIKNEGDKPKLDF (SEQ ID NO: 151)

[0107] In some embodiments the Cas9 protein can be *N. meningitidis* Cas9 and may comprise or consist of the amino acid sequence:

MAAFKPNPINYILGLDIGIASVGWAMVEIDEDENPICLIDLGV RVFERAEVPKTGDSLAMARRLARSVRRLT
 RRAHRLLRARLLKREGVLQAADFENGLIKSLPNTPWQLRAAALDRKLT PLEWSAVLLHLIKHRGYLS
 QRKNEGETADKELGALLKGVADNAHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFSRKDLQAE
 ILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCTFEP AEPKAAKNTYTAERFIWLT
 NNLRILEQGSERPLTDTERATLMDEPYRKSCLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAY
 HAISRALEKEGLKDKKSPLNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKFVQISL
 KALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTTEKIYLPPIPADEIRNPV VLRALSQARKVINGVVRRYG
 SPARIHETAREVGKSFKDRKEIEKRQEENRKDREKAAAKFREYFPNFVGE PKSKDILKRLYEQQHGKCLY
 SGKEINLGRLEKGYVEIDHALPFSRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSREWQEFKAR
 VETS RFPRSKQRILLQKFDDEDGFKERNLNDTRYVNRFLCQFVADRMRLTGKGKKRVFASNGQITNLLR
 GFWGLRKVRAENDRHHALDAVVVACSTVAMQKQITRFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQP
 WEFFAQEVMIRVFGKPDGKPEFEEADTPEKLR TLLAEKLSRPEAVHEYVTPLFVSRAPNRKMSGQGH
 METVKSARKLDEGVSVLRVPLTQLKLDLEKMNRREREPKLYEALKARLEAHKDDPAKAFAPFYKYDK
 AGRNTQQVKAVRVEQVQKTGVVVRNHNGIADNATMVRVDVFEKGDKYYLVPIYSWQVAKGILPDRA
 VVQKDEEDWQLIDDSFNFKFLSPNDLVEVITKKARMFYGFASCHRGTGNINIRIHDL DHKIGKNGILE
 GIGVKTALSFKYQIDELGKEIRPCRLKKRPPVR (SEQ ID NO: 152)

[0108] In some embodiments the Cas9 protein can be *Parvibaculum. lavamentivorans* Cas9 and may comprise or consist of the amino acid sequence:

MERIFGFDIGTTSIGFSVIDYSSTQSAGNIQRLGVRIFPEARDPDGTPLNQRRQKRMRRQLRRRRRIRRKAL
 NETLHEAGFLPAYGSADWPVVMADPEYELRRRGLEEGLSAYEFGRAIYHLAQHRHFKGRELEESDTPDPD
 VDDEKEAANERAATLKALKNEQTTLGAWLARRPPSDRKRGIHAHRNVVAEEFERLWEVQSKFHPALKSE
 EMRARISDTIFAQRPVFWRKNTLGEGRFMPGPEPLCPKGSWLSQQRRLMLEKLNLAAGGNARPLDAEERD
 AILSKLQQQASMSWPGVRSALKALYKQRGEPGAEKSLKFNLELGGESKLLGNALAKLADMFGPDWPAH
 PRKQEIRHAVHERLWAADYGETPDKKRVIILSEKDRKAHREAAANSFVADFGITGEQAAQLQALKLPTGW
 EPYSIPALNLFLAELEKGERFGALVNGPDWEGWRRTNFPHRNQPTGEILDKLPSPASKEERERISQLRNPTV
 VRTQNELRKVVNNLIGLYGKPDRIEIVGRDVGKSKREREIEIQSGIRRNEKQRKKATEDLIKNGIANPSRDD
 VEKWILWKEGQERCPYTGDIQGFNALFREGRYEVEHIWPRSRSFDNSPRNKTLCKRDVNIEKGNRMPFEAF
 GHDEDRWSAIQIRLQGMVSAKGGTGMSPGKVKRFLAKTMPEDFAARQLNDTRYAAKQILAQLKRLWPD
 MGPEAPVKVEAVTGQVTAQLRKLWTLNNILADDGEKTRADHRHHAIDALTVACTHPGMTNKLRSRYWQL
 RDDPRAEKPALTPPWDITRADA EKA VSEIVVSHRVRKKVSGPLHKETTYGDTGTDIKTKSGTYRQFVTRKK
 IESLSKGELDEIRDPRIKEIVAAHVAGRGGDPKKAFFPYPCVSPGGPEIRK VRLTSKQQLNLMAQTGNGYAD
 LGSNHIIAIYRLPDGKADFEIVSLFDASRRLAQRNPIVQRTRADGASFVMSLAAGEAIMIPEGSKKGIWIVQ
 GVWASGQVVLERD TDADHSTTTRPMPNPILKDDAKKVSIDPIGRVRPSND (SEQ ID NO: 153)

[0109] In some embodiments the Cas9 protein can be *Corynebacter diphtheria* Cas9 and may comprise or consist of the amino acid sequence:

MKYHVGIDVGTFSVGLAAIEVDDAGMPIKTLVSHIHDSGLDPDEIKSAVTRLASSGIARRTRRLYRRKRR
 RLQQLDKFIQRQGWVIELEDYSDPLYPWK VRAELAASYIADEKERGEKLSVALRHIARHRGWRNPYAKV
 SSLYLPDGPSDAFKAIREEIKRASGQVPETATVGQMVTLCELGTLKLRGEGGVL SARLQQSDYAREIQEIC
 RMQEIGQELYRKIIDVVFAAESPKGSASSR VGKDPLQPGKNRALKASDAFQRYRIAALIGNLRVVRDGEKRI
 LSVEEKNLVFDHLVNLTPKKEPEWVTIAEILGIDRGQLIGTATMTDDGERAGARPPHTDTRNSIVNSRIAPL
 VDWWKTASALEQHAMVKALSNAEVDDFDSPEGAKVQAFFADLDDDVHAKLDSLHLPVGRAAYS EDTLV
 RLTRRMLSDGV DLYTARLQEFGIEPSWTPPTPRIGEPVGNPAVDRVLKTVSRWLESATKTWGAPERVIIEHV
 REGFVTEKRAREMDGDMRRRAARNAKLFQEMQEKLNVQGKPSRADLWRYQSVQRQNCQACAYCGSPITF
 SNSEMDHIVPRAGQGSTNTRENLVAVCHRCNQSKGNTPF AIWAKNTSIEGVSVKEA VERTRHWVTD TGM
 RSTDFKFKFTKAVVERFQRATMDEEIDARSMESVAWMANELRSRVAQHFA SHGTTVRVYRGS LTAEARRA
 SGISGKLFKFDG V GK SRLDRRHHAIDAA VIAFTSDYVAETLAVRSNLKQSQAHRQEAPQWREFTGKDAEH
 RAAWRVWCQKMEKLSALLTEDLRDDR VVVM SNVRLRLGNGSAHKETIGKLSKVKLSSQLSVSDIDKASS
 EALWCAL TREP GFDPK EGLPANPERHIRVNGTHVYAGDNIGLFPVSAGSIALRGGYAELGSSFH HARVYKI
 TSGKKPAFAMLRVYTIDLLPYRNQDLFSVELKPQTMSMRQA EKKLRDALATGNAEYLGWL VVDDDEL VVD
 TSKIATDQVKA VEAELGTIRRWRVDGFFSPSKLRLRPLQMSKEGIKKESAPELSKIIDRPGWLPV NKLFS D
 GNVTVVRRDSLGRVRLESTAHL PVTWKVQ (SEQ ID NO: 154)

[0110] In some embodiments the Cas9 protein can be *Streptococcus pasteurianus* Cas9 and may comprise or consist of the amino acid sequence:

MTNGKILGLDIGIASVGVGIIIEAKTGKVVHANSRLFSAANAENNAERRGFRGSRRLNRRKKHRVKRVRDLF
 EKYGIVTDFRNLNLPYELRVKGLTEQLKNEELFAALRTISKRRGISYLLDDAEDDSTGSTDYAKSIDENRRL
 LKNKTPGQIQLERLEKYGQLRGNFTVYDENGAEHRLINVFSTSDYEKEARKILETQADYNKKITAEFIDDYV
 EILTQKRKYHYHGPNEKSRDYGRFRTDGTTLENIFGILIGKCNFYDPDEYRASKASYTAQEYNFLNDLNNLK
 VSTETGKLSTEQKESLVEFAKNTATLGPALLKEIAKILDCKVDEIKGYREDDKGGKPDHLTFEPYRKLKFNL
 ESINIDDLREVIDKLADILTLNTEREGIEDAIKRNLPNQFTEEQISEIIVRKSQSTAFNKGWHSFSAKLMNE
 LIPELYATSDEQMTILTRLEKFKVNKSSKNTKTIDEKEVTDEIYNPVAKSVRQTIKIINA AVKKYGDFDKI
 VIEMPRDKNADDEKKFIDKRKENKKEKDDALKRAAYLYNSSDKLPDEVFHGNKQLETKIRLWYQQGER
 CLYSGKPISIQELVHNSNNFEIDHILPLSLSFDDSLANKVLVYAWTNQEKGQKTPYQVIDSMDAAWSFREM
 KDYVLKQKGLGKKKRDYLLTTENIDKIEVKKKFIERNLVDTRYASRVVLSLQALRELKGDTKVSVVRG
 QFTSQLRRKWKIDKSRETYHHHAVDALIIAASSQLKLWEKQDNPMFVDYGKNQVVDKQTGEILSVSDDEY
 KELVFQPPYQGFVNTISSKGFEDILFSYQVDSKYNRKVS DATIYSTRKAKIGKDKKEETYVLGKIKDIYSQ
 NGFDTFIKKYNKDKTQFLMYQKDSL TWENVIEVILRDYPTTKKSEDGKNDVK CNPFEEYRREGLICKYSK
 KGKGTPIKSLKYDYDKLGNCIDITPEESRNK VILQSINPWRADVFNPETLKYELMGLKYSDSLSEKGTGNY
 HISQEKYDAIKEKEGIGKSEFKFTLYRNDLILIKDIASGEQEIYRFLSRTMPNVNHYVELKPYDKEKFDNVQ
 ELVEALGEADKVGRCIKGLNKPNIYKVRTDVLGNKYFVKKKGDKPKLDFKNNKK (SEQ ID NO: 155)

[0111] In some embodiments the Cas9 protein can be *Neisseria cinerea* Cas9 and may comprise or consist of the amino acid sequence:

MAAFKPNPMNYILGLDIGIASVGWAIVEIDEEENPIRLIDLGVRVFERAEVPKTGDSLAAARRLARSVRRLT
 RRRARHLLRARRLLKREGVLQAADFENGLIKSLPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLS
 QRKNEGETADKELGALLKGVADNTHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFNRKDLQAE
 NLLFEKQKEFGNPHVSDGLKEGIETLLMTQRPALSGDAVQKMLGHCTFEPTPKAAKNTYTAERFVWLTK
 LNNLRILEQGSRPLTDTERATLMDEPYRKSCLTYAQARKLLDLDATAFFKGLRYGKDNAEASTLMMEMKA
 YHAISRALEKEGLKDKKSPLNLSPELQDEIGTAFSLFKTDEDITGRLKDRVQPEILEALLKHISFDKQVQISLK
 ALRRIVPLMEQGNRYDEACTEYGDHYGKKNTTEKIYLPPIPADEIRNPVLRALSQARKVINGVVRRYGSP
 ARIHIETAREVGKSFKDRKEIEKRQEENRKDREKSAKFREYFPNFVGEPKSKDILKRLRYEQQH GKCLYSG
 KEINLGRLEKGYVEIDHALPFSRTWDDSFNNKVLALGSENQNKGNQTPYEYFNGKDNSREWQEFKARVE
 TSRFPKSKQRILLQKFDDEDGFKERNLNDTRYINRFLCQFVADHMLLTGKGRVVFASNGQITNLLRGFWG
 LRKVRANDRHHALDAVVVACSTIAMQQKITRFVRYKEMNAFDGKTIDKETGEVLHQAHPQPWEFFA
 QEVMIRVFGKPDGKPEFEEADTPEKLRLLAEKLSRPEAVHKYVTPLFISRAPNRKMSGQGHMETVKS
 RLDEGISVLRVPLTQLKLDLEKMNREPERKLYEALKARLEAHKDDPAKAFAPFYKYDKAGNRTQQV
 KAVRVEQVQKTGVVHNHNGIADNATIVRVDVFEKGGKYYLVPIYSWQVAKGILPDRAVVQKDEEDW
 TVMDDSFEFKFLYANDLIKLTAKKNEFLGYFVSLNRATGAIDIRTHDSTKKGKNGIFQSVGVKTALS
 FQKYQIDELGKEIRPCRLKKRPPVR (SEQ ID NO: 156)

[0112] In some embodiments the Cas9 protein can be *Campylobacter lari* Cas9 and may comprise or consist of the amino acid sequence:

MRILGFDIGINSIGWAFVENDELKDCGVRIFTKAENPKNKESLALPRRNARSSRRRLKRRKARLIAIKRILAK
ELKLNKYDYVAADGELPKAYEGSLASVYELRYKALTQNLETKDLARVILHIAKHRGYMKNKNEKKSNDK
KGKILSALKNNALKLENYQSVGEYFYKEFFQKYKKNTKNFIKIRNTKDNYNLCVSSDLEKELKLILEKQK
EFGYNYSEDFINEILKVAFFQRPLKDFSHLVGACTFFEEEEKRACKNSYSAWEFVALTKIINEIKSLEKISGEIV
PTQTINEVLNLILDKGSITYKKFRSCINLHESISFKSLKYDKENAENAKLIDFRKLVEFKKALGVHLSRQEL
DQISTHITLIKDNVCLKTVLEKYNLSNEQINNLEIEFNDYINLSFKALGMILPLMREGKRYDEACEIANLKP
KTVDEKKDFLPAFCDSIFAHELSNPVVNRAISEYRKVLNALLKKYGVHVKIHELEARDVGLSKKAREKIEK
EQKENQAVNAWALKECENIGLKASAKNILKLLWKEQKEICISGNKISIEHLKDEKALEVDHIYPYRSFD
DSFINKVLVFTKENQEKLNKTPEAFGKNIEKWSKIQTALQNLPHYKKNKILDENFKDKQQEDFISRNLNDT
RYIATLIAKYTKEYLNFLLLSENENANLKSGEKGSKIHVQTISGMLTSVLRHTWGFDDKDRNNHLHHALDA
IIVAYSTNSIIKAFSDFRKNQELLKARFYAKELTSDNYKHQVKKFFEPFKSFREKILSKIDEIFVSKPPRRARR
ALHKDTFHSENKIIDKCSYNSKEGLQIALSCGRVRKIGTKYVENDTIVRVDIFKKQNKFYAIPYAMDFALGI
LPNKIVITGDKNNPKQWQTIDESYEFCFLYKNDLILLQKKNMQEPEFAYYNDFSISTSSICVEKHDNKF
ENLTSNQKLLFSNAKEGSKVESLGIQNLKVFKEYIITPLGDKIKADFQPRENISLKTSSKYGRL (SEQ ID
NO: 157)

[0113] In some embodiments the Cas9 protein can be *T. denticola* Cas9 and may comprise or consist of the amino acid sequence:

MKKEIKDYFLGLDVGTVGSVWAVTDDYKLLKANRKDLWGMRCFETAETAEVRRRLHRGARRRIERRKK
RIKLLQELFSQEIAKTDEGFFQRMKESPFYAEDKTIQENTLFNDKDFADKTYHKAYPTINHLIKAWIENKV
KPDPRLLYLACHNIIKKRGHFLFEGDFDSENQFDTSIQALFEYLREDMEVDIDADSQKVKELKDSSSLKNS
KQSRNLKILGLKPSDKQKKAITNLISGNKINFADLYDNPDLKDAEKNSISFSKDDFDALSDDLASILGDSFEL
LLKAKAVYNCSVLSK VIGDEQYLSFAKVKIYEKHKTDLTKLKNVIKHFHFKDYKVFVGYNKNEKNNNNY
SGYVGVCKTKSKKLIINNSVNQEDFYKFLKTILSAKSEIKEVNDILTEIETGTFLPKQISKNAEIPYQLRKME
LEKILSNAEKHFSFLKQKDEKGLSHSEKIIMLLTFKIPYYIGPINDNHKKFFPDRCWVVKKEKSPSGKTPW
FFDHIDKEKTAFAFITSRTNFCTYL VGESVLPKSSLLYSEYTVLNEINNLIIDGKNICDIKQKIYEDLFKK
YKKITQKQISTFIKHEGICNKTDEVIILGIDKECTSSLSYIELKNIFGKQVDEISTKNMLEEIRWATIYDEGE
GKTILKTKIKAEYGYCSDEQIKILNLKFSGWGRLSRKFLFETVTSEMPGFSEPVNIITAMRETQNNLMELLS
SEFTFTENIKKINSGFEDAQFSYDGLVKPLFLSPSVKMLWQTLKLVKEISHITQAPPKFIEMAKGAEL
EPARTKTRLKILQDL YNNCKNDADAFSSEIKDLSGKIENEDNLRRLSDKLYLYYTQLGKCMYCGKPIEIGH
VFDTSNYDIDHIYPQSKIKDDISISNRVLVCCSSCNKEDKYPLKSEIQSKQRGFWNFLQRNNFISLEKLNRLT
RATPISDDETAKFARQLVETRQATKVAKVLEKMFPEKIVYSKAETVSMFRNKFIVKCREINDFHHAH
DAYLNIVVGNVYNTKFTNPNWFIKEKRDNPKIADTYNYYKVFYDVKRNNITAWEKGKTIITVKDMLKR
NTPIYTRQAACKGELFNQTIMKKGLGQHPLKKEGPFNSISKYGGYNKVSAAYYTLIEYEEKGNKIRSLETI

PLYLVKDIQKDQDVLKSYLTDLLGKKEFKILVPKIKINSLKINGFPCHITGKTNDSFLLRPAVQFCCSNNEV
LYFKKIIRFSEIRSQREKIGKTISPYEDLSFRSYIKENLWKKTKNDEIGEKEFYDLLQKKNLEIYDMLLTKHKD
TIYKRPNSATIDILVKGKEKFKSLIENQFEVILEILKLFSAATRNVSDDLQHIGGSKYSVAKIGNKISSLDNCI
LIYQSITGIFEKRIDLKLV (SEQ ID NO: 158)

[0114] In some embodiments the Cas9 protein can be *S. mutans* Cas9 and may comprise or consist of the amino acid sequence:

MKKPYSIGLDIGTNSVGWAVVTDDYKVPKMKVLGNTDKSHIEKNLLGALLFDSGNTAEDRRLKRTAR
RRYTRRRNRILYLQEIFSEEMGKVDDSFHRLSDSFLVTEDKRGERHPIFGNLEEEVKYHENFPTIYHLRQYL
ADNPEKVDLRLVYLALAHIIKFRGHFLIEGKFDTRNNDVQRLFQEFLLAVYDNTFENSSLQEQNQVVEEILTD
KISKSARKDRVLKLPNEKSNRFAEFLKLIVGNQADFKKHFELEEKAPLQFSKDTYEELEVLLAQIGDNY
AELFLSAKKLYDSILLSGILTVTDVGTKAPLSASMIQRYNEHQMDLAQLKQFIRQKLSKDYNEVFSVSKD
GYAGYIDGKTNQEAFYKYLKGLLNKIEGSGYFLDKIEREDFLRKQRTFDNGSIPHQIHLQEMRAIIRRAEF
YPFLADNQDRIEKLITFRIPYYVGPLARGKSDFAWLSRKSADKITPWNFDEIVDKESSAEAFINRMTNYDLY
LPNQKVLPHSLLYEKFTVYNELTKVKYKTEQGKTAFFDANMKQEIFDGVFKVYRKVTKDKLDMDFLEKE
FDEFRIVDLTGLDKENKVFNASYGTYHDLCKILDKDFLDNSKNEKILEDIVLTLTLFEDREMIRKRENYSD
LLTKEQVKKLERRHYTGWRLSAELIHGIRNKESRKTILDYLIIDDGNSNRNFMQLINDDALSFKEEIAKAQV
IGETDNLNQVSDIAGSPAIAKKGILQSLKIVDELVKIMGHQPENIVVEMARENQFTNQGRNSQQRLKGLTD
SIKEFGSQLKEHPVENSQQLQNDRLFLYYLQNGRDMYTGEELDIDYLSQYDIDHIIPQAFIKDNSIDNRVLTSS
KENRGKSDDVPSKDVVRKMKSYWSKLLSAKLITQRKFDNLTKAERGGLTDDDKAGFIKRQLVETRQITKH
VARILDERFNTETDENKKIRQVKIVTLKSNLVSNFRKEFELYKREINDYHHAHDAYLNAVIGKALLGVY
PQLEPEFVYGDYPHFHGHKENKATAKFFYSNIMNFFKDDVRTDKNGEIIWKKDEHISNIKKVLSYPQVN
IVKKVEEQTGGFSKESILPKGNSDKLIPRKTCKFYWDTKKYGGFDSPIVAYSILVIADIEKGKSKKLLTKV
VGVTIMEKMTFERDPVAFLEKGYRNVQEENIILPKYSLFKLENGRKRLLASARELQKGNIEVLPNHLGT
LLYHAKNIHKVDEPKHLDYVDKHKDEFKELLDVVSNFSSKTYLAEGNLEKIKELYAQNGEDLKECLASSFI
NLLTFTAIGAPATFKFFDKNIDRKRYTSTTEILNATLIHQSIITGLYETRIDLNKLGDD (SEQ ID NO: 159)

[0115] In some embodiments the Cas9 protein can be *S. thermophilus* CRISPR 3 Cas9 and may comprise or consist of the amino acid sequence:

MTKPYSIGLDIGTNSVGWAVTTDNYKVPKMKVLGNTSKKYIKKNLLGVLLFDSGITAEGRRLKRTARR
RYTRRRNRILYLQEIFSTEMATLDDAFFQRLDDSFLVPDDKRDSKYPIFGNLVEEKAYHDEFPTIYHLRKYL
ADSTKKADLRLVYLALAHMIKYRGHFLIEGFEFNSKNNDIQKNFQDFLDYNAIFESDLSLENSKQLEEIVKD
KISKLEKKDRILKLPGEKNSGIFSEFLKLIVGNQADFRKCFNLDEKASLHFSKESYDEDLETLLGYIGDDYS
DVFLKAKKLYDAILLGSFLTVTDNETEAPLSSAMIKRYNEHKEDLALLKEYIRNISKTYNEVFKDDTKNG
YAGYIDGKTNQEDFYVYLKLLAEFEGADYFLEKIDREDFLRKQRTFDNGSIPYQIHLQEMRAILDKQAKF
YPFLAKNKERIEKILTFRIPYYVGPLARGNSDFAWSIRKRNEKITPWNFEDVIDKESSAEAFINRMTSFDLYL
PEEKVLPKHSLLYETFNVYNELTKVRFIAESMRDYQFLDSKQKQKDIVRLYFKDKRKVTDKDIIEYLHAIYGY

DGIELKGIEKQFNSSLSTYHDLLNIINDKEFLDSSNEAIIIEIHTLTIFEDREMIKQRLSKFENIFDKSVLKKL
 SRRHYTGWGLSAKLINGIRDEKSGNTILDYLDGIDSNRNFMQLIHDDALSFKKKIQAQIIGDEDKGNIKE
 VVKSLPGSPAIAKKGILQSIKIVDELVKVMGGRKPESIVVEMARENQYTNQGKSNSQQRLKRLEKSLKELGS
 KILKENIPAKLSKIDNNALQNDRLYLQNGKDMYTGDDLDIDRLSNYDIDHIIPQAFKDNKSIDNKVLS
 SASNRGKSDDVPSLEVVKRRTFWYQLLQSKLISQRKFDNLTKAERGGSPEDKAGFIQRQLVETRQITKH
 VARLLDEKFNKKDENNRAVRTVKIITLTKSTLVSQFRKDFELYKREINDFHHAHDAYLNAVVASALLKK
 YPKLEPEFVYGDYPKYNSFRERKSATEKVYFYNSIMNIFKKSISLADGRVIERPLIEVNEETGESVWNKESDL
 ATVRRVLSYPQVNVVKVEEQNHGLDRGKPKGLFNANLSSKPKPNSNENLVGAKEYLDPKKYGGYAGIS
 NSFTVLVKGTEKGAKKKITNVLEFQGISILDRINYRKDKLNFLLEKGYKDIELIIEPKYSLFELSDGSRML
 ASILSTNNKRGEIHKGNQIFLSQKFVKLLYHAKRISNTINENHRKYVENHKKEFEELFYIIEFNENYVGAK
 KNGKLLNSAFQSWQNSIDELCSSFIGPTGSEKGLFELTSRGSAADEFELGVKIPRYRDTYTPSSLLKDATLI
 HQSVTGLYETRIDLAKLGEG (SEQ ID NO: 160)

[0116] In some embodiments the Cas9 protein can be *C. jejuni* Cas9 and may comprise or consist of the amino acid sequence:

MARILAFDIGISSIGWAFSENDELKDCGVRIFTKVENPKTGESLALPRRLARSARKRLARRKARLNHLKHLI
 ANEFKLNIEDYQSFDESLAKAYKGLISPYELRFRALNELLSKQDFARVILHIAKRRGYDDIKNSDDKEKG
 AILKAIKQNEEKLANYQSVGEYLYKEYFQKFKENSKEFTNVRNKKESYERCIASFLKDELKLIFKKQREFG
 FSFSKKFEEVLSVAFYKRALKDFSHLVGNCSFFTDEKRAPKNSPLAFMFVALTRIINLLNKLKNTGILYTK
 DDLNALLNEVLKNGTLTYKQTKLLGLSDDYEFKGEKGTYFIEFKKYKEFIKALGEHNSQDDLNEIAKDI
 TLIKDEIKLKKALAKYDLNQNQIDSLSKLEFKDHLNLSFKALKLVTPLMLEGKKYDEACNELNLKVAINED
 KKDFLPAFNETYKDEVTPVVRRAIKEYRKLNLKLYGKVKHINIELAREVGKNHSQRAKIEKEQNE
 NYKAKKDAELECEKLGKINSKILKRLRFKEQKEFCAYSGEKIKISDLQDEKMLEIDHIYPYSRFSDDSYM
 NKVLVFTKQNEKLNQTPFEAFGNDSAKWQKIEVLAKNLPTKKQKRILDKNYKDKKEQKNFKDRNLNDR
 YIARLVNNTKDYLDLPLSDDENTKLNDRQKGSKVHVEAKSGMLTSALRHTWGFSKDRNNHLHHAID
 AVIIAYANNSIVKAFSDFKKEQESNSAELYAKKISELDYKNRKRKFFEPFSGFRQKVLKIDEIFVSKPERKKP
 SGALHEETFRKEEFYQSYGGKEGVLKALELGKIRKVNKIVKNGDMFRVDIFKHKKTNKFYAVPIYTMD
 FALKVLPNKAVARSKKGEIKDWILMDENYEFCSLYKDSLILIQTKDMQEPEFVYNAFTSSTVSLIVSKHD
 NKFETLSKNQKILFKNANEKEVIAKSIGIQNLKVFEKYIVSALGEVTKAEFRQREDFKK (SEQ ID NO: 161)

[0117] In some embodiments the Cas9 protein can be *P. multocida* Cas9 and may comprise or consist of the amino acid sequence:

MQTTNLSYILGLDLGIASVGVAVVEINENEDPIGLIDVGVRIFERAEVPKTGESLALSRRLARSTRRLIRRA
 HRLLLAKRFLKREGILSTIDLEKGLPNQAWELRVAGLERLSAIEWGAVLLHLIKHRGYLSKRKNESQTNN
 KELGALLSGVAQNHQLQSDDYRTPAELALKKFAKEEGHIRNQRGAYTHTFNRLDLAELNLLFAQQHQF
 GNPHCKEHIQQYMTPELLMWQKPAISGEAILKMLGKCTHEKNEFKAAKHTYSAERFVWLTKLNNLRILED
 GAERALNEEERQLLINHPYEKSKLTYAQVRKLLGLSEQAIFKHLRYSKENAESATFMELKAWHAIRKALEN

QGLKDTWQDLAKKPDLLDEIGTAFSLYKTDEDIQQYLTKNVPNSVINALLVSLNFDKFIELSLKSLRKILPL
 MEQGKRYDQACREIYGHYGEANQKTSQLLPAIPAQEIRNPVVLRTLSQARKVINAIIRQYGS PARVHIETG
 RELGKSFKERREIQKQEDNRKRESAVQKFKELFSDFSSEPKSKDILKFRLEYEQQH GKCLYS GKEINIHL
 NEKGYVEIDHALPFSRTWDDSFNNKVLVLA SENQNKGNQTPYEWLQ GKINSERWKNFVALVLGSQCSAA
 KKQRLLTQVIDDNKFIDRNLNDTRYIARFLSNYIQENLLL VGKNKKNVFTPNGQITALLRSRWGLIKARENN
 NRHHALDAIVVACATPSMQKITRFRIRFKEVHPYKIENRYEMVDQESGEIISPHFPEPWAYFRQEVNIRVFD
 NHPD TVLKEMLPDRPQANHQFVQPLFVSRAPTRKMSGQGHMETIKSAKRLAEGISVLRIPLTQLKPNLLEN
 MVNKEREPALYAGLKARLAEFNQDPAKAFATPFYKQGGQVKAIRVEQVQKSGVLVRENNGVADNASIV
 RTDVIKNNKFFLVPIYTWQVAKGILPNKAIVAHKNEDEWEEMDEGAKFKFSLFPNDLVELTKKEYFFGY
 YIGLDRATGNISLKEHDGEISKGKDG VYRVGVKLALSFEKYQVDELGKNRQICRPQQRQVR (SEQ ID NO:
 162)

[0118] In some embodiments the Cas9 protein can be *F. novicida* Cas9 and may comprise or consist of the amino acid sequence:

MNFKILPIAIDLGVKNTGVFSAFYQKGTSLERLDNKNKGVYELSKDSYTLMMNRTARRHQRRGIDRKQL
 VKRLFKLIWTEQLNLEWDKDTQQAISFLFNRRGFSFITD GYSPEYLNIVPEQVKAILMDIFDDYNGEDDLDS
 YLKLATEQESKISEIYNKLMQKILEFKLMKLC TDIKDDKVSTKTLKEITSYEFELLADYLANYSESLKTQKFS
 YTDKQGNL KELSYYHDKYNIQEFLKRHATINDRILD TLLTDDLDIWNFNFEKFD FDKNEEKLQNQEDKD
 HIQAHLHFFVFAVNKIKSEMASGGRHRSQYFQEITNVLDENNHQEGYLKNFCENLHNKKYSNLSVKNLNVN
 LIGNLSNLELKPLRKYFNDKIHAKADHWDEQKFTETYCHWILGEWRVGVKDQDKKD GAKYSYKDL CNEL
 KQKVTKAGLVDFLELDPCRTIPPYLDNNNRKPPKCQSLILNPKFLDNQYPNWQQYLQELKQLQSIQNYLD
 SFETDLKVLKSSKDQPYFVEYKSSNQQIASGQRDYKDL DARILQFIFDRVKASDELLLNEIYFQAKKLLKQKA
 SSELEKLESSKKLDEVIANSQLSQILKSQHTNGIFEQGTFLHLVCKYYKQRQRARDSRLYIMPEYRYDKKLH
 KYNNTGRFDDDNQLTYCNHKPRQRYQLLNDLAGVLQVSPNFLKDKIGSDDDLFISKWLVEHIRGFKKA
 CEDSLKIQKDNRGLLNHNKINIARNTKGKCEKEIFNLICKIEGSEDKKGN YKHGLAYELGVLLFGEPNEASKP
 EFDRKIKKFNSIYSAQIQQIAFAERKGNANTCAVCSADNAHRMQQIKITEPVEDNKDKIILSAKAQRLPAIP
 TRIVDGA VKKMATILAKNIVDDNWQNIKQVLSAKHQLHIPITESNAFEFEPALADVKGKSLKDRRKKALE
 RISPENIFKDKNNRIKEFAKGISAYSGANLTDGDFDGAKEELDHIIPRSHKKYGTLNDEANLICVTRGDNKN
 KGNRIFCLRDLADNYKQFETDDLEIEKKIADTIWDANKKDFKFGNYRSFINLTPQEQA FRHALFLADE
 NPIKQAVIRAINNRNRTFVNGTQRYFAEVLANNIYLRAKKENLNTDKISFDYFGIPTIGNRGI AEIRQLYEK
 VDSDIQAYAKGDKPQASYSHLIDAMLAF CIAADEHRNDGSIGLEIDKNYSLYPLDKNTGEVFTKDIFSQIKIT
 DNEFSDKKLVRKKAIEGFNTHRQMTRDGIYAENYLPILIHKELNEVRKGYTWKNSEEIKIFKGGKYDIQQL
 NNLVYCLKFVDKPISIDIQISTLEELRNILTTN NIAATAEYYYINLKTQKLHEYYIENYNTALGYKKYSKEME
 FLRSLAYRSERVKIKSIDDVKQVLDKDSNFIIGKITLPFKKEWQRLYREWQNTTIKDDYEFLK SFFNVKSITK
 LHKKVRKDFSLPISTNEGKFLVKRKTDWNNFIYQILNDSRSDGTPFIPAFDISKNEIVEAII DSFTSKNIF
 WLPKNIELQKVDNKNIFAIDTSKWFEVETPSDLRDIGIATIYKIDNNSRPKVRVKLDYVIDDDSKINYFMN
 HSLKSRYPDKVLEILKQSTIIEFESSGFNKTIKEMLGMKLAGIYNETSNN (SEQ ID NO: 163)

[0119] In some embodiments the Cas9 protein can be *Lactobacillus buchneri* Cas9 and may comprise or consist of the amino acid sequence:

MKVNNYHIGLDIGTSSIGWVAIGKDGKPLRVKGGKTAIGARLFQEGNPAADRRMFRTTRRRLSRRKWRLKL
 LEEIFDPYITPVDSTFFARLKQSNLSPKDSRKEFKGSMLFPDLTDMQYHKNYPTIYHLRHALMTQDKKFDIR
 MVYLAIIHHIVKYRGNFLNSTPVDSFKASKVDFVDQFKKLNELYAAINPEESFKINLANSEDIGHQFLDPSIRK
 FDKKKQIPKIVPMMNDKVTDRNLNGKIASEIIHAILGYKAKLDVVLQCTPVDSKPWALKFDDEDIDAKLEK
 ILPEMDENQQSIVAILQNLYSQVTLNQIVPNGMSLSESMIEKYNDHHDHLKLYKKLIDQLADPKKKA VLLK
 AYSQYVGGDGK VIEQA EFWSSVKNLDDSEL SKQIMDLIDAEK FMPKQRTSQNGVIPHLHQRELDEIIH
 QSKYYPWLVEINPNKHDHLAKYKIEQLVAFRVPYVYVGPMPKQDAESAETVFSWMERKGTETGQITPW
 NFDEK VDRKASANRFIKRMTTKDTYLIGEDVLPDESLLYEKFKVLNELNMVRVNGKLLK VADKQAIFQDL
 FENYKHVSVKKLQNYIAKTGLPSDPEISGLSDPEHFNNSLGTYNDFKFLFGSKVDEPDLQDDFEKIVEWST
 VFEDKKILREKLNEITWLSQQKDVLESSRYQGWGRLSKKLLTGIVNDQGERIIDKLWNTNKNFMQIQSDD
 DFAKRIHEANADQMQA VDVEDVLADAYTSPQNKKAIRQVVKVVDIQAAMGGVAPKYISIEFTRSED RNP
 RRTISRQRQLENTLKDTAKSLAKSINPELLSELDNAAKSKKGLTDRLYL YFTQLGKDIYTGEPINIDELNKYD
 IDHILPQAFIKDNSLDNRVLVLTAVNNGKSDNVPLRMFGAKMGHFWKQLAEAGLISKRKLK NLQTDPTIS
 KYAMHGFIRRLVETSQVIKLVANILGDKYRNDDTKIIETARMNHQMRDEFGFIKREINDYHHAFDAYL
 TAFLGRYLYHRYIKLRPYFVYGDFKFKFREDKVTMRNFNHLHDLTDDTQEKIADAETGEVIWDRENSIQQLK
 DVYHYKFMLISHEVYTLRGAMFNQTVYPASDAGKRKLIPVKADRPVNVYGGYSGSADAYMAIVRIHNKK
 GDKYRVVGVPMRALDRLDAAKNVSDADFDRAKDV LAPQLTKTKKSRKTGEITQVIEDFEIVLGKVMYR
 QLMIDGDKKFM LGSSTYQYNAKQLVLSQSVKTLASKGRLDPLQESMDYNNVYTEILDKNVQYFSLYDM
 NKFRHKLNLGFSKIFSPNHNVDGNTKVSSGKREILQEILNGLHANPTFGNLKDVGITTPFGQLQQPNGILL
 SDETKIRYQSPTGLFERTVSLKDL (SEQ ID NO: 164)

[0120] In some embodiments the Cas9 protein can be *Listeria innocua* Cas9 and may comprise or consist of the amino acid sequence:

MKKPYTIGLDIGTNSVGWAVLTDQYDLVKRKMKIAGDSEKKQIKKNFWGVRLFDEGQTAADRRMARTA
 RRIERRRRNRISYLGIFAEEMSKTDANFFCRLSDSFYVDNEKRNSRHPFFATIEEEVEYHKNYPTIYHLREE
 LVNSSEKADLRLVYLALAHIIKYRGNFLIEGALDTQNTSVDGIYKQFIQTYNQVFASGIEDGSLKKLEDNKD
 VAKILVEKVTRKEKLERILKLYPGEKSAGMFAQFISLIVGSKGNFQKPFDLIEKSDIECAKDSYEEDLESLLA
 LIGDEYAELFVA AKNAYS AVVLSSIITVAETETNAKLSASMIERFDTHEEDLGELKAFIKLHLPKHYYEIEFSN
 TEKHGYAGYIDGKTKQADFYKYMKMTLENIEGADYFIAKIEKENFLRKQRTFDNGAIPHQLHLEEELEAILH
 QQAKYYPFLKENYDKIKSLVTRIPYFVGPLANGQSEFAWLTRKADGEIRPWNIEEKVDFGKSAVD FIEKM
 TNKDTYLPKENVLPKHSLCYQKYL VYNELTKVRYINDQGKTSYFSGQEKEQIFNDFKQKRKVKKDLEL
 FLRNMSHVESPTIEGLEDSFNSSYSTYHDLLKVGIKQEILDNPVNTEMLNIVKILTVFEDKRMIEQLQQFS
 DVL DGVV LKKLERRHYTGWGRLSAKLLMGIRDKQSHLTILDYLMNDDGLNRNLMQLINDSNLSFKSIEK
 EQVTTADKDIQSIVADLAGSPAIKKGILQSLKIVDELVSVMGYPPQTIVVEMARENQTTGKGKNNRPRYKS

LEKAIKEFGSQILKEHPTDNQELRNNRLYYLQNGKDMYTGQDLDIHNL SNYDIDHIVPQSFITDNSIDNL
 VLTSSAGNREKGGDVPPEIVRKRKVFWEKLYQGNLMSKRKFDYLTKAERGGLTEADKARFIHRQLVETR
 QITKNVANILHQRFNYEKDDHGNTMKQVRIVTLKSALVSQFRKQFQLYKVRDVNDYHHAHDAYLNGVV
 ANTLLKVYPQLEPEFVYGDYHQFDWFKANKATAKKQFYTNIMLFFAQKDRIIDENGEILWDKKYLDTVKK
 VMSYRQMNIIVKKTEIQKGEFSKATIKPKGNSSKLIPRKTNWDPMKYGGLDSPNMAYAVVIEYAKGKNKLV
 FEKKIIRVTIMERKAFEKDEKAFLEEQGYRQPKVLAKLPKYTYECEGRRRMLASANEAQKGNQQVLPN
 HLVTLLHHAANCEVSDGKSLDYIESNREMF AELLAHVSEFAKRYTLAEANLNKINQLFEQNKEGDIKAI AQ
 SFVDLMAFNAMGAPASFKFFETTIERKRYNNLKELLNSTIYQSITGLYESRKRLDD (SEQ ID NO: 165)

[0121] In some embodiments the Cas9 protein can be *L. pneumophila* Cas9 and may comprise or consist of the amino acid sequence:

MESSQILSPIGIDLGGKFTGVCLSHLEAFAELPNHANTKYSVILIDHNNFQLSQAQRRA TRHRVRNKKRNQF
 VKRVALQLFQHILSRDLNAKEETALCHYLNNRGYTYVDTDLDEYIKDETTINLLKELLPSESEHNFIDWFLQ
 KMQSSEFRKILVSKVEEKDDELKNAVKNIKNFITGFEKNSVEGHRHRKVYFENIKSDITKDNQLDSIKKK
 IPSVCLSNLLGHLSNLQWKNLHRYLAKNPKQFDEQTFGNEFLRMLKNFRHLKGSQESLAVRNLIQQLEQSQ
 DYISILEKTPPEITIPPYEARNTNGMEKDQSLLLNPEKLNLYPNWRNLIPGIIDAHFPLEKDLEHTKLRDRKR
 IISPSKQDEKRDSYILQRYL DLNKKIDFKIKKQLSFLGQKQLPANLIETQKEMETHFNSSLVSVLIQIASAY
 NKEREDAAQGIWFDNAFSLCELSNINPPRKQKILPLLVGAILSEDFINNKDKWAKFKIFWNTHKIGRTSLKS
 KCKEIEEARKNSGNAFKIDYEEALNHPEHSNNKALIKIITIPDIIQAIQSHLGHNDSQALIYHNPFSLSQLYTI
 LETKRDGFHKNCVAVTCENYWRSQKTEIDPEISYASRLPADSVRPFDGVLARMMQRLAYEIAMAKWEQIK
 HIPDNSSLLIPIYLEQNRFEFEESFKKIKGSSSDKTLEQAIEKQNIQWEEKFQRIINASMNICPYKGASIGGQGE
 IDHIYPRSLSKKHFGVIFNSEVNLIYCSSQGNREKKEEHYLLEHLSPLYLKHQFGTDNVSDIKNFISQNVANI
 KKYISFHLLTPEQQKAARHALFLDYDDEAFKTITKFLMSQQKARVNGTQKFLGKQIMEFLSTLADSKQLQL
 EFSIKQITAEVHDHRELLSKQEPKLVKSRQQSFP SHAIDATLTMSIGLKEFPQFSQELDNSWFINHLMPDEV
 HLNPVRSKEKYNKPNISSTPLFKDSL YAERFIPVWVKGETFAIGFSEKDLFEIKPSNKEKLFLLKTYSTKNP
 GESLQELQAKSKAKWL YFPINKTLALEFLHHYFHKEIVTPDDTTVCHFINSRLYYTKKESITVKILKEPMPVL
 SVKFESSKKNVLGSKHTIALPATKDWERLFNHPNFLALKANPAPNPKEFNEFIRKYFLSDNNPNSDIPNNG
 HNIKPQKHKAVRKFVSLPVIPGNAGTMMRIRKDNKGQPLYQLQTIDDTPSMGIQINEDRLVKQEVLM DA
 YKTRNLSTIDGINNSEGQAYATFDNWL TLPVSTFKPEI IKLEMKPHSKTRRYIRITQSLADFIKTIDEALMIKP
 SDSIDDPLNMPNEIVCKNKLFGNELKPRDGMKIVSTGKIVTYEFESDSTPQWIQTL YVTQLKKQP (SEQ ID
 NO: 166)

[0122] In some embodiments the Cas9 protein can be *N. lactamica* Cas9 and may comprise or consist of the amino acid sequence:

MAAFKPNPMNYILGLDIGIASVGWAMVEVDEEENPIRLIDLGVRVFERAEVPKTGDSLAMARRLARSVRL
 TRRRAHRLLRARLLKREGVLQDADFENGLVKSLPNTPWQLRAAALDRKLTCLEWSAVLLHLVKHRGY
 LSQRKNEGETADKELGALLKGVADNAHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFSRKDLQA

ELNLLFEKQKEFGNPHVSDGLKEDIETLLMAQRPALSGDAVQKMLGHCTFEPAPKAAKNTYTAERFIWL
 TKLNNLRILEQGSERPLDTERATLMDEPYRKSCLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEM
 KAYHAISRALEKEGLKDKKSPNLSTELQDEIGTAFSLFKTDKIDITGRLKDRVQPEILEALLKHISFDKVFQIS
 LKALRRIVPLMEQGKRYDEACAEIYGDHYCKKNAEKKIYLPPIPADEIRNPVLRALSQARKVINCVRRY
 GSPARIHIETAREVGKSFKDRKEIEKRQEENRKDREKAAAKFREYFPNFVGEPEKSKDILKLRLYEQQHGKCL
 YSGKEINLVRNEKGYVEIDHALPFSRTWDDSFNNKVLVLGSENQKGNQTPYEYFNGKDNSREWQEFKA
 RVETSRFPRSKKQRILLQKFDEEGFKERNLNDTRYVNRFLCQFVADHILLTGKGGKRRVFASNGQITNLLRGF
 WGLRKRVTENDRHHALDAVVVACSTVAMQKITRFVRYKEMNAFDGKTIDKETGEVLHQKAHPQPWE
 FFAQEV MIRVFGKPDGKPEFEEADTPEKLRLLAEKLSRPEAVHEYVTPLFVSRAPNRKMSGQGHMETVK
 SAKRLDEGISVLRVPLTQLKLGLEKMNRREREPKLYDALKAQLETHKDDPAKAFAPFYKYDKAGSRTQ
 QVKA VRIEQVQKTGVWVRNHNGIADNATMVRVDVFEKGGKYLLVPIYSWQVAKGILPDRAVVAFKDEE
 DWTVMDDSFERFVLYANDLIKLTAKKNEFLGYFVSLNRATGAIDIRTHDSTDSTKGGNGIFQSVGVKTALS
 FQKNQIDELGKEIRPCRLKKRPPVR (SEQ ID NO: 167)

[0123] In some embodiments the Cas9 protein can be *N. meningitidis* Cas9 and may comprise or consist of the amino acid sequence:

MAAFKPNPINYILGLDIGIASVGWAMVEIDEDENPICLIDLGVRFERAEVPKTGDSLAMARRLARSVRRLT
 RRAHRLLRARRLLKREGVLQAADFENGLIKSLPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLS
 QRKNEGETADKELGALLKGVADNAHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFSRKDLQAE
 ILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCTFEPAPKAAKNTYTAERFIWLTKL
 NNLRLILEQGSERPLDTERATLMDEPYRKSCLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAY
 HAISRALEKEGLKDKKSPNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKVFQISL
 KALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTTEKIYLPPIPADEIRNPVLRALSQARKVINGVRRYGSPAR
 IHIETAREVGKSFKDRKEIEKRQEENRKDREKAAAKFREYFPNFVGEPEKSKDILKLRLYEQQHGKCLYSGKE
 INLGRNEKGYVEIDHALPFSRTWDDSFNNKVLVLGSENQKGNQTPYEYFNGKDNSREWQEFKARVETS
 RFPRSKKQRILLQKFDEEDGFKERNLNDTRYVNRFLCQFVADRMRLTGKGGKRRVFASNGQITNLLRGFWGL
 RRVRAENDRHHALDAVVVACSTVAMQKITRFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQ
 EVMIRVFGKPDGKPEFEEADTPEKLRLLAEKLSRPEAVHEYVTPLFVSRAPNRKMSGQGHMETVKSAR
 LDEGVSVLRVPLTQLKLDLEKMNRREREPKLYEALKARLEAHKDDPAKAFAPFYKYDKAGNRTQQVK
 AVRVEQVQKTGVWVRNHNGIADNATMVRVDVFEKGDKYLLVPIYSWQVAKGILPDRAVVAQKDEEDW
 QLIDDSFNFKFSLHPNDLVEVITKKARMEFYFASCHRG TG NINIRIHDL DHKIGKNGILEGIGVKTALS FQKY
 QIDELGKEIRPCRLKKRPPVR (SEQ ID NO: 168)

[0124] In some embodiments the Cas9 protein can be *B. longum* Cas9 and may comprise or consist of the amino acid sequence:

MLSRQLLGASHLARPVSYSYNVQDNDVHCSYGERCFMRGKRYRIGIDVGLNSVGLAAVEVSDENSPVRL
 NAQSVIHDGGVDPQKNKEAITRKNMSGVARRTRMRRRKRERLHKLDMLLGKFGYPVIEPESLDKPFEEW

HVRAELATRYIEDDELRRRESISIALRHMARHRGWRNPYRQVDSLISDNPYSKQYGELKEKAKAYNDDATA
 AEEESTPAQLVVAMLDAGYAEAPRLRWRTGSKKPDAEGYLPVRLMQEDNANELKQIFRVQRPADDEWKP
 LFRSVFYAVSPKGSAEQRVGQDPLAPEQARALKASLAFQEYRIANVITNLRKIDASAELRKLTVDEKQSIYD
 QLVSPSSEDITWSDLCDFLGFKRSQKGVGSLTEDGEERISSRPPRLTSVQRIYESDNKIRKPLVAWWKSAS
 DNEHEAMIRLLSNTVDDIKVREDVAYASAIEFIDGLDDDALTKLDSVDLPSGRAAYSVELQKLTRQMLTT
 DDDLHEARKTLFNVTDSWRPPADPIGEPLGNPSVDRVLKKNVRYLMNCQQRWGNPVSVNIEHVRSFSSV
 AFARKDKREYEKNNEKRSIFRSSLSEQLRADEQMEKVRESDLRRLEAIQRQNGQCLYCGRTITFRTCEMDH
 IVPRKGVGSTNTRTNFAAVCAECNRMKSNTPFIAWARSEDAQTRGVSLAEAKKRVTMFTFNPKSYAPREV
 KAFKQAVIARLQQTEDDAAIDNRSIESVAWMADELHRRIDWYFNAKQYVNSASIDDAEAETMKTTVSVFQ
 GRVTASARRAAGIEGKIHFQSQSKTRLDRRHHAVDASVIAMMNTAAAQTLMERESLRESQRLIGLMPGER
 SWKEYPYEGTSRYESFHLWLDNMDVLELLNDALDNDRIA VMQSQRVVLGNSIAHDATIHPLEKVPLGSA
 MSADLIRRASTPALWCALTRLPDYDEKEGLPEDSHREIRVHDTRY SADDEMGGFFASQAAQIAVQEGSADIG
 SAIHHARVYRCWKTNAKGVRYFYGMIRVFQTDLLRACHDDLFTVPLPPQSISMRYGEPVVQALQSGNA
 QYLGSLVVGDEIEMDFSSLDVDGQIGEYLQFFSQFSGGNLAWKHVVVDGFFNQTLRIRPRYLA AEGLAK
 AFSDDVVPDGVQKIVTKQGWLPPVNTASKTAVRIVRRNAFGEPRLSSAHHMPCSWQWRHE (SEQ ID NO:
 169)

[0125] In some embodiments the Cas9 protein can be *A. muciniphila* Cas9 and may comprise or consist of the amino acid sequence:

MSRSLTFSFDIGYASIGWAVIASASHDDADPSVCGCGTVLFPKDDCQAFKRREYRRLRRNIRSRRVRIERIG
 RLLVQAQIITPEMKETSGHPAPFYLAASEALKGHRTLAPIELWHVLRWYAHNRGYDNNASWSNSLSEGGN
 GEDTERVKHAQDLMDKHGTATMAETICRELKLEEGKADAPMEVSTPAYKNLNTAFPRLIVEKEVRRILELS
 APLIPGLTAEIIEIAQHHPHTTEQRGVLLQHGIKLARRYRGSLLFGQLIPRFDNRIISRPCVTWAQVYEAELK
 KGNSEQSARERAELKSKVPTANCPEFYEYRMARILCNIRADGEPLSAEIRRELMNQARQEGKTKASLEKAI
 SSRLGKETETNVSNYFTLHPDSEEALYLNPAVEVLQRSGIGQILSPSVYRIANRLRRGKSVTPNYLLNLLKS
 RGESGEALEKKIEKESKKKEADYADTPLKPKYATGRAPYARTVLKVVVEILDGEDPTRPARGEAHPDGEL
 KAHDGCLYCLLDTSSVNQHQKERRLDTMTNNHLVRHRMLILDRLLKDLIQDFADGQKDRISRVCVEVG
 KELTTFSAMDSKIKRELTLRQKSHTDAVNRLKRKLPKALSANLIRKCRIAMDMNWTCPFTGATYGDHE
 LENLELEHIVPHSFRQSNALSSLVLTWPGVNRMKGQRTGYDFVEQEENPVPDKPNLHICSLNNYRELVEK
 LDDKKGHEDDRRKRKALLMVRGLSHKHQSQNHEAMKEIGMTEGMMTQSSHLMKLACKSIKTSPLD
 AHIDMIPGAVTAEVRKAWDVFGVFKELCPEAADPDSGKILKENLRSLSLTHLHHALDACVLGLIPYIIPAHN
 GLLRRVLAMRRIPEKLIPQVRPVANQRHYVLNDDGRMMLRDLASLKENIREQLMEQRVIQHVPA DMGG
 ALLKETMQRVLSVDGSGEDAMVSLSKKKDGKKEKNQVKASKLVGVFPEGPSKALKAAIEIDGNYGVA
 LDPKPVVIRHIKVFKRIMALKEQNGGKPVRLKKGMLIHLTSSKDPKHAGVWRIESIQDSKGGVKLDLQRA
 HCAVPKNKTHECNWREVDLISLLKQYQMKRYPTS YTGTPR (SEQ ID NO: 170)

[0126] In some embodiments the Cas9 protein can be *O. laneus* Cas9 and may comprise or consist of the amino acid sequence:

METTLGIDLGTNSIGLALVDQEEHQILYSGVRIFPEGINKDTIGLGEKEESRNATRRAKRQMRRQYFRKKLR
 KAKLLELLIAYDMCPLKPEDVRRWKNWQKQKSTVRQFPDTPAFREWLNQNPYELRKQAVTEDVTRPEL
 GRILYQMIQRRGFLSSRKGKEEGKIFTGKDRMVGIDETRKNLQKQTLGAYLYDIAPKNGEKYRFRTERVRA
 RYTLRDMYIREFEIHWQRQAGHLGLAHEQATRKKNFLEGSATNVRNSKLITHLQAKYGRGHVLIEDTRITV
 TFQLPLKEVLGGKIEIEEQLFKFSNESVLFWQRPLRSQKSLLSKCVFEGRNFDYDPVHQKWIIAGTPAPLSH
 PEFEEFRAYQFINNIYGKNEHLTAIQREAVFELMCTESKDFNFEEKIPKHLKLFKFNFD DTTKVPACTTISQL
 RKLFPHPVWEEKREEIWHCFYFYDDNTLLFEKLQKDYALQTNDEKIKIRLSESYGNVSLKAIRRNIPYK
 KGYAYSTAVLLGGIRNSFGKRFEYFKEYEPEIEKAVCRILKEKNAEGEVIRKIKDYLVHNRFGFAKNDRAFQ
 KLYHHSQAITTAQKERLPETGNLRNPIVQQGLNELRRTVNKLLATCREKYGPSFKFDHIHVEMGRELRSS
 KTEREKQSRQIRENEKKNEAAKVLAEYGLKAYRDNIQKYLLYKEIEEKGGTVCCPYTGKTLNISHTLGSD
 NSVQIEHIIPYSISLDDSLANKTLCDATFNREKGE LTPYDFYQKDP SPEK WGASSWEEIEDRAFLLPYAKAQ
 RFIRRPQESNEFISRQLNDTRYISKKA VEYLSAICSDVKAFPGQLTAE LRHLWGLNNILQSAPDITFPLPVA
 TENHREYYVITNEQNEVIRLFPKQGETPRTEKGELLLTGEVERK VFRCKGMQEFQTDVSDGKYWRRIKLSS
 SVTWSPLFAPKPISADGQIVLKGRIEKGVFVCNQLKQKLTGLPDGSYWISLPVISQTFKEGESVNNSKLT SQ
 QVQLFGRVREGIFRCHNYQCPASGADGNFWCTLD TDTAQP AFTPIKNAPPGVGGGQIILTG DVDDK GIFHA
 DDDLHYELPASLPKGKYYGIFTVESCDPTLIPIELSAPKTSKGENLIEGNIWVDEHTGEVRFDPKKNREDQR
 HHADAIVIALSSQSLFQRLSTYNARRENKKRGLD STEHFSPWPGF AQDVRQSVVPLLVS YKQNP KTLCKI
 SKTLYKDGKKIHS CGNAV RGLH KETVY GQRTAPGATEKSYHIRKDIRELKT SKHIGKVVDITIRQMLLKH
 LQENYHIDITQEFNIPSN AFFKEGVYRIFLPNKHGEPVPIKKIRMKEELGNAERLKD NINQYVNPRNNHHVMI
 YQDADGNLKEEIVSFWSVIERQNQGQPIYQLPREGRNIVSILQINDTFLIGLKEEPEVYRNDLSTLSKHL YR
 VQKLSGMYTFRHHLASTLNNEREEFRIQSLEAWKRANPVKVQIDEIGRITFLNGPLC (SEQ ID NO: 171).

[0127]

[0128] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a CRISPR Cas protein or portion thereof. In some embodiments, the CRISPR Cas protein comprises a Type V CRISPR Cas protein. In some embodiments, the Type V CRISPR Cas protein comprises a Cpf1 protein. Exemplary Cpf1 proteins of the disclosure may be isolated or derived from any species, including, but not limited to, a bacteria or an archaea. Exemplary Cpf1 proteins of the disclosure may be isolated or derived from any species, including, but not limited to, *Francisella tularensis* subsp. *novicida*, *Acidaminococcus* sp. *BV3L6* and *Lachnospiraceae* bacterium sp. *ND2006*. Exemplary Cpf1 proteins of the disclosure may be nuclease inactivated.

[0129] Exemplary wild type *Francisella tularensis* subsp. *Novicida* Cpf1 (FnCpf1) proteins of the disclosure may comprise or consist of the amino acid sequence:

```

1 MSIQEFVVK YSLSKTLRFE LIPQGKTLEN IKARGLILDD EKRAKDYKKA KQIIDKYHQF
61 FIEEILSSVC ISEDLQNYIS DVYFKLKKSD DDNLQKDFKS AKDTIKKQIS EYIKDSEKFK
121 NLFNQNLIDA KKGQESDLIL WLKQSKDNGI ELFKANSDIT DIDEALEI IK SFKGWTTYFK
181 GFHENRKNVY SSNDIPTSII YRIVDDNLPK FLENKAKYES LKDKAPEAIN YEQIKKDLAE
241 ELTFDIDYKT SEVNQRVFSL DEVFEIANFN NYLNQSGITK FNTIIGGK FV NGENTKRKGI
301 NEYINLYSQQ INDKTLKKYK MSVLFKQILS DTESKSFVID KLEDDSDVVT TMQSFYEQIA
361 AFKTVEEKSI KETLSLLFDD LKAQKLDLSK IYFKNDKSLT DLSQQVFDDY SVIGTAVLEY
421 ITQQIAPKNL DNPSKKEQEL IAKKTEKAKY LSLETIKLAL EEFNKHRDID KQCRFEEILA
481 NFAAIPMI FD EIAQNKDNLA QISIKYQNGG KKDLLQASAE DDVKAIKDLL DQTNLLHKL
541 KIFHISQSED KANILDKDEH FYLVFEECYF ELANIVPLYN KIRNYITQKP YSDEKFKLNF
601 ENSTLANGWD KNKEPDNTAI LFIKDDKYLL GVMNKKNNKI FDDKAIKENK GEGYKKIVYK
661 LLPGANKMLP KVFFSAKSIK FYNPSEDILR IRNHSTHTKN GSPQKGYEKF EFNIEDCRKF
721 IDFYKQSISK HPEWKDFGFR FSDTQRYNSI DEFYREVENQ GYKLTFFENIS ESYIDSVVNQ
781 GKLYLFQIYN KDFSAYSKGR PNLHTLYWKA LFDERNLQDV VYKLNGEAEL FYRKQSI PKK
841 ITHPAKEAIA NKNKDNPKKE SVFEYDLIKD KRFTEDKFFF HCPITINFKS SGANKFNDEI
901 NLLLKEKAND VHILSIDRGE RHLAYYTLVD GKGNI IKQDT FNIIGNDRMK TNYHDKLAAI
961 EKDRDSARKD WKKINNIKEM KEGYLSQVHV EIAKLVI EYN AIVVFEDLNF GFKRGRFKVE
1021 KQVYQKLEKM LIEKLNLYLVF KDNEFDKTGG VLRAYQLTAP FETFKKMGKQ TGIYYVPAG
1081 FTSKICPVTG FVNQLYPKYE SVSKQEFFS KFDKICYNLD KGYFEFSFDY KNFGDKAAKG
1141 KWTIASFGSR LINFRNSDKN HNWDTRVEYP TKELEKLLKD YSIEYGHGEC IKA AICGESD
1201 KKFFAKLTSV LNTILQMRNS KTGTELDYL I SPVADVNGNF FDSRQAPKNM PQDADANGAY
1261 HIGLKLMLL GRIKNNQEGK KLNLVIKNEE YFEFVQNRNN (SEQ ID NO: 172).

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[0130] Exemplary wild type *Lachnospiraceae* bacterium sp. *ND2006* Cpf1 (LbCpf1) proteins of the disclosure may comprise or consist of the amino acid sequence:

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1 AASKLEKFTN CYLSKTLRF KAIPVGKTQE NIDNKRLLE DEKRAEDYK G VKKLLDRYYL
61 SFINDVLHSI KLKLNLYNIS LFRKKTRTEK ENKELNLEI NLRKEIAKAF KGAAGYKSLF
121 KKDI IETILP EAADDKDEIA LVNSFNGFTT AFTGFFDNRE NMFSEEAKST SIAFRGINEN
181 LTRYISNMDI FEKVD AIFDK HEVQEI KEKI LNSDYDVEDF FEGEFFNFVL TQEGIDVYNA
241 IIGGFVTEG EKIKGLNEYI NLYNAKTKQA LPKFKPLYKQ VLSDRESLSF YGEGYTSDEE
301 VLEVFRNTLN KNSEIFSSIK KLEKLFKNFD EYSSAGIFVK NGPAISTISK DIFGEWNLIR
361 DKWNAEYDDI HLKKKAVVTE KYEDDRRSF KKIGSFSLEQ LQEYADADLS VVEKLKEIII
421 QKVDEIYKVY GSSEKLFAD FVLEKSLKKN DAVVAIMKDL LDSVKS FENY IKAFFGEGKE
481 TNRDESFYGD FVLAYDILLK VDHIYDAIRN YVTQKPYSK KFKLYFQNPQ FMGGWDKDKKE
541 TDYRATILRY GSKYYLAIMD KKYAKCLOKI DKDDVNGNYE KINYKLLPGP NKMLPKVFFS
601 KKW MAYNPS EDIQKIYKNG TFKKGDMFNL NDCHKLIDFF KDSISRYPKW SNAYDFNFSE
661 TEKYKDIAGF YREVEEQGYK VSFESASKKE VDKLVEEGKL YMFQIYNKDF SDKSHGTPNL
721 HTMYFKLLFD ENNHGQIRLS GGAELFMRRR SLKKEELVH PANSPIANKN PDNPKTTTL
781 SYDVYKDKRF SEDQYELHIP IAINKCPKNI FKINTEVRVL LKHDDNPYVI GIDRGERNLL
841 YIVVVDGKGN IVEQYSLNEI INNFGIRIK TDYHSLDDK EKERFEARQN WTSIENIKEL
901 KAGYISQVH KICELVEKYD AVIALEDLNS GFKNSRVKVE KQVYQKFEKM LIDKLNMYMD
961 KKSNPCATGG ALKGYQITNK FESFKSMSTQ NGFIFYIPAW LTSKIDPSTG FVNLLKTKYT
1021 SIADSKKFIS SFDRIMYVPE EDLFEFALDY KNFSRTDADY IKKWKLYSYG NRIRIFAAAK
1081 KNNVFAWEEV CLTSAYKELF NKYGINYQQG DIRALLCEQS DKAFYSSFMA LMSLMLQMRN
1141 SITGRTDVDF LISPVKNSDG IFYDSRNYEA QENAILPKNA DANGAYNIAR KVLWAIQQFK
1201 KAEDEKLDKV KIAISNKEWL EYAQTSVK (SEQ ID NO: 173).

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[0131] Exemplary wild type *Acidaminococcus sp. BV3L6* Cpf1 (AsCpf1) proteins of the disclosure may comprise or consist of the amino acid sequence:

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1  MTQFEGFTNL  YQVSKTLRFE  LIPQGKTLKH  IQEQGFIEED  KARNDHYKEL  KPIIDRIYKT
61  YADQCLQLVQ  LDWENLSAAI  DSYRKEKTEE  TRNALIEEQA  TYRNAIHDFY  IGRTDNLTD
121  INKRHAEIYK  GLFKAELFNG  KVLKQLGTVT  TTEHENALLR  SFDKFTTYFS  GFYENRKNVF
181  SAEDISTAIP  HRIVQDNFPP  FKENCHIFTR  LITAVPSLRE  HFENVKKAIG  IFVSTSIEEV
241  FSFPFYNQLL  TQTQIDLYNQ  LLGGISREAG  TEKIKGLNEV  LNLAIQKNDE  TAHIIASLPH
301  RFIPLFKQIL  SDRNTLSFIL  EEFKSDEEVI  QSFCKYKTL  RNENVLETAE  ALFNELNSID
361  LTHIFISHKK  LETISSALCD  HWDTLRNALY  ERRISELTGK  ITKSAKEKVQ  RSLKHEDINL
421  QEIIISAAGKE  LSEAFKQKTS  EILSHAHAAL  DQPLPTTLKK  QEEKEILKSQ  LDSLLGLYHL
481  LDWFAVDES  EVDPEFSARL  TGIKLEMEPS  LSFYNKARNY  ATKPPYSVEK  FKLNFQMPTL
541  ASGWDVNKEK  NNGAILFVKN  GLYYLGIMPK  QKGRYKALS  EPTEKTSEGF  DKMYDYFDP
601  AAKMIPKCST  QLKAVTAHFQ  THTPILLSN  NFIEPLEITK  EIYDLNNEPK  EPKKFQTAYA
661  KKTGDQKGYR  EALCKWIDFT  RDFSLSKYTK  TSIDLSSLRP  SSQYKDLGEY  YAEINPLLYH
721  ISFQRIAEKE  IMDAVETGKL  YLFQIYNKDF  AKGHHGKPNL  HTLYWTGLFS  PENLAKTSIK
781  LNGQAELFYR  PKSRMKRMAH  RLGEKMLNKK  LKDQKTPIPD  TLYQELYDYV  NHRLSHDLS
841  EARALLPNVI  TKEVSHEIIK  DRRFTSDKFF  FHPITLNYQ  AANSPSKFNQ  RVNAYLKEHP
901  ETPIIGIDRG  ERNLIYITVI  DSTGKILEQR  SLNTIQQFDY  QKKLDNREKE  RVAARQAWSV
961  VGTIKDLKQG  YLSQVIHEIV  DLMIHYQAV  VLENLNFGFK  SKRTGIAEKA  VYQOFEKMLI
1021  DKLNCLVLKD  YPAEKVGGVL  NPYQLTDQFT  SFAKMGTSQ  FLFYVPAPYT  SKIDPLTGFV
1081  DPFVWKTIKN  HESRKHFLG  FDFLHYDVKT  GDFILHFKMN  RNLSFQRLP  GFMPAWDIVF
1141  EKNETQFDAQ  GTPFIAGKRI  VPVIENHRFT  GRYRDLYPAN  ELIALLEEKG  IVFRDGSNIL
1201  PKLLENDSSH  AIDTMVALIR  SVLQMRNSNA  ATGEDYINSP  VRDLNGVCFD  SRFQNPWPM
1261  DADANGAYHI  ALKGQLLLNH  LKESKDLKLQ  NGISNQDWLA  YIQELRN (SEQ ID NO:
174) .

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[0132] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a CRISPR Cas protein. In some embodiments, the CRISPR Cas protein comprises a Type VI CRISPR Cas protein or portion thereof. In some embodiments, the Type VI CRISPR Cas protein comprises a Cas13 protein or portion thereof. Exemplary Cas13 proteins of the disclosure may be isolated or derived from any species, including, but not limited to, a bacteria or an archaea. Exemplary Cas13 proteins of the disclosure may be isolated or derived from any species, including, but not limited to, *Leptotrichia wadei*, *Listeria seeligeri serovar 1/2b (strain ATCC 35967 / DSM 20751 / CIP 100100 / SLCC 3954)*, *Lachnospiraceae bacterium*, *Clostridium aminophilum DSM 10710*, *Carnobacterium gallinarum DSM 4847*, *Paludibacter propionicigenes WB4*, *Listeria weihenstephanensis FSL R9-0317*, *Listeria weihenstephanensis FSL R9-0317, bacterium FSL M6-0635 (Listeria newyorkensis)*, *Leptotrichia wadei F0279*, *Rhodobacter capsulatus SB 1003*, *Rhodobacter capsulatus R121*, *Rhodobacter capsulatus DE442* and *Corynebacterium ulcerans*. Exemplary Cas13 proteins of the disclosure may be DNA nuclease inactivated. Exemplary Cas13 proteins of the disclosure include, but are not limited to, Cas13a, Cas13b, Cas13c, Cas13d

and orthologs thereof. Exemplary Cas13b proteins of the disclosure include, but are not limited to, subtypes 1 and 2 referred to herein as Csx27 and Csx28, respectively.

[0133] Exemplary Cas13a proteins include, but are not limited to:

Cas13a number	Cas13a abbreviation	Organism name	Accession number	Direct Repeat sequence
Cas13a1	LshCas13a	Leptotrichia shahii	WP_018451595.1	CCACCCCAATATCGAAGGGGACTAA AAC (SEQ ID NO: 175)
Cas13a2	LwaCas13a	Leptotrichia wadei	WP_021746774.1	GATTAGACTACCCCAAAAACGAAG GGGACTAAAAC (SEQ ID NO: 176)
Cas13a3	LseCas13a	Listeria seeligeri	WP_012985477.1	GTAAGAGACTACCTCTATATGAAAG AGGACTAAAAC (SEQ ID NO: 177)
Cas13a4	LbmCas13a	Lachnospiraceae bacterium MA2020	WP_044921188.1	GTATTGAGAAAAGCCAGATATAGTT GGCAATAGAC (SEQ ID NO: 178)
Cas13a5	LbnCas13a	Lachnospiraceae bacterium NK4A179	WP_022785443.1	GTTGATGAGAAGAGCCCAAGATAG AGGGCAATAAC (SEQ ID NO: 179)
Cas13a6	CamCas13a	[Clostridium] aminophilum DSM 10710	WP_031473346.1	GTCTATTGCCCTCTATATCGGGCTGT TCTCCAAAC (SEQ ID NO: 180)
Cas13a7	CgaCas13a	Carnobacterium gallinarum DSM 4847	WP_034560163.1	ATTAAAGACTACCTCTAAATGTAAG AGGACTATAAC (SEQ ID NO: 181)
Cas13a8	Cga2Cas13a	Carnobacterium gallinarum DSM 4847	WP_034563842.1	AATATAAACTACCTCTAAATGTAAG AGGACTATAAC (SEQ ID NO: 182)
Cas13a9	Pprcas13a	Paludibacter propionigenes WB4	WP_013443710.1	CTTGTGGATTATCCCAAAATTGAAG GGAACTACAAC (SEQ ID NO: 183)
Cas13a10	LweCas13a	Listeria weihenstephanensis FSL R9-0317	WP_036059185.1	GATTAGAGTACCTCAAAATAGAAG AGGTCTAAAAC (SEQ ID NO: 184)
Cas13a11	LbfCas13a	Listeriaceae bacterium FSL M6-0635 (Listeria newyorkensis)	WP_036091002.1	GATTAGAGTACCTCAAAACAAAAG AGGACTAAAAC (SEQ ID NO: 185)

Cas13a12	Lwa2cas13a	Leptotrichia wadei F0279	WP_021746774.1	GATATAGATAACCCCAAAAACGAA GGGATCTAAAAC (SEQ ID NO: 186)
Cas13a13	RcsCas13a	Rhodobacter capsulatus SB 1003	WP_013067728.1	GCCTCACATCACCGCCAAGACGACG GCGGACTGAAC (SEQ ID NO: 187)
Cas13a14	RcrCas13a	Rhodobacter capsulatus R121	WP_023911507.1	GCCTCACATCACCGCCAAGACGACG GCGGACTGAAC (SEQ ID NO: 188)
Cas13a15	RcdCas13a	Rhodobacter capsulatus DE442	WP_023911507.1	GCCTCACATCACCGCCAAGACGACG GCGGACTGAAC (SEQ ID NO: 189)

[0134] Exemplary wild type Cas13a proteins of the disclosure may comprise or consist of the amino acid sequence:

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1  MGNLFGHKRW  YEVRDKKDFK  IKRKVKVKNR  YDGNKYILNI  NENNNKEKID  NNFIRKYIN
61 YKKNNDNILE  FTRKFHAGNI  LFKLGKKEGI  IRIENDDDFL  ETEEVVLYIE  AYGKSEKLKA
121 LGITKKKIID  EAIRQGITKD  DKKIEIKRQE  NEEEEIEIDIR  DEYTNKTLND  CSIILRIIEN
181 DELETKKSIY  EIFKNINMSL  YKIIIEKIIEN  ETEKVFENRY  YEEHLREKLL  KDDKIDVILT
241 NFMEIREKIK  SNLEILGFVK  FYLVGGDKK  KSKNKKMLVE  KILNINVDLT  VEDIADFKVIK
301 ELEFWNITKR  IEKVKKVNE  FLEKRRNRTY  IKSYVLLDKH  EKFKIERENK  KDKIVKFFVE
361 NIKNSIIEK  IEKILAEFKI  DELIKKLEKE  LKKGNCDTEI  FGIFKKHYKV  NFDSKKFSKK
421 SDEEKELYKI  IYRYLKGRIE  KILVNEQKVR  LKKMEKIEIE  KILNESILSE  KILKRVKQYT
481 LEHIMYLGKL  RHNDIDMTTV  NTDDFSRLHA  KEELDLELIT  FFASTNMELN  KIFSRENINN
541 DENIDFFGGD  REKNYVLDKK  ILNSKIKIIR  DLDFIDNKNN  ITNNFIRKFT  KIGTNERNRI
601 LHAISKERDL  QGTQDDYKVV  INIIQNLKIS  DEEVSKALNL  DVVFKDKKNI  ITKINDIKIS
661 EENNDIKYL  PSFSKVLPEI  LNLRYRNNPKN  EPFDTIETEK  IVLNALIYVN  KELYKKLILE
721 DDLEENESKN  IFLQELKKT  GNIDEIDENI  IENYKNAQI  SASKGNNAI  KKYQKQVIEC
781 YIGYLRKNYE  ELDFDFDFKM  NIQEIKKQIK  DINDNKTYER  ITVKTSDKTI  VINDDFEYII
841 SIFALLNSNA  VINKIRNRFF  ATSVWLNTSE  YQNIIDILDE  IMQLNLTNRNE  CITENWNLNL
901 EEFIQMKKEI  EKDFDDFKIQ  TKKEIFNNY  EDIKNNILTE  FKDDINGCDV  LEKKLEKIVI
961 FDDETKFEID  KKSNIQDEQ  RKLSNINKKD  LKKKVDQYIK  DKDQEIKSKI  LCRIIFNSDF
1021 LKKYKKEIDN  LIEDMESENE  NKFQEIYYPK  ERKNELYIYK  KNLFNLGNP  NFDKIYGLIS
1081 NDIKMAKAF  LFNIDGKNIR  KNKISEIDAI  LKNLNDKLN  GYSKEYKEYI  KKLKENDDF
1141 AKNIQNKYK  SFEKDYNRVS  EYKIRDLE  FNYLNKIESY  LIDINWKLAI  QMARFERDMH
1201 YIVNGLREL  IIKLSGYNTG  ISRAYPKRNG  SDGFYTTTAY  YKFFDEESYK  KFEKICYGFG
1261 IDLSENSEIN  KPENESIRNY  ISHFYIVRNP  FADYSIAEQI  DRVSNLLSYS  TRYNNSTYAS
1321 VFEVFKKDVN  LDYDELKKKF  KLIGNNDILE  RLMKPKKVS  VLELESYNSDY  IKNLIIELLT
1381 KIENNTDTL (SEQ ID NO: 190).

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[0135] Exemplary Cas13b proteins include, but are not limited to:

Species	Cas13b Accession	Cas13b Size (aa)
Paludibacter propionicigenes WB4	WP_013446107.1	1155
Prevotella sp. P5-60	WP_044074780.1	1091
Prevotella sp. P4-76	WP_044072147.1	1091
Prevotella sp. P5-125	WP_044065294.1	1091
Prevotella sp. P5-119	WP_042518169.1	1091
Capnocytophaga canimorsus Cc5	WP_013997271.1	1200
Phaeodactylibacter xiamenensis	WP_044218239.1	1132

<i>Porphyromonas gingivalis</i> W83	WP_005873511.1	1136
<i>Porphyromonas gingivalis</i> F0570	WP_021665475.1	1136
<i>Porphyromonas gingivalis</i> ATCC 33277	WP_012458151.1	1136
<i>Porphyromonas gingivalis</i> F0185	ERJ81987.1	1136
<i>Porphyromonas gingivalis</i> F0185	WP_021677657.1	1136
<i>Porphyromonas gingivalis</i> SJD2	WP_023846767.1	1136
<i>Porphyromonas gingivalis</i> F0568	ERJ65637.1	1136
<i>Porphyromonas gingivalis</i> W4087	ERJ87335.1	1136
<i>Porphyromonas gingivalis</i> W4087	WP_021680012.1	1136
<i>Porphyromonas gingivalis</i> F0568	WP_021663197.1	1136
<i>Porphyromonas gingivalis</i>	WP_061156637.1	1136
<i>Porphyromonas gulae</i>	WP_039445055.1	1136
<i>Bacteroides pyogenes</i> F0041	ERI81700.1	1116
<i>Bacteroides pyogenes</i> JCM 10003	WP_034542281.1	1116
<i>Alistipes</i> sp. ZOR0009	WP_047447901.1	954
<i>Flavobacterium branchiophilum</i> FL-15	WP_014084666.1	1151
<i>Prevotella</i> sp. MA2016	WP_036929175.1	1323
<i>Myroides odoratimimus</i> CCUG 10230	EHO06562.1	1160
<i>Myroides odoratimimus</i> CCUG 3837	EKB06014.1	1158
<i>Myroides odoratimimus</i> CCUG 3837	WP_006265509.1	1158
<i>Myroides odoratimimus</i> CCUG 12901	WP_006261414.1	1158
<i>Myroides odoratimimus</i> CCUG 12901	EHO08761.1	1158
<i>Myroides odoratimimus</i> (NZ_CP013690.1)	WP_058700060.1	1160
<i>Bergeyella zoohelcum</i> ATCC 43767	EKB54193.1	1225
<i>Capnocytophaga cynodegmi</i>	WP_041989581.1	1219
<i>Bergeyella zoohelcum</i> ATCC 43767	WP_002664492.1	1225
<i>Flavobacterium</i> sp. 316	WP_045968377.1	1156
<i>Psychroflexus torquis</i> ATCC 700755	WP_015024765.1	1146
<i>Flavobacterium columnare</i> ATCC 49512	WP_014165541.1	1180
<i>Flavobacterium columnare</i>	WP_060381855.1	1214
<i>Flavobacterium columnare</i>	WP_063744070.1	1214
<i>Flavobacterium columnare</i>	WP_065213424.1	1215
<i>Chryseobacterium</i> sp. YR477	WP_047431796.1	1146
<i>Riemerella anatipestifer</i> ATCC 11845 = DSM 15868	WP_004919755.1	1096
<i>Riemerella anatipestifer</i> RA-CH-2	WP_015345620.1	949
<i>Riemerella anatipestifer</i>	WP_049354263.1	949
<i>Riemerella anatipestifer</i>	WP_061710138.1	951
<i>Riemerella anatipestifer</i>	WP_064970887.1	1096
<i>Prevotella saccharolytica</i> F0055	EKY00089.1	1151
<i>Prevotella saccharolytica</i> JCM 17484	WP_051522484.1	1152
<i>Prevotella buccae</i> ATCC 33574	EFU31981.1	1128
<i>Prevotella buccae</i> ATCC 33574	WP_004343973.1	1128
<i>Prevotella buccae</i> D17	WP_004343581.1	1128
<i>Prevotella</i> sp. MSX73	WP_007412163.1	1128
<i>Prevotella pallens</i> ATCC 700821	EGQ18444.1	1126
<i>Prevotella pallens</i> ATCC 700821	WP_006044833.1	1126

Prevotella intermedia ATCC 25611 = DSM 20706	WP_036860899.1	1127
Prevotella intermedia	WP_061868553.1	1121
Prevotella intermedia 17	AFJ07523.1	1135
Prevotella intermedia	WP_050955369.1	1133
Prevotella intermedia	BAU18623.1	1134
Prevotella intermedia ZT	KJJ86756.1	1126
Prevotella aurantiaca JCM 15754	WP_025000926.1	1125
Prevotella pleuritidis F0068	WP_021584635.1	1140
Prevotella pleuritidis JCM 14110	WP_036931485.1	1117
Prevotella falsenii DSM 22864 = JCM 15124	WP_036884929.1	1134
Porphyromonas gulae	WP_039418912.1	1176
Porphyromonas sp. COT-052 OH4946	WP_039428968.1	1176
Porphyromonas gulae	WP_039442171.1	1175
Porphyromonas gulae	WP_039431778.1	1176
Porphyromonas gulae	WP_046201018.1	1176
Porphyromonas gulae	WP_039434803.1	1176
Porphyromonas gulae	WP_039419792.1	1120
Porphyromonas gulae	WP_039426176.1	1120
Porphyromonas gulae	WP_039437199.1	1120
Porphyromonas gingivalis TDC60	WP_013816155.1	1120
Porphyromonas gingivalis ATCC 33277	WP_012458414.1	1120
Porphyromonas gingivalis A7A1-28	WP_058019250.1	1176
Porphyromonas gingivalis JCVI SC001	EOA10535.1	1176
Porphyromonas gingivalis W50	WP_005874195.1	1176
Porphyromonas gingivalis	WP_052912312.1	1176
Porphyromonas gingivalis AJW4	WP_053444417.1	1120
Porphyromonas gingivalis	WP_039417390.1	1120
Porphyromonas gingivalis	WP_061156470.1	1120

[0136] Exemplary wild type *Bergeyella zoohelcum* ATCC 43767 Cas13b (BzCas13b) proteins of the disclosure may comprise or consist of the amino acid sequence:

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1 menktslgnn iyynpfkppd ksyfagyfna amentdsvfr elgkrlkgke ytsenffdai
61 fkenislvey eryvklldsy fpmarlldkk evpikerken fkknfkgiik avrdlnrfyt
121 hkehgeveit deifgvldem lkstvlvtvkk kkvktdktk ilkksiekql dilcqqkkley
181 lrdtarkiee krrnqrerge kelvapfkys dkrddliaai yndafdvvid kkkdskless
241 kakyntksdp qqeegdlkip isknqvfl1 slfltkqeih afkskiagfk atvideatvs
301 eatvshgkns icfmatheif shlaykklkr kvrtaeinyg eaenaqlsv yaketlmmqm
361 ldelskvpdv vyqnlsevdq ktfiedwney lkenngdvgt meeeqvihpv irkryedkfn
421 yfairfldef aqfptlrfqv hlgnylhdsr pkenlisdr ikekitvfgr lselekkal
481 fikntetned rehyweifpn pnydfpkeni svndkdfpia gsildrekqp vagkigikvk
541 llnqqyvsev dkavkahqk qrkaskpsiq niieivpin esnpkeavf gggptaylsm
601 ndihsilyef fdkwekkkek lekkgekelr keigkelekk ivgkiqaiq qiiddktnak
661 ilkpyqdgn taidkeklik dlkqeqnilq klkdeqtvre keyndfiayq dknreinkvr
721 drnhkqylkd nlkrkypeap arkevlyyre kgkvavwlan dikrfmptdf knewkgeqhs
781 llqkslayye qckeelknll pekvfqhlpf klggyfqqky lyqfytcyld krleyisglv
841 qqaenfxsen kvfkkvenec fkflkkqnyt hkeldarvqs ilgypifler gfmdekptii
901 kgktfkgnea lfadwfryyk eyqnfqtfyd tenyplvele kkqadrkrkt kiyyqqkndv
961 ftllmakhif ksvfkqdsid qfsledlyqs reerlgnqr arqtgerntn yiwnktvdlk

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1021 lcdgkitven vklknvgdfi kyeydgrvga flkyeeniew qaflikeske eenypyvver
 1081 eiegyekvrr eellkevhli eeyilekvkd keilkkgdnq nfkyylngl lkqlknedve
 1141 sykvfnlnte pedvniqlk qeatdleqka fvltyrnkf ahnqlpkkef wdycqekyqk
 1201 ektyaey faevfkkeke alik (SEQ ID NO: 191).

[0137] In some embodiments of the compositions of the disclosure, the sequence encoding the first RNA binding protein comprises a sequence isolated or derived from a CasRX/Cas13d protein. CasRX/Cas13d is an effector of the type VI-D CRISPR-Cas systems. In some embodiments, the CasRX/Cas13d protein is an RNA-guided RNA endonuclease enzyme that can cut or bind RNA. In some embodiments, the CasRX/Cas13d protein can include one or more higher eukaryotes and prokaryotes nucleotide-binding (HEPN) domains. In some embodiments, the CasRX/Cas13d protein can include either a wild-type or mutated HEPN domain. In some embodiments, the CasRX/Cas13d protein includes a mutated HEPN domain that cannot cut RNA but can process guide RNA. In some embodiments, the CasRX/Cas13d protein does not require a protospacer flanking sequence. Also see WO Publication No. WO2019/040664 & US2019/0062724, which is incorporated herein by reference in its entirety, for further examples and sequences of CasRX/Cas13d protein, without limitation, specific reference is made to

[0138] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig6049000251:

LYLTSFGKGN AAVIEQKIEP ENGYRVTGMQ ITPSITVNKA TDESVRFRVK RKIAQKDEFI	60
ADNPMHEGRH RIEPSAGSDM LGLKTKLEKY YFGKEFDDNL HIQIIYNILD IEKILAVYST	120
NITA	124

(SEQ ID NO: 54).

[0139] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig546000275:

MDSYRPKLYK LIDFCIFKHY HEYTEISEKN VDTLRAAVSE EQKESFYADE AKRLWGIFDK	60
QFLGFCKKIN VWVNGSHEKE ILGYIDKDAY RKSVDVSYFS KFLYAMSFFL DGKEINDLLT	120
TLINKFDNIA SFISTAKELD AEIDRILEKK LDPVTGKPLK GKNSFRNFIA NNVIENKRFI	180
YVIKFCNPKN VLKLVKNTKV TEFVLKRMPE SQIDRYYSSC IDTEKNPSVD KKISDLAEMI	240
KKIAFDDEFN VRQKTRTREE SLEKERFKAV IGLYLTVVYL LIKNLVNVNS RYVMAFHCLE	300
RDAKLYGINI GKNYIELTED LCRENENSRS AYLARNKRLR DCVKQNIDNA KNMKSKEK	358

(SEQ ID NO: 57).

[0140] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig4114000374:

DTKINPQTWL YQLENTPLDL NEYRDTLDHF FDERFNEINE HFVTQATNL CIMKEVFPDE	60
DFKSIADLYY DFIVVKS YKN IGFSIKKLRE KMLELPEAKR VTSTEMDSVR SKLYKLIDFC	120

IFKHHEKPE TVEMIVSMLR AYTSEDMKE 149

(SEQ ID NO: 61).

[0141] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig721000619:

KEGSTMAKNE KKKSTAKALG LKSSFVVNND IYMTSFGKGN KAVLEKKITE NTIENKSDTT 60
 YFDVINRDPK GFTLEGRRIA DMTAFSNDPK YHVNVVNGKF LEDQLGARSE LEKKVFGRTF 120
 DDNVHIQLIH NILDIEKIMA QYVSDIVYLL HNTIKRDMND DIMGYISIRN SFDDFCHPER 180
 IPDRKAKDNL QKQHDIFFDE ILKCGRLAYF GNAFFEDGSD NKEIAKLKRY KEIYHIIALM 240
 GSLRQSYFHG ENSDKNFQGP TWAYTLESNL TGKYKEFKDT LDKTFDERYE MISKDFGSTN 300
 MVNLQILEEL LKMLYGNVSP 320

(SEQ ID NO: 67).

[0142] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig2002000411:

EKQNKAKYQA IISLYLMVMY QIVKNMIYVN SRYVIAFHCL ERDSNQLLGR FNSRDASMYN 60
 KLTQKFITDK YLNDGAQGC S KKVGNL SHN ITCCSDELRK EYRNQVDHFA VVRMIGKYAA 120
 DIGKFSTWFE LYHYVMQRII FDKRNPLSET ERTYKQLIAK HHTYCKDLVK ALNTPFGYNL 180
 ARYKNLSIGE LFDNRNNYNAK TKET 204

(SEQ ID NO: 69).

[0143] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig13552000311:

LIDFLIYDLY YNRKPARIEE IVDKLRRESVN DEEKESIYSA ETKYVYEALG KVLVRSLLKKY 60
 LNGATIRDLDK NRYDAKTANR IWDISEHSHS GHVNCFCCLI YMTLMLDGK EINDLLTTLV 120
 NKFDNIASF I DVMDELGLEH SFTDNYKMFA DSKAICLDLQ FINSFARMSK IDDEKSKRQL 180
 FRDALVVDI GDKNEDWIEK YLTSDFKRD ENGNKIDGK RDFRNFIANN VIKSARFKYL 240
 VKYSSADGMI KKKNEKLIS FVLEQLPETQ IDRYYESCGL DCAVADRKVR IEKLTGLIRD 300
 MRFDNFRGVN YSNDACKKDK QAKAKYQAI SLYLMVLYQI VKNMIYVNSR YVIAFHCLER 360
 DLLFFNIELD NSYQYSNCNE LTEKFIKDKY MKEGALGFNM KAGRYLTKNI GNCSNELRKI 420
 YRNQVDHFAV VRKIGNYAAD IASVGSWFE 449

(SEQ ID NO: 71).

[0144] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig10037000527:

YMDQNFANS AWAIHVYR NK IQHLDAVRHA DMYIGDIREF HSWFELYHYI IQRRIIDQYA 60
 YESTPGSSRD GSAIIDEERL NPATRRYFRL ITTYKT 96

(SEQ ID NO: 72).

[0145] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig238000329:

RYDKDRSKIY TMMDFVIYRY YIDNNNSID FINKLRSSID EKSKEKLYNE EANRLWNKLLK 60

```

EYMLYIKEFN  GKLASRTPDR  DGNISEFVES  LPKIHRLPR  GQKISNFSKL  MYLLTMFLDG      120
KEINDLLTTL  INKFENIQGF  LDIMPEINVN  AKFEPEYVFF  NKSHEIAGEL  KLIKGFQMG      180
EPAATLKLEM  TADAIKILGT  EKEDAELIKL  AESLFKDENG  KLLGNKQHGGM  RNFIGNNVIK     240
SKRFHYLIRY  GDPAHLHKIA  TNKNVRFVL  GRIADMQKKQ  GQKGKNQIDR  YEVVCVGNKD     300
IKKTIEEKID  ALTDIIVNMN  YDQFEKKAV  IENQNRGKTF  EEKNKYKRDN  AEREKFKKII     360
SLYLTVIYHI  LKNIVNVNSR  YILGFHCLER  DKQLYIEKYN  KDKLDGFVAL  TKFCLGDEER     420
YEDLKAKAQA  SIQALETANP  KLYAKYMNYS  DEEKKEEFKK  QLNREVRKNA  RNAYLKNIKN     480
YIMIRLQLRD  QTDSSGYLCG  EFRDKVAHLE  VARHAHEYI                                519
    
```

(SEQ ID NO: 73).

[0146] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig2643000492:

```

NGEIVSLAEK  EAFSAKIADK  NIGCKIENKQ  FRHPKGYDVI  ADNPIYKGGSP  RQDMLGLKET      60
LEKRYFSPSD  SIDNVRVQVA  HNILDIEKIL  AEYITNAVYS  FDNIAGFGKD  IIGDDFSPVY     120
TYDKFEKSDR  YEYFKNLLNN  SRLGYYQAF  FECDDSKENK  KKKDAIKCYN  IIALLSGLRH     180
W                                                    216
    
```

(SEQ ID NO: 84).

[0147] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig874000057:

```

MSKNKESYAK  GMGLKSALVS  GSKVYMTSFE  GGNDAKLEKV  VENSEIVSLA  EKESFSAEIF      60
KKNIGCKIEN  KKFKHPKRYD  VIADNPLYKG  SVRQDMLGLK  ETLEKRYFNS  ADGTDNVCIQ     120
VIHNILDIEK  ILAEYITNAV  YSFDNIAGFG  EDIIGMGGFK  PIYTYKQFKE  PDKYNKKFDD     180
ILNNSRLGYY  GKAFFEKNDL  KHNPKNKKRD  KNPYILKYDN  ECYIIALLS  GLRHWNIHSH     240
AKDDLVSYRW  LYNLDSILNR  EYISTLNLYL  DDIADDELTE  FSKNSSANVN  YIAETLNIDP     300
SEFAQQYFRF  SIMKEQKNMG  FNVSKLREIM  LDRKELSDIR  DNHRVFDSIR  SKLYTMMDFV     360
IYRYYIEEAA  KTEAENRNLP  ENEKKISEKD  FFVINLRGSF  DENQKEKLYI  EEAKRLWEKL     420
KDIMLKIKEF  RGEKVKEYKK                                444
    
```

(SEQ ID NO: 85).

[0148] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig4781000489:

```

LDKQLDYEYI  RTLNYMFNDI  ADELTRTFSK  NSAANVNYIA  ETLNIDPNKF  AEQYFRFSIM      60
KEQKNLGFNL  TKLRESMLDR  RELSDIRDNH  NVFDSIRPKL  YTMMDFVIYK  HYIDEAKKTE     120
AENKSLPDDR  KNLSEKD                                137
    
```

(SEQ ID NO: 86).

[0149] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig12144000352:

```

RMGEPVANTK  RVMIDAVKI  LGTDLSDDEL  KEMADSFVKD  SDGNLLKKGK  HGMRNFITNN      60
VIKNKRFHYL  IRYGPAHLH  EIAKNEA                                87
    
```

(SEQ ID NO: 87).

[0150] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig5590000448:

VHNNEEKDLI KYTWLYNLDK YLDAEYITTL NYMYNDIGDE LTDSEFSKNSA ANINYIAETL	60
GIDPKTFAEQ YFRFSIMKEQ KNLGFNLTKL REVMLDRKDM SEIRENHND F DSIRAKVYTM	120
MDFVIYRYII EEAQVNAAN KSLPDNEKSL SEKDIFVISL RGSFNEDQKD RLYYDEAQL	180
WSKVGKMLK IKKFRGKDTR KYKNMGTPRI RRLIPEGRDI STFSKLMYAL TMFLDGKEIN	240
DLTTLINKF DNIQSFLKVM PLIGVNAKFA EEYSFFNNSE KIADELRLIK SFARMGEPVA	300
DARRAMYIDA IRILGTDLSD DELKALADSF SLDENGNKLG KGKHGMRNFI INNVITNKRF	360
HYLIRYGNPV HLHEIAKNEA VVKFVLGRIA DIQKKQGQNG KNQIDRYYET CIGK	414

(SEQ ID NO: 88).

[0151] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig525000349:

MSKKENRKS Y VKGLGLKSTL VSDSKVYLT FADGSNAKLE KCVENNKIIC ISNDKEAFAA	60
SIANKNVGYK IKNDEKFRHP KGYDIISNNP LLHNSVQQD MLGLKNVLEK RYFGKSSGGD	120
NNLCIQIHN IIDIEKILSE YIPNVVYAFN NIAGFKDEHN NIIDIIGTQT YNSSYTYADF	180
SKDKSDKKYI EFQKLLKNKR LGYWGKAFFT GQGNNAKVRQ ENQCFHIAL LISLRNWATH	240
SNELDKHTR TWLYKLDLTDN ILNAEYVKTLY NYLYDTIAD LTKSFSKNGA VNVNLYLAKKY	300
NIKDDLPGFS EQYFRFSIMK EQKNLGFNIS KLRENMLDFK DMSVI	345

(SEQ ID NO: 89).

[0152] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig7229000302:

KKISSLTFC LGESDEKLLK ALAKSLEEL KTNSKLYEN YIKYSDERKA EEAKRQINRE	60
RAKTAMNAHL RNTKWNDIMY GOLKDLADSK SRICSEFRNK AAHLEVARYA HMYINDISEV	120
KSYFRLYHYI MQRRIIDVIE NNPKAKYEGK VKVYFEDVKK NKKYNKLLK LMCVPGYCI	180
PRFKNLSIEQ MFDMNEDNS DKKKEK	206

(SEQ ID NO: 90).

[0153] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig3227000343:

IGDISEVNSY FQLYHYIMQR ILIDKIGSKT TGKAKEYFDS VIVNKYDDR LLKLLCSPLG	60
YCLTRYKDLS IEALFDMNEA AKYDKLNKER KNKKK	95

(SEQ ID NO: 91).

[0154] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Gut_metagenome_contig7030000469:

SIRSKLYTMM DFVIYRYIE ESAKAAAENK PSESDFVIR LRGSFNENQK EELYIEEAER	60
LWKKFGEIML KIKEFRGEKV KEYKKEVPRI ERILPHGKDI SAFSKLMYML SMFLD	115

(SEQ ID NO: 92).

[0155] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d gut_metagenome_P17E0k2120140920, c87000043:

```
MYFSKMIYML TYFLDGKEIN DLLTTLISKF DNIKEFLKIM KSSAVDVECE LTAGYKLFND      60
SQRITNELFI VKNIASMRKP AASAKLTMFR DALTLGIDD KITDDRISEI LKLKEKGKGI      120
HGLRNFITNN VIESSRFVYL IKYANAQKIR EVAKNEKVVV FVLGGIPDTQ IERYYKSCVE      180
FPDMNSSLEA KRSELARMIK NISFDDFKNV KQQAKGRENV AKERAKAVIG LYLT          234
```

(SEQ ID NO: 93).

[0156] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OBVH01003037.1, human gut metagenome sequence (also found in WGS contigs emb|OBXZ01000094.1| and emb|OBJF01000033.1|):

```
MAKKKRITAK ERKQNHRELL MKKADSNAEK EKAKKPVVEN KPDTAISKDN TPKPNKEIKK      60
SKAKLAGVVKW VIKANDDVAY ISSFGKGNNS VLEKRIMGDV SSNVNKDSHM YVNPKYTKKN      120
YEIKNGFSSG SSLVTYPNKP DKNSGMDALC LKPYFEKDFE GHIFTDNMHI QAIYNIFDIE      180
KILAKHITNI IYTVNSFDRN YNQSNDTIG FGLNYRVPYS EYGGGKDSNG EPKNQSKWEK      240
RDNFIKFYNE SKPHLGYEYEN IFYDHGEPIS EEKFNLYLNI LNFIRNNTFH YKDDDIELYS      300
ENYSEEFVFI NCLNKFVKNK FKNVKNFIS NEKNNLYIIL NAYGKDTENV EVVKKYSKEL      360
YKLSVLKTNK NLGVNVKCLR ESAIEYGYCP LPYDKEKEVA KLSSVKHKLY KTYDFVITHY      420
LNSNDKLLLE IVETLRLSKN DDEKENVYKK YAEKLFKADD VINPIKAISK LFARKGNKLF      480
KEKIIIKKEY IEDVSDKNI YDFTKVIFFM TCFLDGKEIN DLLTNIISKL QVIEDHNNVI      540
KFISNNKDAV YKDYSKYAI FRNAGKIATE LEAIKSIARM ENKIENAPQE PLLKDALLSL      600
GVSDDTKMLE NTYNKYFDSK EKTDKQSQKV STFLMNNVIN NNRFKYVIKY INPADINGLA      660
KNRYLVKFLV SKIPEEQIDS YYKLFSEEE PGCEKIKLL TKKISKLNFO TLFENNKIPN      720
VEKEKKKAI TLYFTIVYIL VKNLVNINGL YTLALYFVER DGYFYKDICG KKDKKSYND      780
VDYLLPEIF SGSKYREETK NLKLPKEKDR DIMKKYLPND KDREKYNKFF TAYRNNIVHL      840
NIIAKLSELT KNIDKDINSY FDIYHYCTQR VMFNKYCKEKN DVVLAKMKDL AHIKSDCNEF      900
SSKHTYPFSS AVLRFMNLPF AYNVPRFKNL SYKKFFDKQ          939
```

(SEQ ID NO: 94).

[0157] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig tpg|DJXD01000002.1| (uncultivated Ruminococcus assembly, UBA7013, from sheep gut metagenome):

```
MKKQKSKKTV SKTSGLKEAL SVQGTVIMTS FGKGNMANLS YKIPSSQKPQ NLNSSAGLKN      60
VEVSGKKIKF QGRHPKIATP DNPLFKPQPG MDLLCLKDKL EMHYFGKTFD DNIHIQLIYQ      120
ILDIEKILAV HVNNIVFTLD NVLHPQKEEL TEDFIGAGGW RINLDYQTLR GQTNKYDREFK      180
NYIKRKELLY FGEAFYHENE RRYEEDIFAI LTLALSARQF CFHSDLSSDE SDHVNSFWLY      240
QLEDQLSDEF KETLSILWEE VTERIDSEFL KTNTVNLHIL CHVFPKESKE TIVRAYYEFL      300
IKKSFKNMGF SIKKLRREIML EQSDLKSFKE DKYNSVRAKL YKLFDFIITY YYDHHAFEKE      360
ALVSSLRSSL TEENKEEYI KTARTLASAL GADFKKAAAD VNAKNIRDYQ KKANDYRISF      420
```

EDIKIGNTGI	GYFSELIYML	TLLLDGKEIN	DLTTLINKF	DNIISFIDIL	KKLNLEFKFK	480
PEYADFFNMT	NCRYTLEELR	VINSIARMQK	PSADARKIMY	RDALRILGMD	NRPDEEIDRE	540
LERTMPVGAD	GKFIKKGQGF	RNFIASNVIE	SSRFHYLVRY	NNPHKTRTLV	KPNVVKFVL	600
EGIPETQIKR	YFDVCKGQEI	PPTSDKSAQI	DVLARIISSV	DYKIFEDVPQ	SAKINKDDPS	660
RNFSDALKKQ	RYQAIVSLYL	TVMYLITKNL	VYVNSRYVIA	FHCLEERDAFL	HGVTLPKMKN	720
KIVYSQLTTH	LLTDKNYTTY	GHLKNQKQHR	KWYVLVKNNL	QNSDITAVSS	FRNIVAHISV	780
VRNSNEYISG	IGELHSYFEL	YHYLVQSMIA	KNNWYDTSHQ	PKTAEYLNLL	KKHHTYCKDF	840
VKAYCIPFGY	VVPRYKNLTI	NELFDRNNPN	PEPKKEEV			877

(SEQ ID NO: 95).

[0158] An exemplary direct repeat sequence of CasRX/Cas13d Metagenomic hit (no protein accession): contig tpg|DJXD01000002.1| (uncultivated Ruminococcus assembly, UBA7013, from sheep gut metagenome) (SEQ ID NO: 95) comprises or consists of the nucleic acid sequence:

CasRX/Cas13d DR:

caactacaac cccgtaaaaa tacggggttc tgaaac 36

[0159] (SEQ ID NO: 96).

[0160] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig OGZC01000639.1 (human gut metagenome assembly):

MKKKNIRATR	EALKAQKIKK	SQENEALKKQ	KLAEEAAQKR	REELEKKNLA	QWEETSAEGR	60
RSRVKAVGVK	SVFVVGDDLY	LATFGNGNET	VLEKKITPDG	KITTFPEEET	FTAKLKFAQT	120
EPTVATSIGI	SNGRIVLPEI	SVDNPLHTTM	QKNTIKRSAG	EDILQLKDVL	ENRYFDRSFN	180
DDLHIRLIYN	ILDIEKILAE	YTTNAVFAID	NVSGCSDDFL	SNFSTRNQWD	EFQNPEQHRE	240
HFGNKDNVIC	SVKKQQDLFF	NFFKNNRIGY	FGKAFFHAES	ERKIVKKTEK	EVYHILTLIG	300
SLRQWITHTS	EGGISRLWLY	QLEDALSREY	QETMNNCYN	TIYGLQKDFE	KTNAPNLNFL	360
AEILGKNASE	LAEPYFRFII	TKEYKNLGFS	IKTLREMLLD	QPDLQEIREN	HNVDYSIRSK	420
LYKMIDFVLV	YAYSNERKSK	ADALASNLRS	AITEDAKKRI	YQNEADQLWT	SYQELFKRIR	480
GFKGAQVKEY	SSKNMPIPIQ	KQIQNILKPA	EQVTYFTKLM	YLLTMFLDGK	EINDLLTTLI	540
NKFDNISSLL	KTMEQLELQT	TFKEDYTFQ	QSSRLCKEIT	QLKSFARMGN	PISNLKEVMM	600
VDAIQILGTE	KSEQELQSMA	CFFFRDKNGK	KLNTGEHGMR	NFIGNNVISN	TRFQYLIRYG	660
NPQKLHTLSQ	NETVVRVFLS	RIAKNQRVQG	MNGKNQIDRY	YETCGGTNSW	SVSEEEKINF	720
LCKILTNSY	DQFQDVKQSG	AEITAEKRRK	KERYKAIISL	YLTVLYQLIK	NLVNINARYI	780
IAFHCLERDA	ILYSSKFNTS	INLKKRYTAL	TEMILGYETD	EKARRKDTRT	VYEKAEAAKN	840
RHLKNVKWNC	KTRENLENAD	KNAIVAERNI	VAHLWIIRDA	DRFITGMGAM	KRYFDCYHYL	900
LQRELGYILE	KSNQGSEYTK	KSLEKVQQYH	SYCKDFLHML	CLPFAYCIPR	YKNLSIAELF	960
DRHEPEAEPK	EEASSVNNSQ	FITT				984

(SEQ ID NO: 97).

[0161] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OHBM01000764.1 (human gut metagenome assembly):

```

XXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX      60
XXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX      120
XXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX      180
XXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXHPLQKRYR YLTSTNLKSF          240
ETYKNNLVNK KKFDLDRVVK IPQLAYFGSA FYNTPEDTSA KITKTKIKSN EEIYYTFMLL          300
STARNFSAHY LDRNRAKSSD AEDFDGTSVI MYNLDNEELY KKLYNKKVHM ALTGMKKVLD          360
ANFNKVEHL NNSFIKNSAK DFVILCEVLG IKS RDEKTKF VKDYDFVVR KNYKHLGFSV          420
KELRELLFAN HDSNKYIKEF DKISNKKFDS VRSRLNRLAD YIIYDYNNKN NAKVSDLVKY          480
LRAAADDEQK KKIYLNESIN LVKSGILERI KKILPKLNGK IIGNMQPDST ITASMLHNTG          540
KDWHPISENA HYFTKWIYTL TLFMDGKEIN DLVTTLINKF DNIA SFIEVL KSQSVCTHFS          600
EERKMFI DSA EICSELSAMN SFARMEAPGA SSKRAMFVEA ARILGDNRSK EELEEYFDL          660
FDKSASKKEK GFRNFIRNNV VDSNRFKYL T RYDTSSVKA FSNKALVKF AIKDIPQEQI          720
LRYNSCFGA SERYNDGMS DKLVEAIGKI NLMQFNGVIQ QADRNLPEE KKKANAQKEK          780
YKSIIRLYLT VCYLFFKNLV YVNSRYYSAF YNLEKDRSLF EINGELKPTG KFDEGHY TGL          840
VKLFIDNGWI NPRASAYLTV NLANSDETAI RTFRNTAEHL EALRNADKYL NDLKQFDSYF          900
EIIHYITQRN IKEKCEMLKE QTVKYNNDDL KYHGYSKDFV KALCVPF GYN LPRFKNLSID          960
ALFDKNDKRE KLKKG FED                                978

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(SEQ ID NO: 98).

[0162] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OHCP01000044.1 (human gut metagenome assembly):

```

MAKKITAKQK REEKERLNKQ KWAKNDSVII VPETKEEIKT GEIQDNNRKR SRQKSQAKAM          60
GLKAVLSFDN KIAIASFVSS KNAKSSHIER ITDKEGTTIS VNSKMFESSV NKRDI NIEKR          120
ITIEEPQQDG TIKKEEKGVK STTCNPYFKV GGDYIGIKE IAEEHFFGRA FPNENLRVQI          180
AYNIFDVQKI LGTFVNIIY SFYNLSRDEV QSDNDVIGML YSISDYDRQK ETETFLQAKS          240
LLKQTEAYYA YFDDVFKNK KPDKNKEGDN SKQYQENLRH NFNILRVLSF LRQICMHAEV          300
HVSDDEGCTR TQNYTDSLEA LFNISKAFGK KMP ELKTLID NIYSKGINAI NDEFVKN GKN          360
NLYILSKVYP NEKREVL LRE YNFVVCKEG SNIGISTRKL KETMIAQNMP SLKEENTYRN          420
KLYTVMNFIL VRELKNCATI REQMIKELRA NMDEEEGRDR IYSKYAKEIY LYVKDKL KLM          480
LNVFKEEAEG IIPGKEDPV KFSHGKLDKK EIESFCLT TK NTEDITKVIY FLCKFLDGKE          540
INELCCAMMN KLDGISDLIE TAKQCGEDVE FVDQFKCLSK CATMSNQIRI VKNISR MKKE          600
MTIDNDTIFL DALELLGRKI EK YQDKNGD YVKDEKGGKV YTKDYNFQD MFFEGKNHRV          660
RNFVSNVVIK SKWFSYVVRY NKPAECQALM RNSKLVKFAL DELPDSQIEK YISVFG EKS          720
SSSNEEMRRE LLKLCDFSV RGFLDEIVLL SEDEM KQDK FSEK EKKSL IRLYLTIVYL          780
ITKSMVKINT RFSIACATYE RDYILLQSE KAERAWEKGA TAFALTRKFL NHDKPTFEQY          840
YTREREISAM PQEKRKELRK ENDQLLKKTH YSKHAYCYIV DNVNNTGAV ANDNGRGLPC          900
LSEKNDNANL FLEM RNKIVH LNVVHDMVKY INEIKNITSY YAFFCYVLQR MIIGNNSNEQ          960
NKFKAKYSKT LQEGTYSKD LMWV LNPFA YNLPRYKNLS NEQLFYDEEE RMEKIVGRKN          1020

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DSR

1023 (SEQ ID NO:

99).

[0163] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OGDF01008514.1| (human gut metagenome assembly):

MTETKPKRED	IAKTPAAKSR	SKAAGLKSTF	AVNGSVLLTS	FGRGNDVPE	KLITEKAVSE	60
INTVKPREFSV	EKPATSYSSS	FGIKSHISAT	ADNPLAGRAP	VGEDAIHAKE	VLEQRVFGKT	120
FSDDNIHIQL	IYNILDIRKI	LSTYANNVVF	TINSMRRLDE	YDREQDYLG	LYTGNSYERL	180
LDIADKYAVD	GEDWRNTAAG	ISNDFEKKQF	QTINGFWDLL	DMIEPYMCYF	SEAFFCETTV	240
KDPDSGRIVP	CLEQRSDGDI	YNILRILSIV	RQTCMHDNAS	MRTVMFTLGQ	NSVRDRKNGF	300
DELAELLDYL	YDEKIDIVNR	DFLRNQNNI	ELLSRIYGSS	ADSPERDLV	QNFYDFRVLS	360
QDKNLGFSIK	KLREKLLDSP	ALSVVRSKKY	DTMRSKIYSL	IDFMIYRKFS	ENHVAVDDEV	420
EELRSLLTED	EKESAYSRWA	ETLINDGFAQ	EILVKLLPQT	DPAVIGKIKG	KKLLNDSIAG	480
IKLKKDASFF	TKIINVLCMF	QDGKEINELV	SSLVNKFANI	QSFVDVMRSQ	GIDSGFTADY	540
AMFAESGRIS	RELHILKGIA	RMQHSIAGLG	DVKIYGSDDK	FHGVSRRVYT	DAAYILGFGE	600
RSEDNDGYVD	DYVSSKLLGG	ADKNLRFIT	NNVIKRRFL	YTVRYMNPKR	AKKLVQNDAL	660
VVLALSGIPE	TQIDRYKSC	IEKRSFNPDL	NEKIAALSEM	ITTLKIDDFE	DVKQNPEKNA	720
NYEAKKNQRI	SKERYKACIG	LYLTVLYLIC	KNLVKINARY	SIAIGCLERD	TQLHGVDFKG	780
AAYMTRDVEI	AKGWINPKK	TVKSIKEQYA	FLTPYIFTTY	RNMIAHLAAV	TNAYKYIPQM	840
DRFKSWFHL	HTVIQHSLIQ	QYEDRDYGR	KGAPVVSERV	LQLLEQCREH	SNYSRDLLHI	900
LNLFPGYNLP	RYLNLSSSEK	FDANAI				926

[0164] (SEQ ID NO: 100).

[0165] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OGPN01002610.1 (human gut metagenome assembly):

MAKKITAKQK	REEKERLNKQ	KWAKQDTPVV	PKSKTEEKPV	AASDDKLLKT	TQVKKVQTKS	60
KAKAMGLKTV	LSFDDKIAIA	SFVNDKKTCL	PHIERITDKS	GTTIHENARM	FDSSVDEQNV	120
NIEKRMTIEE	KQNDGTFKKD	EKDVKATICN	PYFKTCGKDY	IGIKDVAEKY	FFGKTFFPEN	180
LRVQIAYNVF	DIQKILGTYV	NNIIYSFYNL	RRDGKSDVDI	IGSLYAFADF	DNQLKDKPAF	240
REAKDLLKNT	EAYFSYFGDV	FKKSKKGKGD	ENNEDYEKNL	RHNFNVLRLV	SFLRQICTHA	300
YVKCTGGAKN	NGDSTKVEAE	SLDALFNITE	YFAKTAPELS	KTINEIYKEG	IDRINNDFVT	360
NGKNNLYILS	KVYPDMQRNE	LVKKYYQFVV	CKEGNNVGIN	TRKLKESIIS	QHPWITTPQD	420
NNKANDYESC	RHKLYTIMCF	ILVAELDAHE	SIRDNMVAEL	RANMDGDDGR	DAIYEKYAKD	480
IYHIVKDKLL	AMQKVFDEEL	VPVKVEGKND	PQQFTHGKLG	KKEIESFCLS	DKNTSDIAKV	540
VYFLCNFLDG	KEINELCCAM	MNKFDGIGDL	IDTAKQCGEE	VKFIEEFACL	SNCRKITNDI	600
RVAKSISKMK	NKVNIDNDII	YLDIAIELLGR	KIEKYQKDEN	GKILLGTDGK	RLYTQEYKYF	660
NDMFFNAGNH	KVRNFIANNV	MQSKWFFYVV	RYNKPAEQCI	IMRNKTLVKF	TLDDLDPMQI	720
QRYYSVFGD	NNMPAVDEMR	KRLLDKINQF	SVRGFLDELD	EIVLMSDEES	KRNKSSEKEQ	780
KKSLIRLYLT	IAYLITKSMV	KINTRFSIAC	AMYERDYALL	CQSEMKGGPW	DGGAQALAVT	840

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RKFLNHDREV  FDRYCAREAE  IARLPSEERK  PLRKANDKLL  KQTHYTNHSY  TYIVNNLNSF      900
TDIDYCAKDV  GLPAPNDKND  NASILGEMRN  DIAHLNIVHD  MVKYIEELKD  ISSYYAFYCY      960
VLQRRLVGKD  PNCQNKFKAK  YAKELNDYGT  YNKNLMWMLN  LPFAYNLPRY  KNLSSEFLFY     1020
DMEYNKKDDE                                     1030
    
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(SEQ ID NO: 101).

[0166] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): from contig emb|OBLI01020244 and emb|OBLI01038679 (from pig gut metagenome):

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MAKKITAKQR  REERERQNKQ  KWAKKQADAT  AVFECEADIK  PADSKDEDCT  NIYIKREKKK      60
TQAKAMGLKT  VLGFDNKIAI  ASFMSKDSK  SSHIERITDP  NGKTIREDVR  MFDSNVDECS     120
INLEKRMVTE  ERQKDGTIKK  DEKDVKSTIC  NPYSNECGKD  YIGIKSVAEE  LFFGRTFPND     180
NLRVQIAYNI  FDIQKILGTY  INNIIYSFYN  LSRDESQSDN  DVIQGLYMLK  DFDGQKETDT     240
FRQARALLER  TEAYYSYFDN  VFKKIDKNKK  KSDDCKRERN  EILRYNFNVL  RVLSFLRQIC     300
AHAQVKISNE  HDREKGGGLV  DSLDALFNIS  RFFDAVAPEL  NEVINSVYSK  GIDDINDNFV     360
KNGKNNFYIL  SKIYPEVARE  DLLREYFFV  VSKEGNNIGI  STKKLKEAII  VQDMSYIKSE     420
DYDTPYRNKLY  TVLCFILVKE  LNERTTIREQ  MVADLRANMN  GDIGREDIYS  KYAKIIYAQV     480
KPRFDTMKA  FEEEAKDVIV  PDKKPKVFS  HGKLDKNEIE  RFCITSANTD  SVAKIIYFLC     540
KFLDGKEINE  LCCAMMNKLD  GINDLIETAE  QCGAKVEFVD  KFSVLSNCET  ISDQIRIVKS     600
ISKMKKEIAI  DNDTIFLDAL  ELLGRKIDKY  KKDATGKYLK  DENGKYLISK  EYDDFQYMEF     660
KDSHRVRNFI  SNSVIKSKWF  SYIVRYNQPS  ECRAIMKNKT  LVKFALDELP  DLQIQRYFVA     720
LYGDEDLPSY  GEMRKILLKK  LHDFSIGFGL  DEIVLLSDLD  MESQDKYCEK  EQKKSFLRFLY   780
LTIAYLITKS  MVKINTRFSI  ACATYERDYA  LLCASNKQER  AWSSGATALA  LTRRFLNQDK     840
LIFEKHYARE  GEISKLPKEE  RKAMRKVNDQ  LLKRTHFSKH  SYCYIVDNVN  RLTGGECRTD     900
KRVLPVLENE  NDNAGILLDF  RKTIAHLNVV  HKMVDYVDEI  KGITSYYAFF  CYVLQRMVLG     960
NNLNEKNAIK  EKYSATVKSF  GTYSKDFMWL  INLPFAYNLP  RYKNLSNEQL  FYDEEERNET    1020
EEQIDRL                                           1027
    
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(SEQ ID NO: 102).

[0167] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig OIZX01000427.1:

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MAKKKKTARQ  LREEMQQQRK  QAIQKQQEQR  QEKAAAARET  AAPEQPAAAP  VPKRQRKSLA      60
KAAGLKSNEI  LDPQRRTTVM  TAFGQGSTAI  LEKQIVDRAI  SDLQPVQQFQ  VEPASAAKYR     120
LKNSRVRFPN  VTADDPLYRR  KGGFVPGMD  ALRRKNVLEQ  RFFGKSFADN  IHIQMIYSIL     180
DIHKILAAAS  GHIVHLLNIV  NGSKDRDFIG  MAAHVLYNE  LNEEAKRSIA  DFCKSPRLIY     240
YSAAFYETLD  NGKSERRSNE  DIFNILALMT  CLRNFSHHS  IAIKVKDYSA  AGLYNLRRLG     300
PDMKKMLDTF  YTEAFIQLNQ  SFQDHNTNL  TCLFDILNIS  DSARQQLAE  ERYRYVVFKE     360
QKNLGFVSRK  LREEMLLLDP  AAVIADKRYD  TCRSKLYNLM  DFLILRVYRT  GRADRCDKLP     420
EALRAALTDE  EKAVVYHKEA  LSLWNEMRTL  ILDGLLPQMT  PENLSRSLGQ  KRKGELSLDD     480
AMLKECLYEP  GPVPEAAPE  EANAEIFCRM  IYLATLFMDG  KEINTLLTTL  ISKFENIAAF     540
LQTMEOQLNIE  AELGPEYAMF  TRSRAVAEQL  RVINSFALMK  KPQVNAKQQL  YRAAVTLLGT     600
EDPDGVTDEM  LCIDPVTGKM  LPPNQRRHGD  TGLRNFIANN  VVESRRFQYL  IRYSDPAQLH     660
    
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QLASNKKLVR FVLSSIPDTQ INRYEETCGQ	TRLAGRAAKV EFLTDMIAAI RFDQFRDVNQ	720
KERGANTQKE RYKAMLGLYQ TVLYLAVKNL	VNINARYVMA FHCVERDMFL YDGELTDPKG	780
ESVSAFLAVN GKKGVQPQYL LLTQLFIRRD	YLKRSACEQI QHNMENISDR LLREYRNAVA	840
HLNVIAHLAD YSADMREITS YYGLYHYLMQ	RHLFKRHAWQ IRQPERPTEE EQKLIEQEQK	900
QLAWEKALFD KTLQYHSYNK DLVKALNAPF	GYNLARYKNL SIEPLFSKEA APAAEIKATH	960
A		961

(SEQ ID NO: 103).

[0168] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig OCTW011587266.1:

MKQNDRENNN KIKKSAKAV GVKSLARLSD	GSTVVSSFVK GAAAELES LI TGGEIRKLS D	60
KAILEITDDT QNKNAYNVKS SRIPNLTART	DKLSDKSGMD DLGFKRELEL EVFGQCFDDS	120
IHIQIAHAVF DIQKSLAAVI PNVLYTLNNL	DRSYSTDNTS DKKDIIGNTL NYQHSYSEFN	180
VEKRGEFTEY YNAAKDRFSY FPDILCVLEK	VNGKDRYQPK SEKDAENVLS SVNMLRNSLF	240
HFAPKSNQDG ARIAVFKNQF DSDFSHITST	VNKIYSAKIA GVNENFLNNE GNNLYIILKA	300
TNWDIKKIVP QLYRFSVLKS DKNMGFNMRK	LREFAVESKN IDLSRLNDKF LTNNRKKLYK	360
VIDFIIYYHL NKVLKDSFVD DFVAALRASQ	SEEEKEKLYA QYSERLFADE GLKSAIKKAV	420
DMISDTPKSN FKMKTPLDKA LIENIKVNSD	ASDFCKLIYV FTRFLDGKEI NILLNSLIKK	480
FQDIHSFNTT VKKLSENNLI INADYVDDYS	LFEQSGTVAR ELMLIKSISK MDFGLDNINL	540
SFMYDDALRT LGVSDENLPE VKREYFGKTK	NLSAYIRNNV LENRRFKYVI KYIHPSDVQK	600
IACNKALAGF VLNRMPTQI KRYYDSLINK	GATDIAQAQAK ALLDCITGIS FDAIKDDKHL	660
HKSKEKSPQR SADREKRAM LTLYYTIVYI	FVKQMLHINS LYTIGFFYLE RDQRFIYSRA	720
KKENKNPSKN SYLNDFRSVT AYFIPSEIMK	RIEKENKGF LEDFEALWNS CGKTSRLRKE	780
DVLLYARYIS PDHALKNYKM ILNSYRNKIA	HINVIMSAGK YTGGIKRMDS YFSVFQHLVQ	840
CDILSNPNK GKCFESESLK PLLLDMKFDG	TDEKLYSKRL TRALNIPFGY NVPRYKNLTF	900
EKIYLKSSIN E		911 (SEQ ID NO:

104).

[0169] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OGNF01009141.1:

MADIDKKKSS AKAAGLKSTF VLENNKLLMT	SFGNGNKAVI EKIIDEKVDS INEPEVFSVT	60
PCDKKFELQP AKRGLAADSL VDNPLKSKKT	AGDDAIHSRK FLERQFFDGN TFNDNIHIQL	120
IYNILDIEKI LSVHVNDIVY SVNNILSRGE	GMEYNDYIGT LNLKSFETYK NNLVNKKKFD	180
LDRVKKIPQL AYFGSAFYNT PEDTSAKITK	TKIKSNEEYI YTFMLLSTAR NFSAHYLDNR	240
RAKSSDAEDF DGTSMVIMYL DNEELYKKLY	NKKVHMALTG MKKVLDFANFN KKVEHLNNSF	300
IKNSAKDFVI LCEVLGIKSR DEKTKFVKDY	YDFVVRKNYK HLGFSVKELR ELLFANHDSN	360
KYIKEFDKIS NKKFDSVRSR LNRLADYIY	DYNNKNNAKV SDLVKYLRAA ADDEQKKKIY	420
LNESINLVKS GILERIKKIL PKLNGKIIGN	MQPDSITITAS MLHNTGKDWH PISENAHYFT	480
KWIYTLTFLM DGKEINDLVT TLINKFDNIA	SFIEVLKSQS VCTHFSEERK MFIDSAEICS	540
ELSAMNSFAR MEAPGASSKR AMFVEAARIL	GDNRSKEELE EYFDTLFDKS ASKKEKGFRN	600
FIRNNVVDSDN RFKYLTRYTD TSSVKAFSNN	KALVKFAIKD IPQEQLIRYY NSCFGASERY	660
YNDGMSDKLV EAIGKINLMQ FNGVIQQADR	NMLPEEKKKA NAQKEKYKSI IRLYLTVCYL	720

FFKNLVYVNS RYYSAFYNLE KDRSLFEING ELKPTGKFDE GHYTGLVKLF IDNGWINPRA	780
SAYLTVNLAN SDETAIRTFR NTAEHLEALR NADKYLNDLK QFDSYFEIYH YITQRNIKEK	840
CEMLKEQTVK YNNDLLKYHG YSKDFVKALC VPFYGNLPRF KNLSIDALFD KNDKREKLKK	900
GFED	904

(SEQ ID NO: 105).

[0170] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig emb|OIEN01002196.1:

MERQKRKMS KSKMAGVKS FVIGDELLMT SFGDGDDAVL EKDIDENGVV NDCRNPAAYD	60
AVYGTDSIRV KKTNNNIRAK VNNPLAKSNI RSEESALFRT RVNEYKREQK DKYETLFFGK	120
TFDDNIHQQL ISKILDIEKT FSVVIGNIVY AINNLSLEQS IDRPIDIFGD KNTQGISLRE	180
DNDYLKTMPL RCEYLFHNIL NSDSDNNSKM NYNKVNGKKE EKDNRRNENI EKLKKALEVI	240
KIIRVDSFHG VDGIKGDQKF PRSKYNLAVN YNEEIQTIS EPFNRRKVEEV QQDFYRNSCV	300
NIDFLKEIMY GSNYTDRGSD SLECSYFNFA ILKQNKMGF SITSIRECLL DLYELNFESM	360
QNLRRPRANSF CDFLIYDYIC KNESERANLV DCLRSAASEE EKKNIFYQTA ERVKEKFRNA	420
ENRISRFDAS YIKNSREKNL SGGSSLPKYS FIEGFTKRSK KINDNDEKNA DLFCNMLYYL	480
AQFLDGKEIN IFLTSIHNI FQNIDSFLKVM KEKGMECKFQ KDFKMFHSHAG HVAKKIEIVI	540
SLAKMKKTLT FYNAQALKDA VTILGVSKKH QYLDMNSYLD FYMFDNRSGA TGKNAGKDHN	600
LRNFLVSNVI RSRKFNYLSR YSNLAEVKKL AQNPSTLVQFV LSRIEPLIC RYESSQGIS	660
SEGITIDEQI KKLTTGIIVDM NIDSFENINN GEIGMRYSKA TPQSIERRNQ MRVCVGLYLN	720
VLYQIEKNLM NVNARYVLAF AFAERDALML NFTLEECKKN KKRSSGGFSF IEMTQFFIDK	780
KLFKVATEAI KKNVLKYNGN PESLNHIPGE YICKNMEGYH ENTVRNFRNM VAHLTAVARV	840
PLYISEVTQI DSYALYHYC MQMNILQGIE QSGKILDNIK LKNALENARV HRTYSKDAVK	900
YLCLPFAYNI SRYKALTIKD LFDWTEYSCK KDE	933

(SEQ ID NO: 106).

[0171] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Metagenomic hit (no protein accession): contig e-k87_11092736:

MKRQKTFAPR IGIKSTVAYG QGKYAITTFG KGSKAETIAVR SADPPEETLP TESDATLSIH	60
AKFAKAGRDG REFKCGDVDE TRIHTSRSEY ESLISNPAES PREDYLGKGLG TLERKFFGDE	120
YPKDNLRIQI IYSILDIQKI LGLYVEDILH FVDGLQDEPE DLVGLGLGDE KMQKLLSKAL	180
PYMGFFGSTD VFKVTKKREE RAAADEHNAK VFRALGAIQ KLAHFKWKES LAIFGANANM	240
PIRFFQGATG GRQLWNDVIA PLWKKRIERV RKSFLSNSAK NLWVLYQVFK DDTDEKPKAR	300
ARQYYHFSVL KEGKNLGFNL TKTREYFLDK FFPIFHSSAP DVKRKVDTFR SKFYAILDFI	360
IYEASVSVAN SGQMGKVAPW KGAIIDNALVK LREAPDEEAK EKIYNVLAAS IRNDSLFLRL	420
KSACDKFGAE QNRPVFPNEL RNNRDIRNVR SEWLEATQDV DAAAFVQLIA FLCNFLEGKE	480
INELVTALIK KFEGIQALID LLRNLEGVDS IRFENEFALE NDDKGNMAGR IARQLRLLAS	540
VGKMKPDMTD AKRVLYKSAL EILGAPPDEV SDEWLAENIL LDKSNNDYQK AKKTVNPFNR	600
YIAKNVITSR SFYYLVRYAK PTAVRKLMSN PKIVRYVLKR LPEKQVASYY SAIWTQSESN	660
SNEMVKLIEM IDRLTTEIAG FSAVLKDKK DSIVSASRES RAVNLEVERL KKLTTLYMSI	720
AYIAVKSIVK VNARYFLAYS ALERDLYFFN EKYGEEFRLH FIPYELNGKT CQFEYLAILK	780
YYLARDEETL KRKCEICEEI KVGCEKHKKN ANPPYEYDQE WIDKKKALNS ERKACERRLH	840
FSTHWAQYAT KRDNMAKHP QKWYDILASH YDELLALQAT GWLATQARND AEHLNPNVNEF	900

DVYIEDLRRY PEGT¹PKNKDY HIGSYFEIYH YIRQRAYLEE VLAKRKEYRD SGSFTDEQLD 960
 KLQKILDDIR ARGSYDKNLL KLEYLPPFAYN LPRYKNLTTE ALFDDDSVSG KKRVAEWREER 1020
 EKTREAEREQ RRQR 1034

(SEQ ID NO: 107).

An exemplary direct repeat sequence of CasRX/Cas13d Metagenomic hit (no protein accession):
 contig e-k87_11092736 (SEQ ID NO: 107) comprises or consists of the nucleic acid sequence:

CasRX/Cas13d Direct repeat 1: gtgagaagtc tccttatggg gagatgctac

(SEQ ID NO: 108).

[0172] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Ga0129306_1000735:

MQKQREQQTV TDESERKKKP LKSGAKAAGL KSVFVLSEGG ELLTSFGRGN EAVPEKRVTG 60
 GTIANARTDN KEAFSAALQN KRFEVFGRTA GSSDDPLAVS RAPGQDLIGA KTALEERYFG 120
 RAFADNIHQ VIYAIQDINK ILAVHANNIV YTLNNDREA DPETDDFIGS GYLTLKNTFE 180
 TYCDPAALNE REREKVTVSK QHFDAFMQNP RLAYYGNFAF RKLSKAERLA RGREIFDKES 240
 PERRQEILGS RGKNKSVDDDE IRALAPEWVK REERDVYSEL VLMSELRQSC FHGQKNSAR 300
 IFRLDNDLGP GVDGARELLD RLYAEKINDL RSFDKTSASS NFRLLFNAYH ADNEKKKELA 360
 QEFYRFVSLK VSKNTGFSIR TLREKIIEDH AAQYRDKIYD SMRKKLFSTF DFFLWRFYEE 420
 REDEAEELRA CLRAARSDEE KEQIYAEAAA SCWPSVKPFV ESVAATLCDV VKGRTKLNKL 480
 KLSADESTLV RNAIDGVRIS PRASYFTKLI YLMTLFLDGK EINDLLTTLI HAFENIDSFL 540
 SVLGSERLER TFDANYRIFA DSGVIAQELR AVNSFARMTT EPFNKLVMF EDAAQLFGMS 600
 GGLVEHAEEL REYLDNKMLD KTKLRLLPDG KVD¹TGFRNFI ISNVTESRRF RYLVRYCEPR 660
 AVR¹DYMSCRP LIRLTLRDMP DTILRRYYEQ SVGAATVDRE RILD¹TLADKL LSLRFTDFEN 720
 VNQRANAERN REKQMMGII SLYLNVAYQI VKNLVYV¹NAR YTMAYHCAER DTE¹LLNAAG 780
 EGNLLRRDRS WPARLHLPRR ALARRRRDVE VMERDVARGP EAYNRDEWLG LVRTLRRREKR 840
 VCDNLHNNYA YLCGADAEPG DASLSLLFVY RNKAAHLSVL NKGGR¹LSGDL KEAKSWFYVY 900
 HFLMQRVLEE EFRNTQALPE RLRELLMAE RYRGCSKDLI KVLNLTFAYN LPRYKNLSID 960
 GRFDKNHPDP SDE 973

(SEQ ID NO: 109).

[0173] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Ga0129317_1008067:

MKKQKKSIVK AAGLKSFAFVV GDSVYLTSFG KGNAARLDTK INPDNSTERY VSDSEKHTLK 60
 INSITDTELRLSGPFPKQAE AKNPTHKKDN EQKNTRQDML GLKSTLEK¹FY FGSTFDDNIH 120
 IQIIHNIQDI AKILAAHSNN AGYALDNMLA YQGV¹EFSDMI GYMGTSRTFD NYDPNHKNNK 180
 DFFRFLKLPRLGYFGSAFYS QKGKDFEKRS DEEVYNICAL MGQIRQCCFH GKQEKYQLKW 240
 LYNFHNFKSN KPFLDTLDKH FDEMIDRINK NFIKNNT¹PDILILSGLYPDM AKKELVRLFY 300
 DFTTVKEYKN MGF¹SVK¹KLRE KMLESE¹EASD FRDKDYDSVR RKLYKLMDFC IYYLYYSDSE 360
 RNENLVSRRL ESLTDENKDI IYSKEAKIVW NELRKKFSTI LDNVKGSNIK KLE¹NVKEKFI 420
 SEDEFDDIKL DIDISYFSKL MYVMCYFLDG KEINDLLTTL VSKFDNIGSI IEAATQIGIN 480
 IEFIDDFKFF DRSKDISVEL NIIRNFARMQ APVPNAKRAM QEDAIRILGG SEEDIFSILD 540

DMTGYDKSGK KLAQSKKGFR NFIINNVVES SRFKYIVRYS NPQKIRKLAN NSVVVGFVLG 600
 KLPDAQIESY FNSCLPNRVY STPDKARES L RDM LHNISFN DFADVKQDDR RATPEEKVEK 660
 ERYKAIIGLY LTVMYHLVKN LVYVNSRYVM AFHCLERDAM HYDVSLDNYR DLIRHLISEG 720
 DSSCNHFISH NRRMRDCIEE NVKNSEQLIF GKEDAVIRFR NNVAHL SAIR NAN EYIGDIR 780
 EITSYFALYH YLMQRKLIDD CKVNDTAHKY FEQLTKYKTY VMDMVKALCS PFGYNLPRFK 840
 NLSIEGKFDM HESK 854

(SEQ ID NO: 110).

[0174] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d Ga0224415_10048792:

MSKKENRKS Y VKGLGLKSTL VSDSKVYLT T FADGSNAKLE KCVENNKIIC ISNDKEAF AA 60
 SIANKNVGYK IKNDEKFRHP KGYDIISNNP LLHNNSVQQD MLGLKNVLEK RYFGKSSGGD 120
 NNLCIQI IHN IIDIEKILSE YIPNVVYAFN NIAGFKDEHN NIIDIIGTQT YNSSYTYADF 180
 SKDKSDKKYI EFQKLLKNKR LGYWGKAFFT GQGNNAKVRQ ENQCFHIIAL LISLRNWATH 240
 SNELDKHTKR TWLYKLDDTN ILNAEYVKTL NYLYDTIAD E LTKSFSKNGA VNVNYLAKKY 300
 NIKDDLPGFS EQYFRFSIMK EQKNLGFNIS KLRENMLDFK DMSVIRDDHN RYDKDRSKIY 360
 TMMDFVIYRY YIDNNNDSID FINKLRSSID EKSKEKLYNE EANRLWNK LK EYMLYIKEFN 420
 GKLASRTPDR DGNISEFVES LPKIHRL LPR GQKISNFSKL MYLLTMFLDG KEINDLLTTL 480
 INKFENIQGF LDIMPEINVN AKFEPEYVFF NKSHEIAGEL KLIKGF AQMG EPAATLKLEM 540
 TADAIKILGT EKEDAELIKL AESLFKDENG KLLGNKQHGM RNFIGNNVIK SKRFHYLIRY 600
 GDPAHLHKIA TNKNVVRFVL GRIADMQKKQ GQKGKNQIDR YYEVCVGNKD IKKTIEEKID 660
 ALTDIIIVNMN YDQFEK KAV IENQNRGKTF EEKNKYKRDN AEREKFKKII SLYLTVIYHI 720
 LKNIVNVNSR YILGFHCLER DKQLYIEKYN KDKLDGFVAL TKFCLGDEER FEDLKAKAQA 780
 SIQALETANP KLYAKYMNYS DEEKKEEFKK QLNRRERVKNA RNAYLKNIKN YIMIRLQLRD 840
 QTDSSGYLCG EFRDKVAHLE VARHAHEYIG NIKEVNSYFQ LYHYIMQCRL YDVLKNNTKA 900
 EAMVKGKAKE YFEALEKEGT YNDKLLKIAC VPFGYCIPRY KNLSMEELFD MNEEKKFKKK 960
 APENT 965 (SEQ ID NO:
 111).

[0175] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence

CasRX/Cas13d 160582958_gene49834:

MKNSVTFKLI QAQENKEAAR KKAKDIAEQ A RIAKRNGVVK KEENRINRIQ IEIQ TQKKS N 60
 TQNAYHLKSL AKAAGVKS VF AIGNDLLMTG FGPGN DATIE KRVFQNR AIE TLSSPEQYSA 120
 EFQNKQFKIK GNIKVLNHST QKMEEIQTEL QDNYNRPHF D LLGCKNVLEQ KYFGRTFSDN 180
 IHVQIAYNIM DIEKLLTPYI NNIIYTLNEL MRDNSKDDFF GCDSHF SVAY LYDELKAGYS 240
 DRLKTKPNLS KNIDRIWNNF CNYMNSDSGN TEARLAYFGE LFYKPKETGD AKSDYKTHLS 300
 NNQKEEWELK SDKEVYNI FA ILCDLRH FCT HGESITPSGK PFPYNLEKNL FPEAKQVLNS 360
 LFEEKAESLG AEAFGKTAGK TDVSI LLKVF EKEQASQKEQ QALLKEYYDF KVQKTYKNMG 420
 FSIKKLEAI MEIPDAAKFK DDLYSSLRHK LYGLDFDILV KHFLDTS DSE NLQNNDIFRQ 480
 LRACRCEEEK DVYRSIAVK VWEKVKKEL NMFQVVVIP SLSKDELKQM EMTKNT ELLS 540
 SIETISTQAS LFSEMI FMMT YLLDGKEINL LCTSLIEKFE NIASFNEVLK SPQIGYETKY 600
 TEGYAFFKNA DKTAKELRQV NNMARMTKPL GGVNTKCVMY NEAAKILGAK PMSKAELESV 660

FNLDNHDYTY SPSGKKIPNK NFRNFIINNV ITSRRFLYLI RYGNPEKIRK IAINPSIISF	720
VLKQIPDEQI KRYYPFCIGK RTDDVTLMRD ELGKMLQSVN FEQFSRVNKK QNAKQNPNGE	780
KARLQACVRL YLTVPYLFIK NMVNINARYV LAHFCLERDH ALCFNSRKLN DDSYNEMANK	840
FQMRKAKKE QYEKEYKCKK QETGTAHTKK IEKLNQQIAY IDKDIKMHS YTCRNYRNLV	900
AHLNVVSKLQ NYVSELPNDY QITSYFSFYH YCMLGLMEK VSSKNIPLVE SLKNEANDAQ	960
SYSAKKTLEY FDLIEKNRTY CKDFLKALNA PFSYNLPRFK NLSIEALFDK NIVYEQADLK	1020
KE	1022

(SEQ ID NO: 112).

[0176] An exemplary direct repeat sequence of CasRX/Cas13d proteins may comprise or consist of the sequence

CasRX/Cas13d 160582958 _gene49834 (SEQ ID NO: 112) comprises or consists of the nucleic acid sequence: CasRX/Cas13d DR:

gaactacacc cctctgttct ttaggggtc taacac	36
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(SEQ ID NO: 113).

[0177] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d 250twins_35838_GL0110300:

MGNKQVSAQ KRRENAKLCN QQKARQAESQ RDKIKNMNVE KMNINTNDI KHTKTTAKKL	60
GLKSTIIADK KIILTSFINE QSSKTANIEK VAGFKGDTID TISYTPRMFR SEINPGEIVI	120
SKGDDLSEFA NPANFPIGRD YVKIRSALEK QYFGKEFPED NLHVQIAYNV ADIKKILSVY	180
INNIIYMFYN LARSEEYDIF YNSQSENSGR DCDVIGSLY QASYRNQDAN RFEKDGKKA	240
IDSLDDTRA YTYFDGLFS VPKREDDGKI KESEKEKAKD QNFDVLRLLS VGRQLTFHSD	300
KSNNEAYLFD LSKLTRAADQ ENRRQDIQSL LNILNSTCRS NLEGVNGDFV KHAKNNLYVL	360
NQLYPSLKAN DLIGEYYNFI VKKENRNIGI RLITVRELI EHNITNLKDS KYDITRNKIY	420
TVLNFILFRE IQENSIAIKN FREKLRSTEK AEQPALYQAF ANKIYPMQA KFAKAIDLFE	480
EQYKTKFKSE FKGGISIENM QQQNILLQTE NIDYFSKYVL FLTQKFLDGKE INELLCALIN	540
KFDNIADLLD ISKQIGTPVV FCADYESLND AAKIAENIRL IKNIAHLRPA IQEAQSSKDN	600
ADAAGTPATL LIDAYNMLNT DIQLVYGEAA YEELRKLDFE RKNGTQYNKK GKKVDVYDHK	660
FRNFLINVI KSKWFFYIAK YVKPADCAKM MSNKKMIEFA LRDLPETQIK RYYYTITGNE	720
ALGDAESLKG VIIEQLHAFS IKNTLLSIKN MGEGEYKIQQ IGSSKEKKA IVNLYLTVAY	780
LLTKSLVKVN IRFSIAFGCL ERDLVLQKKS EKKFDAINE ILLEDDKIRK ECDKERAQAK	840
TLPRELAQER FAQIKRRESG CYFKSYHVYD YLSKNSNEFK QNHIDFAVTS YRNNVEHLNV	900
VHCMTKYFSE VKDVKSYYGV YCYIMQRMLC DELIKNQDK PDVRQTFEEY NRLLKDHGTY	960
SKNLMWLLNF PFAYNLARYK NLSNEDLFNA KNNDQKSK	998

(SEQ ID NO: 114).

[0178] Exemplary CasRX/Cas13d proteins may comprise or consist of the sequence:

CasRX/Cas13d 250twins_36050_GL0158985:

MKKKHQSAAE KRQVKLKNQ EKAQKYASEP SPLQSDTAGV ECSQKKTQVVS HIASSKTLAK	60
AMGLKSTLVM GDKLVITSFA ASKAVGGAGY KSANIEKITD LQGRVIEEHE RMFSADVGEK	120

NIELSKNDCH TNVNNPVVTN IGKDYIGLKS RLEQEFGKT FENDNLHVQL AYNILDIKKI 180
 LGTYVNNIIY IFYNLNRAGT GRDERMYDDL IGTLYAYKPM EAQQTYLLKG DKDMRRFEEV 240
 KQLLQNTSAY YVYGTLF EK VKAKSKKEQR AKEAEIDACT AHNYDVLRL L SLMRQLCMHS 300
 VAGTAFKLAE SALFNIEDVL SADLKEILDE AFSGAVNKL N DGFVQHSGNN LYVLQQLYPN 360
 ETIERIAEKY YRLTVRKEDL NMGVNIKKLR ELIVGQYFPE VLDKEYDLSK NGDSVVTYRS 420
 KIYTVMNYIL LYLEDHDSS RESMVEALRQ NREGDEGKEE IYRQFAKKVW NGVSGLFGVC 480
 LNLFKTEKRN KFRSKVALPD VSGAAYMLSS ENIDYFVKML FFVCKFLDGK EINELLCALI 540
 NKFNDIADIL DAAAQCGSSV WFDVSYRFFE RSRRI SAQIR IVKNIASKDF KSKKDSDES 600
 YPEQLYLDAL ALLGDVISKY KQNRDGSVVI DDQGNVLT E QYKRFYEFF EEIKRDESGG 660
 IKYKKS GKPE YNHQRRNFIL NNVLKS KWFF YVVKYNRPSS CRELMKNKEI LRFVLRDIPD 720
 SQVRRYFKAV QGEEAYASAE AMRTRLVDAL SQFSVTACLD EVGGMTDKEF ASQRAVDSKE 780
 KLRAIIRLYL TVAYLITKSM VKVNTREFSIA FSVLERDYLL IDGKKKSSD YTGEDMLALT 840
 RKFVGEDAGL YREWKEKNAE AKDKYFDKAE RKKVLRQNDK MIRKMHFTPH SLNYVQKNLE 900
 SVQSNGLAAV IKEYRNAVAH LNIINRLDEY IGSARADSY SLYCYCLQMY LSKNF SVGYL 960
 INVQKQLEEH HTYMKDLMWL LNI PFAYNLA RYKNLSNEKL FYDEEAAA EK ADKAENERGE 1020

(SEQ ID NO: 115).

[0179] Yan et al. (2018) *Mol Cell*. 70(2):327-339 (doi: 10.1016/j.molcel.2018.02.2018) and Konermann et al. (2018) *Cell* 173(3):665-676 (doi: 10.1016/j.cell/2018.02.033) have described CasRX/Cas13d proteins and both of which are incorporated by reference herein in their entireties. Also see WO Publication Nos. WO2018/183703 (CasM) and WO2019/006471 (Cas13d), which are incorporated herein by reference in their entirety.

[0180] Exemplary wild type Cas13d proteins of the disclosure may comprise or consist of the amino acid sequence:

[0181] **Cas13d (*Ruminococcus flavefaciens* XPD3002) sequence:**

1 IEKKKSFAGK MGVKSTLVSG SKVYMTTFAE GSDARLEKIV EGDSIRSVNE GEAFSAEMAD
 61 KNAGYKIGNA KFSHPKGYAV VANNPLYTGP VQDMLGLKE TLEKRYFGES ADGNDNICIQ
 121 VIHNIIDIEK ILAEYITNAA YAVNNISGLD KDIIGFGKFS TVYTYDEFKD PEHHRAAFNN
 181 NDKLINAIKA QYDEFDFLD NPRLGYFGQA FFSKEGRNYI INYGNECYDI LALLSGLAHW
 241 VVANNEESR ISRTWLYNLD KNLDNEYIST LNYLYDRITN ELTNSFSKNS AANVNYIAET
 301 LGINPAEFAE QYFRFSIMKE QKNLGFNITK LREVMLDRKD MSEIRKNHKV FDSIRTKVYT
 361 MMDFVIYRY I EEDAKVAAA NKSLPDNEKS LSEKDIFVIN LRGSFNDDQK DALYYDEANR
 421 IWRKLENIMH NIKEFRGNKT REYKKKDAPR LPRILPAGRD VSAFSKLMYA LTMFLDGKEI
 481 NDLLTTLINK FDNIQSFLKV MPLIGVNAKF VEEYAFFKDS AKIADELRLI KSFARMGEPI
 541 ADARRAMYID AIRILGTNLS YDELKALADT FSLDENGK L KKGKHGMRNF IINNVISNKR
 601 FHYLIRYGD P AHLHEIAKNE AVVKFVLGRI ADIQKQGGON GKNQIDRYYE TCIGKDKGKS
 661 VSEKVDALTK IITGMNYDQF DKKRSVIEDT GRENAEREKF KKIISLYLTV IYHILKNIVN
 721 INARYVIGFH CVERDAQLYK EKG YDINLKK LEEKGFSSVT KLCAGIDETA PDKRK DVEKE
 781 MAERAKESID SLESANPKLY ANYIKYSDEK KAEFTRQIN REKAKTALNA YLRNTKWNVI
 841 IREDLLRIDN KTCTLFANKA VALEVARYVH AYINDIAEVN SYFQLYHYIM QRIIMNERYE
 901 KSSGKVSEYF DAVNDEKKYN DRLLKLLCVP FG YCIPRFKN LSIEALFDRN EAAKFDKEKK
 961 KVSGNS (SEQ ID NO: 45).

[0182] Exemplary wild type Cas13d proteins of the disclosure may comprise or consist of the amino acid sequence:

[0183] Cas13d (contig e-k87_11092736):

MKRQKTFAKRIGIKSTVAYGQGKYAITTFGKGSKAEIAVRSADPPEETLPTESDATLSIHAKFA
KAGRDGREFKCGDVDETRIHTSRSEYESLISNPAESPREDYLGKGTLEKFFGDEYPKDNLRI
QIIYSILDIQKILGLYVEDILHFVDGLQDEPEDLVGLGLGDEKMQKLLSKALPYMGFFGSTDVF
KVTKKREERAAADEHNAKVFRALGAI RQKLAHFKWKESLAI FGANANMPIRFFQGATGGRQLWN
DVIAPLWKKRIERVRKSFLSNSAKNLWVLYQVFKDDTDEKKKARARQYYHFSVLKEGKNLGFNL
TKTREYFLDKFFPIFHSSAPDVKRKVDTFRSKFYAILDFI IYEASVSVANSQMGKVAPWKGAI
DNALVKLREAPDEEAKEKIYNVLAASIRNDSLFLRLKSACDKFGAEQNRPVFPNELRNNRDIRN
VRSEWLEATQDVDAAAFVQLIAFLCNFLEGKEINELVTALIKKFEGIQALIDLRLNLEGVDSIR
FENEFALFNDDKGNMAGRIARQLRLLASVGMKPDMDAKRVLYKSALEILGAPPDEVSDewLA
ENILLDKSNNDYQKAKKTVNPFERNYIAKNVITSRSFYLVRYAKPTAVRKLMSNPKIVRYVLKR
LPEKQVASYYSAIWTQSESNSNEMVKLIEMIDRLTTEIAGFSFAVLKDKKDSIVSASRESRAVN
LEVERLKKLTTLYMSIAYIAVKSLVKVNARYFIAYSALERDLYFFNEKYGEEFRLHFIPYELNG
KTCQFEYLA I LKY YLARDEETLKRKCEICEEIKVGCEKHKKNNANPPYEYDQEWIDKKKALNSER
KACERRLHFSTHWAQYATKRDENMAKHPQKWYDILASHYDELLALQATGWLATQARNDAEHLNP
VNEFDVYIEDLRRYPEGTPKNKDYHIGSYFEIYHYIRQRAYLEEVLAKRKEYRDSGSFTDEQLD
KLQKILDDIRARGSYDKNLLKLEYLPFAYNLPYKNTTTEALFDDDSVSGKKRVAEWREREKTR
EAEREQRRQR (SEQ ID NO: 46).

[0184] An exemplary direct repeat sequence of Cas13d (contig e-k87_11092736) (SEQ ID NO: 46) comprises or consists of the nucleic acid sequence: Cas13d (contig e-k87_11092736) Direct Repeat Sequence): GTGAGAAGTCTCCTTATGGGAGATGCTAC (SEQ ID NO: 47).

[0185] Exemplary wild type Cas13d proteins of the disclosure may comprise or consist of the amino acid sequence:

[0186] Cas13d (160582958_gene49834):

MKNSVTFKLIQAQENKEAARKKAKDIAEQARIAKRNGVVKKEENRINRIQIEIQTKKSNTQNA
YHLKSLAKAAGVKS VFAIGNDLLMTGFGPGNDATIEKRVFQNRAIETLSSPEQYSAEFQNKQFK
IKGNIKVLNHSTQKMEEIQTELQDNYNRP HFDLLGCKNVLEQKYFGRTFSDNIHVQIAYNIMDI
EKLLTPYINNI IYTLNELMRDNSKDDFFGCDSHFSVAYLYDELKAGYS DR LKTKPNLSKNIDRI

WNNFCNYMNSDSGNTEARLAYFGELFYKPKETGDAKSDYKTHLSNNQKEEWELKSDKEVYNI FA
 ILCDLRHFCTHGESI TPSGKPFYPNLEKNLFPEAKQVLNSLFEEKAESLGAEAFGKTAGKTDVS
 ILLKVFEKEQASQKEQQALLKEYYDFKVQKTYKNMGFS IKKLREAIMI IPDAAKFKDDL YSSLR
 HKLYGLFDFILVKHFLDTSSENLQNNDI FRQLRACRCEEEKDQVYRS IAVKVWEKVKKELNM
 FKQVVVIPSLSKDELKQMEMTKNTELLSSIETISTQASLFSEMI FMMTYLLDGKEINLLCTSLI
 EKFENIASFNEVLKSPQIGYETKYTEGYAFFKNADKTAKELRQVNNMARMTKPLGGVNTKCVMY
 NEAAKILGAKPMSKAELESVFNLDNHDYTYSPSGKKIPNKNFRNFI INNVI TSRRFLYLIRYGN
 PEKIRKIAINPSI ISFVLKQIPDEQIKRYPPCIGKRTDDVTLMRDELGKMLQSVNFEQFSRVN
 NKQNAKQNPNGEKARLQACVRLYLTVPYLFIKNMVNINARYVLAHFHCLERDHALCFNSRKLND
 SYNEMANKFQMRKAKKEQYEKEYKCKKQETGTAHTKKIEKLNQQIAYIDKDIKNMHSYTCRNY
 RNLVAHLNVVSKLQNYVSELPNDYQITSYFSFYHYCMQLGLMEKVSSKNIPLVESLKNEANDAQ
 SYSAKKTLEYFDLIEKNRTYCKDFLKALNAPFSYNLPRFKNLSIEALFDKNIVYEQADLKKE
 (SEQ ID NO: 48) .

[0187] An exemplary direct repeat sequence of Cas13d (160582958_gene49834) (SEQ ID NO: 48) comprises or consists of the nucleic acid sequence:

[0188] Cas13d (160582958_gene49834) Direct Repeat Sequence:

GAACTACACCCTCTGTTCTGTAGGGGTCTAACAC (SEQ ID NO: 49) .

[0189] Exemplary wild type Cas13d proteins of the disclosure may comprise or consist of the amino acid sequence:

[0190] Cas13d (contig tpg|DJXD01000002.1| ; uncultivated *Ruminococcus* assembly, UBA7013, from sheep gut metagenome):

MKKQKSKKTVSKTSGLKEALSVQGTVMITSGKGNMANLSYKIPSSQKPQNLNSSAGLKNVEVS
 GKKIKFQGRHPKIATTDNPLFKPQPGMDLLCLKDKLEMHYFGKTFDDNIHIQLIYQILDIEKIL
 AVHVNNIVFTLDNVLHPQKEELTEDFIGAGGWRINLDYQTLRGQTNKYDRFKNYIKRKELLYFG
 EAFYHENERRYEDI FAILTLLSALRQFCFHSDLSSDES DHVNSFWLYQLEDQLSDEFKETLSI
 LWEEVTERIDSEFLKTNTVNLHILCHVFPKESKETIVRAYYEFLIKKSFKNMGFSIKKLREIML
 EQSDLKSFKEDKYNSVRKLYKLFDFIITYYYDHHAFFEKEALVSSLRSSLTEENKEEIIYIKTAR
 TLASALGADFKKAAADVNAKNIRDYQKKANDYRISFEDIKIGNTGIGYFSELIYMLTLLLDGKE
 INDLLTTLINKFDNIISFIDILKKNLEFKFKPEYADFFNMTNCRYTLEELRVINSIARMQKPS
 ADARKIMYRDALRILGMDNRPDEEIDRELERTMPVGADGKFIKKGQGFNFNFIASNVIESSRFHY

LVRYNPNPHKTRTLVKNPNVVKFVLEGIPETQIKRYFDVCKGQEI PPTSDKSAQIDVLARI ISSV
 DYKIFEDVPPQSAKINKDDPSRNFS DALKKQRYQAI VSLYLTVMYLITKNLVYVNSRYVIAFHCL
 ERDAFLHGVTLPKMNKKIVYSQLTTHLLTDKNYTTYGHLKNQK GHRKQWYVLVKNNLQNSDITAV
 SSFRNIVAHISVVRNSNEYISGIGELHSYFELYHYLVQSMIAKNNWYDTSHQPKTAEYLNK
 HHTYCKDFVKAYCIPFGYVVPYKNTINELFDRNNPNPEPKKEEV (SEQ ID NO: 50) .

[0191] An exemplary direct repeat sequence of Cas13d (contig tpg|DJXD01000002.1| ;
 uncultivated *Ruminococcus* assembly, UBA7013, from sheep gut metagenome) (SEQ ID NO:
 50) comprises or consists of the nucleic acid sequence: Cas13d (contig tpg|DJXD01000002.1| ;
 uncultivated *Ruminococcus* assembly, UBA7013, from sheep gut metagenome) Direct Repeat
 Sequence: CAACTACAACCCCGTAAAAATACGGGGTTCTGAAAC (SEQ ID NO: 51) .

gRNA Target Sequences

[0192] In some embodiments of the compositions of the disclosure, a target sequence of an
 RNA molecule comprises a sequence motif corresponding to the first RNA binding protein
 and/or the second RNA binding protein.

[0193] In some embodiments of the compositions and methods of the disclosure, the sequence
 motif is a signature of a disease or disorder.

[0194] A sequence motif of the disclosure may be isolated or derived from a sequence of
 foreign or exogenous sequence found in a genomic sequence, and therefore translated into an
 mRNA molecule of the disclosure or a sequence of foreign or exogenous sequence found in an
 RNA sequence of the disclosure.

[0195] A sequence motif of the disclosure may comprise or consist of a mutation in an
 endogenous sequence that causes a disease or disorder. The mutation may comprise or consist of
 a sequence substitution, inversion, deletion, insertion, transposition, or any combination thereof.

[0196] A sequence motif of the disclosure may comprise or consist of a repeated sequence. In
 some embodiments, the repeated sequence may be associated with a microsatellite instability
 (MSI). MSI at one or more loci results from impaired DNA mismatch repair mechanisms of a
 cell of the disclosure. A hypervariable sequence of DNA may be transcribed into an mRNA of
 the disclosure comprising a target sequence comprising or consisting of the hypervariable
 sequence.

[0197] A sequence motif of the disclosure may comprise or consist of a biomarker. The biomarker may indicate a risk of developing a disease or disorder. The biomarker may indicate a healthy gene (low or no determinable risk of developing a disease or disorder). The biomarker may indicate an edited gene. Exemplary biomarkers include, but are not limited to, single nucleotide polymorphisms (SNPs), sequence variations or mutations, epigenetic marks, splice acceptor sites, exogenous sequences, heterologous sequences, and any combination thereof.

[0198] A sequence motif of the disclosure may comprise or consist of a secondary, tertiary or quaternary structure. The secondary, tertiary or quaternary structure may be endogenous or naturally occurring. The secondary, tertiary or quaternary structure may be induced or non-naturally occurring. The secondary, tertiary or quaternary structure may be encoded by an endogenous, exogenous, or heterologous sequence.

[0199] In some embodiments of the compositions and methods of the disclosure, a target sequence of an RNA molecule comprises or consists of between 2 and 100 nucleotides or nucleic acid bases, inclusive of the endpoints. In some embodiments, the target sequence of an RNA molecule comprises or consists of between 2 and 50 nucleotides or nucleic acid bases, inclusive of the endpoints. In some embodiments, the target sequence of an RNA molecule comprises or consists of between 2 and 20 nucleotides or nucleic acid bases, inclusive of the endpoints.

[0200] In some embodiments of the compositions and methods of the disclosure, a target sequence of an RNA molecule is continuous. In some embodiments, the target sequence of an RNA molecule is discontinuous. For example, the target sequence of an RNA molecule may comprise or consist of one or more nucleotides or nucleic acid bases that are not contiguous because one or more intermittent nucleotides are positioned in between the nucleotides of the target sequence.

[0201] In some embodiments of the compositions and methods of the disclosure, a target sequence of an RNA molecule is naturally occurring. In some embodiments, the target sequence of an RNA molecule is non-naturally occurring. Exemplary non-naturally occurring target sequences may comprise or consist of sequence variations or mutations, chimeric sequences, exogenous sequences, heterologous sequences, chimeric sequences, recombinant sequences, sequences comprising a modified or synthetic nucleotide or any combination thereof.

[0202] In some embodiments of the compositions and methods of the disclosure, a target sequence of an RNA molecule binds to a guide RNA of the disclosure.

[0203] In some embodiments of the compositions and methods of the disclosure, a target sequence of an RNA molecule binds to a first RNA binding protein of the disclosure.

[0204] In some embodiments of the compositions and methods of the disclosure, a target sequence of an RNA molecule binds to a second RNA binding protein of the disclosure.

RNA Molecules

[0205] In some embodiments of the compositions and methods of the disclosure, an RNA molecule of the disclosure comprises a target sequence. In some embodiments, the RNA molecule of the disclosure comprises at least one target sequence. In some embodiments, the RNA molecule of the disclosure comprises one or more target sequence(s). In some embodiments, the RNA molecule of the disclosure comprises two or more target sequences.

[0206] In some embodiments of the compositions and methods of the disclosure, an RNA molecule of the disclosure is a naturally occurring RNA molecule. In some embodiments, the RNA molecule of the disclosure is a non-naturally occurring molecule. Exemplary non-naturally occurring RNA molecules may comprise or consist of sequence variations or mutations, chimeric sequences, exogenous sequences, heterologous sequences, chimeric sequences, recombinant sequences, sequences comprising a modified or synthetic nucleotide or any combination thereof.

[0207] In some embodiments of the compositions and methods of the disclosure, an RNA molecule of the disclosure comprises or consists of a sequence isolated or derived from a virus.

[0208] In some embodiments of the compositions and methods of the disclosure, an RNA molecule of the disclosure comprises or consists of a sequence isolated or derived from a prokaryotic organism. In some embodiments, an RNA molecule of the disclosure comprises or consists of a sequence isolated or derived from a species or strain of archaea or a species or strain of bacteria.

[0209] In some embodiments of the compositions and methods of the disclosure, the RNA molecule of the disclosure comprises or consists of a sequence isolated or derived from a eukaryotic organism. In some embodiments, an RNA molecule of the disclosure comprises or consists of a sequence isolated or derived from a species of protozoa, parasite, protist, algae,

fungi, yeast, amoeba, worm, microorganism, invertebrate, vertebrate, insect, rodent, mouse, rat, mammal, or a primate. In some embodiments, an RNA molecule of the disclosure comprises or consists of a sequence isolated or derived from a human.

[0210] In some embodiments of the compositions and methods of the disclosure, the RNA molecule of the disclosure comprises or consists of a sequence derived from a coding sequence from a genome of an organism or a virus. In some embodiments, the RNA molecule of the disclosure comprises or consists of a primary RNA transcript, a precursor messenger RNA (pre-mRNA) or messenger RNA (mRNA). In some embodiments, the RNA molecule of the disclosure comprises or consists of a gene product that has not been processed (e.g. a transcript). In some embodiments, the RNA molecule of the disclosure comprises or consists of a gene product that has been subject to post-transcriptional processing (e.g. a transcript comprising a 5' cap and a 3' polyadenylation signal). In some embodiments, the RNA molecule of the disclosure comprises or consists of a gene product that has been subject to alternative splicing (e.g. a splice variant). In some embodiments, the RNA molecule of the disclosure comprises or consists of a gene product that has been subject to removal of non-coding and/or intronic sequences (e.g. a messenger RNA (mRNA)).

[0211] In some embodiments of the compositions and methods of the disclosure, the RNA molecule of the disclosure comprises or consists of a sequence derived from a non-coding sequence (e.g. a non-coding RNA (ncRNA)). In some embodiments, the RNA molecule of the disclosure comprises or consists of a ribosomal RNA. In some embodiments, the RNA molecule of the disclosure comprises or consists of a small ncRNA molecule. Exemplary small RNA molecules of the disclosure include, but are not limited to, microRNAs (miRNAs), small interfering (siRNAs), piwi-interacting RNAs (piRNAs), small nucleolar RNAs (snoRNAs), small nuclear RNAs (snRNAs), extracellular or exosomal RNAs (exRNAs), and small Cajal body-specific RNAs (scaRNAs). In some embodiments, the RNA molecule of the disclosure comprises or consists of a long ncRNA molecule. Exemplary long RNA molecules of the disclosure include, but are not limited to, X-inactive specific transcript (Xist) and HOX transcript antisense RNA (HOTAIR).

[0212] In some embodiments of the compositions and methods of the disclosure, the RNA molecule of the disclosure contacted by a composition of the disclosure in an intracellular space.

In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in a cytosolic space. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in a nucleus. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in a vesicle, membrane-bound compartment of a cell, or an organelle.

[0213] In some embodiments of the compositions and methods of the disclosure, the RNA molecule of the disclosure contacted by a composition of the disclosure in an extracellular space. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in an exosome. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in a liposome, a polymersome, a micelle or a nanoparticle. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in an extracellular matrix. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in a droplet. In some embodiments, the RNA molecule of the disclosure contacted by a composition of the disclosure in a microfluidic droplet.

[0214] In some embodiments of the compositions and methods of the disclosure, a RNA molecule of the disclosure comprises or consists of a single-stranded sequence. In some embodiments, the RNA molecule of the disclosure comprises or consists of a double-stranded sequence. In some embodiments, the double-stranded sequence comprises two RNA molecules. In some embodiments, the double-stranded sequence comprises one RNA molecule and one DNA molecule. In some embodiments, including those wherein the double-stranded sequence comprises one RNA molecule and one DNA molecule, compositions of the disclosure selectively bind and, optionally, selectively cut the RNA molecule.

RNA-Binding Endonucleases

[0215] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a nuclease domain. In some embodiments, the second RNA binding protein binds RNA in a manner in which it associates with RNA. In some embodiments, the second RNA binding protein associates with RNA in a manner in which it cleaves RNA.

[0216] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an RNase.

[0217] In some embodiments, the second RNA binding protein comprises or consists of an RNase1. In some embodiments, the RNase1 protein comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGLCKPVNTFVHEPLVDVQNV
CFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYV
PVHFDASVEDST (SEQ ID NO: 20).

[0218] In some embodiments, the second RNA binding protein comprises or consists of an RNase4. In some embodiments, the RNase4 protein comprises or consists of:

QDGMYQRFLRQHVHPEETGGSDRYCDLMMQRRKMTLYHCKRFNTFIHEDIWNIRSICS
TTNIQCKNGKMNCHHEGVVKVTDCRDTGSSRAPNCRYRAIASTRRVVIACEGNPQVPVH
FDG (SEQ ID NO: 21).

[0219] In some embodiments, the second RNA binding protein comprises or consists of an RNase6. In some embodiments, the RNase6 protein comprises or consists of:

WPKRLTKAHWFEIQHIQPSPLQCNRAMSGINNYTQHCKHQNTFLHDSFQNVAAVCDLL
SIVCKNRRHNCHQSSKPVNMTDCRLTSGKYPQCRYSAQAQYKFFIVACDPPQKSDPPYK
LVPVHLDL (SEQ ID NO: 22).

[0220] In some embodiments, the second RNA binding protein comprises or consists of an RNase7. In some embodiments, the RNase7 protein comprises or consists of:

APARAGFCPLLLLLLLGLWVAEIPVSAKPKGMTSSQWFKIQHMQPSPQACNSAMKNINK
HTKRCKDLNTFLHEPFSSVAATCQTPKIACKNGDKNCHQSHGVPVSLTMCKLTSGKYPNC
RYKEKRQNKSYVVACKPPQKKDSQQFHLVPVHLDRVL (SEQ ID NO: 23).

[0221] In some embodiments, the second RNA binding protein comprises or consists of an RNase8. In some embodiments, the RNase8 protein comprises or consists of:

TSSQWFKTQHVQPSPQACNSAMSINKYTERCKDLNTFLHEPFSSVAITCQTPNIACKNSC
KNCHQSHGPMSTMGELTSGKYPNCRYKEKHLNTPYIVACDPPQQGDPGYPLVPVHLD
KVV (SEQ ID NO: 24).

[0222] In some embodiments, the second RNA binding protein comprises or consists of an RNase2. In some embodiments, the RNase2 protein comprises or consists of:

KPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGN
PNMTCPSNKTRKNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTAPANMFYIVACDNRDQ
RRDPPQYPVVPVHLDRII (SEQ ID NO: 25).

[0223] In some embodiments, the second RNA binding protein comprises or consists of an RNase6PL. In some embodiments, the RNase6PL protein comprises or consists of:

DKRLRDNHEWKKLIMVQHWPETVCEKIQNDCRDPPDYWTIHGLWPKSEGCNRSWPF
NLEEIKKNWMEITDSSLPSPSMGPAPPRWMRSTPRRSTLAEAWNSTGSWTSTGGCALPP
AALPSGDLCCRPSLTAGSRGVGVDLTALHQLLHVHYSATGIIPEECSEPTKPFQIILHHDH
TEWVQSIGMPIWGTISSSESAIGKNEESQPACAVLSHDS (SEQ ID NO: 26).

[0224] In some embodiments, the second RNA binding protein comprises or consists of an RNaseL. In some embodiments, the RNaseL protein comprises or consists of:

AAVEDNHLLIKAVQNEVDLVQQLLEGGANVNFQEEEGGWTPHNAVQMSREDIVEL
LLRHGADPVLRRKNGATPFILAAIAGSVKdLLKLFLSKGADVNECDFYGFTAFMEAAYV
GKVKALKFLYKRGANVNLRRKTKEDQERLRKGGATALMDAAEKGHVEVLKILLDEM
GADVNACDNMGRNALIHALLSSDDSDVEAITHLLLDHGADVNVRRGERGKTPILAVEK
KHLGLVQRLLQEHEIINDTSDGKTALLLAVELKLKKAELLCKRGASTDCGDLVMTA
RRNYDHSLVKVLLSHGAKEDFHPPAEDWKPQSSHWGAALKDLHRIYRPMIGKLLKFFID
EKYKIADTSEGGIYLGIFYEKQEVAVKTFCEGSPRAQREVSCSQSSRENSHLVTFYGSSEH
RGHLFVCVTLCEQTLEACLDVHRGEDVENEDEFARNVLSIFKAVQELHLSCGYTHQD
LQPQNILIDSKKAAHLADFDKSIKWAGDPQEVKRDLEDLGRVLVYVVKKGSISFEDLKA
QSNEEVVQLSPDEETKDLIHRLFHPGEHVRDCLSDLLGHPFFWTWESRYRTLNRVGNES
DIKTRKSESEILRLLQPGPSEHSKSFDKWTTKINECVMKKMKNKFYEKRGNFYQNTVGD
LKFIRNLGEHIDEKHKMKLKGDPSTLYFQKTFPDLVIYVYTKLQNTYRKHFPQTHSP
NKPQCDGAGGASGLASPGC (SEQ ID NO: 27).

[0225] In some embodiments, the second RNA binding protein comprises or consists of an RNaseT2. In some embodiments, the RNaseT2 protein comprises or consists of:

VQHWPETVCEKIQNDCRDPPDYWTIHGLWPKSEGCNRSWPFNLEEIKDLLPEMRAYW
PDVIHSFPNRSRFRWKHEWEKHGTCAAQVDALNSQKKYFGRSLELYRELDLNSVLLKLG
KPSINYQVADFKDALARVYGVIPKIQCLPPSQDEEVQTIGQIELCLTKQDQQLQNC
TEPGEQSPKQEVWLANGAAESRGLRVCEGDPVFYPPPCKTKH (SEQ ID NO: 28).

[0226] In some embodiments, the second RNA binding protein comprises or consists of an RNase11. In some embodiments, the RNase11 protein comprises or consists of:

EASESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVKNTSLSMSKDDMSSTLL

TFRSLHYNDPKGNSSGNDKECCNDMTVWRKVSEANGSCKWSNNFIRSSTEVMRRVHR
 APSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKILTVLTGHSLMSWL
 VCGSKL (SEQ ID NO: 29).

[0227] In some embodiments, the second RNA binding protein comprises or consists of an RNaseT2-like. In some embodiments, the RNaseT2-like protein comprises or consists of:
 XLGGADKRLRDNHEWKKLIMVQHWPETVCEKIQNDCRDPDYWTIHGLWPKSEGNCN
 RSWPFNLEEIKDLLPEMRAYWPDVIHSFPNRSRFWKHEWEKHGTCAAQVDALNSQKKY
 FGRSLELYRELDLNSVLLKLGKPSINYYQTTEEDLNLDVEPTTEDTAAEVTIHVLLHSAL
 FGEIGPRRW (SEQ ID NO: 30).

[0228] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a mutated RNase.

[0229] In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R)) polypeptide. In some embodiments, the Rnase1(K41R) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCRPVNTFVHEPLVDVQNV
 CFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYV
 PVHFDASVEDST (SEQ ID NO: 116).

[0230] In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R, D121E)) polypeptide. In some embodiments, the Rnase1 (Rnase1(K41R, D121E)) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCRPVNTFVHEPLVDVQNV
 CFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYV
 PVHFEASVEDST (SEQ ID NO: 117).

[0231] In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R, D121E, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(K41R, D121E, H119N)) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCRPVNTFVHEPLVDVQNV
 CFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYV
 PVNFEASVEDST (SEQ ID NO: 118).

[0232] In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1. In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(H119N)) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNV
CFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIIVACEGSPYV
PVNFDASVEDST (SEQ ID NO: 119).

[0233] In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGDCKPVNTFVHEPLVDVQNV
CFQEKVTCKDGQGNCYKSNSSMHITDCRLTADSDYPNCAYRTSPKERHIIIVACEGSPYV
PVNFDASVEDST (SEQ ID NO: 120). In some embodiments, the second RNA binding protein

comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N, K41R, D121E)) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGDCRPVNTFVHEPLVDVQNV
CFQEKVTCKDGQGNCYKSNSSMHITDCRLTADSDYPNCAYRTSPKERHIIIVACEGSPYV
PVNFEASVEDST (SEQ ID NO: 121).

In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide. In some embodiments, the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D)) polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGDCKPVNTFVHEPLVDVQNV
CFQEKVTCKDGQGNCYKSNSSMHITDCRLTADSDYPNCAYRTSPKERHIIIVACEGSPYV
PVHFDASVEDST (SEQ ID NO: 122).

In some embodiments, the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1 (R39D, N67D, N88A, G89D, R91D, H119N, K41R, D121E)) polypeptide that comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGDCRPVNTFVHEPLVDVQNV
CFQEKVTCKDGQGNKYKSNSSMHITDCRLTADSDYPNCAYRTSPKERHIIVACEGSPYV
PVNFEASVEDST (SEQ ID NO: 208).

[0234] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a NOB1 polypeptide. In some embodiments, the NOB1 polypeptide comprises or consists of:

APVEHVADAGAFRLRHAALQDIGKNIYTIREVVTEIRDKATRRRLAVLPYELRFKEPLPE
YVRLVTEFSKKTGDYPSLSATDIQVLALTYQLEAEFVGVSHLKQEPQKVKVSSSIQHPET
PLHISGFHLPYKPKPPQETEKGHSACEPENLEFSSFMFWRNPLPNIDHELQELLIDRGEDV
PSEEEEEENGFEEDRKDDSDDDGGGWITPSNIKQIQQEQCDVPEDVRVGCLTTDFAM
QNVLLQMGHLVLA VNGMLIREARSYL RCHGCFKTTSDMSRVFC SHCGNKTLKKVSVT
V (SEQ ID NO: 31).

[0235] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an endonuclease. In some embodiments, the second RNA binding protein comprises or consists of an endonuclease V (ENDOV). In some embodiments, the ENDOV protein comprises or consists of:

AFSGLQRVGGVDVSFVKGDSVRACASLVLSFPELEVVEESRMVSLTAPYVSGFLAFR
EVPFLELVQQLREKEPGLMPQVLLVDGNGVLHHRGFGVACHLGVLTDLPCVGVAKKL
LQVDGLENNALHKEKIRLLQTRGDSFPLLGDSTVLMALRSHDRSTRPLYISVGHMRS
LEAAVRLTCCCFRIFPEPVRQADICSREHIRKS (SEQ ID NO: 32).

[0236] In some embodiments, the second RNA binding protein comprises or consists of an endonuclease G (ENDOG). In some embodiments, the ENDOG protein comprises or consists of:
AELPPVPGGPRGPGELAKYGLPGLAQLKSRESYVLCYDPRTRGALWVVEQLRPERLRG
DGDRRECFREDDSVHAYHRATNADYRGSGFDRGHLAAAANHRWSQKAMDDTFYLS
NVAPQVPHLNQNAWNNLEKYSRSLTRS YQNVYVCTGPLFLPRTEADGKSYVKYQVIGK
NHVAVPTHFFKVLILEAAGGQIELRTYVMPNAPVDEAIPLERFLVPIESIERASGLLFV
PNILARAGSLKAITAGSK (SEQ ID NO: 33).

[0237] In some embodiments, the second RNA binding protein comprises or consists of an endonuclease D1 (ENDOD1). In some embodiments, the ENDOD1 protein comprises or

consists of:

RLVGEEAAGFGCEDKFFYAGTPPAGLAADSHVKICQRAEGAERFATLYSTRDRIPVYSA
FRAPRPAPGGAEQRWLVEPQIDDPNSNLEEAINAEAITSVNSLGSKQALNTDYLDSDYQ
RGQLYPSLSDDVQVATFTLTNSAPMTQSFQERWYVNLHSLMDRALTPQCGSGEDLYIL
TGTVPSDYRVKDKVAVPEFVWLAACCAVPGGGWAMGFVKHTRDSIIEDVMVKDLQ
KLLPFNPQLFQNNCGETEQDTEKMKKILEVVNQQDEERMVQSQKSSSPLSSTRSKRSTL
LPPEASEGSSSFLGKLMGFATPFIKLFQLIYYLVVAILKNIVYFLWCVTKQVINGIESCLY
RLGSATISYFMAIGEELVSIPWKVLKVVAKVIRALLRILCCLLKAICRVLSIPVRVLVDVA
TFPVYTMGAIPVCKDIALGLGGTVSLLFDTAFGTLGGLFQVVFVCKRIGYKVTFDMSG
EL (SEQ ID NO: 34).

[0238] In some embodiments, the second RNA binding protein comprises or consists of a Human flap endonuclease-1 (hFEN1). In some embodiments, the hFEN1 polypeptide comprises or consists of:

MGIQGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVRQGGDVLQNEEGET
TSHLMGMFYRTIRMMENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEKQLQQAQAAG
AEQEVEKFTKRLVKVTKQHNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAA
TEDMDCLTFGSPVLMRHLTASEAKKLPIQEFHLSRILQELGLNQEQFV DLCILLGSDYCE
SIRGIGPKRAVDLIQKHK SIEEIVRRLDPNKYPVPENWLHKEAHQLFLEPEVLDPESVELK
WSEPNEELIKFMCGEKQFSEERIRSGVKRLSKSRQGSTQGRLLDFFKVTGSLSSAKRKE
PEPKGSTKKKAKTGAAGKFKRGK (SEQ ID NO: 35).

[0239] In some embodiments, the second RNA binding protein comprises or consists of a DNA repair endonuclease XPF (ERCC4) polypeptide. In some embodiments, the ERCC4 polypeptide comprises or consists of:

MESGQPARRIAMAPLLEYERQLVLELLD TDGLVVCARGLGADRLLYHFLQLHCHPACL
VLVLNTQPAEEYFINQLKIEGVEHLPRRVTNEITSNSRYEVYTQGGVIFATSRILVVDL
TDRIPSDLITGILVYRAHRIESCQEAFILRLFRQKNKRGFIKAFTDNAVAFDTGFCHVERV
MRNLFVRKLYLWPRFHVAVNSFLEQHKPEVVEIHVSMTPTMLAIQTAILDILNACKEL
KCHNPSLEVEDLSLENAIGKPFDKTIRHYLDPLWHQLGAKTKSLVQDLKILRTLQYLSQ
YDCVTFLNLESRLATEKAFGQNSGWLFLDSSTSMFINARARVYHLPDAKMSKKEKISE
KMEIKEGEGILWG (SEQ ID NO: 124).

[0240] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an Endonuclease III-like protein 1 (NTHL) polypeptide. In some embodiments, the NTHL polypeptide comprises or consists of:

CSPQESGMTALSARMLTRSRS LGPGAGPRGCREEPGLRRREAAAEARKSHSPVKRPRK
 AQRLRVAYEGSDSEKGEAEPLKVPVWEPQDWQQQLVNIRAMRNKKDAPVDHLGTEH
 CYDSSAPPKVRRYQVLLSLMLSSQTKDQVTAGAMQRLRARGLTVDSILQTDDATLGKLI
 YPVGFWRSKVKYIKQTSAILQQHYGGDIPASVAELVALPGVGPMAHLAMAVAWGTV
 SGIAVDTHVHRIANRLRWTKKATKSPEETRAALEEWLPRELWHEINGLLVGFQQQTCLP
 VHPRCHACLNQALCPAAQGL (SEQ ID NO: 123).

[0241] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a human Schlafen 14 (hSLFN14) polypeptide. In some embodiments, the hSLFN14 polypeptide comprises or consists of:

ESTHVEFKRFTTKKVIPRIKEMLPHYVSAFANTQGGYVLIGVDDKSKEVVGCKWEKVNPK
 DLLKKEIENCIEKLPTFHFCCEKPKVNFTTKILNVYQKDVLGDGYVCVIQVEPFCCVFAE
 APDSWIMKDNSVTRLTAEQWVVMMLDTQSAPPSLVTDYNSCLISSASSARKSPGYPIKV
 HKFKEALQ (SEQ ID NO: 36).

[0242] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a human beta-lactamase-like protein 2 (hLACTB2) polypeptide. In some embodiments, the hLACTB2 polypeptide comprises or consists of:

TLQGTNTYLVTGPRRILIDTGEP AIPEYISCLKQALTEFN TAIQEIVVTHWHRDHSGGIG
 DICKSINNDTTYCIKKLPRNPQREEIIGNGEQQYVYLKGDV IKT EGATLRVLYTPGHTD
 DHMALLLEENAI FSGDCILGEGTTVFEDLYDYMN SLKELLKIKADI IYPGHGPVIHNAE
 AKIQQYISHRNIREQQIL TLFRENFEKSFTVMELVKI IYKNTPENLHEMAKHNLLLHLKKL
 EKEGKIFSNTDPDKKWK AHL (SEQ ID NO: 37).

[0243] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an apurinic/aprimidinic (AP) endodeoxyribonuclease (APEX) polypeptide. In some embodiments, the second RNA binding protein comprises or consists of an apurinic/aprimidinic (AP) endodeoxyribonuclease (APEX2) polypeptide. In some embodiments, the APEX2 polypeptide comprises or consists of:

MLRVVSWNINGIRRPLQGVANQEPSNCAAVAVGRILDEL DADIVCLQETKVTRDALTEP

LAIVEGYNSYFSFSRNRSGYSGVATFCKDNATPVAAEEGLSGLFATQNGDVGCYGNMDEFTQEELRALDSEGRALLTQHKIRTWEGKEKTLTLINVYCPHADPGRPERLVFKMRFYRLLQIRAEALLAAGSHVILGDLNTHRPIDHWDAVNLECFEEDPGRKWMDSLLSNLGCQSASHVGPFIDSYRCFQPKQEGAFTCWSAVTGARHLNYGSRLDYVLGDRTLVIDTFQASFLLEPEVMGSDHCPVGAVLSVSSVPAKQCPPLCTRFLPEFAGTQLKILRFLVPLEQSPVLEQSTLQHNNQTRVQTCQNKAAQVRSTRPQPSQVGSSRGQKNLKSYPSPSCPQASPDIELPSLPLMSALMTPKTPEEKAVAKVVKGQAKTSEAKDEKELRTSFWKSVLAGPLRTPLCGGHEREPCVMRTVKKPGPNLGRRFYMCARPRGPPTDPSSRCNFFLWSRPS (SEQ ID NO: 38).

[0244] In some embodiments, the APEX2 polypeptide comprises or consists of:

MLRVVSWNINGIRRPLQGVANQEPSNCAAVAVGRILDELADIVCLQETKVTRDALTEPLAIVEGYNSYFSFSRNRSGYSGVATFCKDNATPVAAEEGLSGLFATQNGDVGCYGNMDEFTQEELRALDSEGRALLTQHKIRTWEGKEKTLTLINVYCPHADPGRPERLVFKMRFYRLLQIRAEALLAAGSHVILGDLNTHRPIDHWDAVNLECFEEDPGRKWMDSLLSNLGCQSASHVGPFIDSYRCFQPKQEGAFTCWSAVTGARHLNYGSRLDYVLGDRTLVIDTFQASFLLEPEVMGSDHCPVGAVLSVSSVPAKQCPPLCTRFLPEFAGTQLKILRFLVPLEQSP (SEQ ID NO: 39).

[0245] In some embodiments, the second RNA binding protein comprises or consists of an apurinic or apyrimidinic site lyase (APEX1) polypeptide. In some embodiments, the APEX1 polypeptide comprises or consists of:

PKRGKKGAVAEDGDELRTPEAKKSKTAAKKNDKEAAGEGPALYEDPPDQKTSPSGKPATLKICSWNV DGLRAWIKKKGLDWVKEEAPDILCLQETKCSENKLP AELQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVPNAGRGLVRLEYRQRWDEAFRKF LKGLASRKPLVLCGDLNVAHEEIDLRNPKGNKKNAGFTPQERQGF GELLQAVPLADSRHLYPNTPYAYTFWTYMMNARSKNVGWRLDYFLLS (SEQ ID NO: 125).

[0246] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an angiogenin (ANG) polypeptide. In some embodiments, the ANG polypeptide comprises or consists of:

QDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGKRSIKAICENK

NGNPHRENLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVACENGLPVHLDQSI
FRRP (SEQ ID NO: 40).

[0247] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a heat responsive protein 12 (HRSP12) polypeptide. In some embodiments, the HRSP12 polypeptide comprises or consists of:

SSLIRRVISTAKAPGAIGPYSQAVLVDRTIYISGQIGMDPSSGQLVSGGVAEEAKQALKN
MGEILKAAGCDFTNVVKTTVLLADINDFNTVNEIYKQYFKSNFPARAAYQVAALPKGS
RIEIEAVAIQGPLTTASL (SEQ ID NO: 41).

[0248] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Zinc Finger CCCH-Type Containing 12A (ZC3H12A) polypeptide. In some embodiments, the ZC3H12A polypeptide comprises or consists of:

GGGTPKAPNLEPPLPEEEKEGSDLRPVVIDGSNVAMSHGNKEVFSCRGILLAVNWFLER
GHTDITVFPVSWRKEQPRPDVPITDQHILRELEKKKILVFTPSRRVGGKRVVCYDDRFIV
KLAYESDGIVVSNPTYRDLQGERQEWKRFIEERLLMYSFVNDKFMPPDDPLGRHGPSLD
NFLRKKPLTLE (SEQ ID NO: 42).

[0249] In some embodiments, the ZC3H12A polypeptide comprises or consists of:

SGPCGEKPVLEASPTMSLWEFEDSHSRQGTTPRGQELAAEEASALELQMKVDFFRKLG
SSTEIHSVLQKLGVQADTNTVLGELVKHGTATERERQTSPDPCQLPLVPRGGGTPKAP
NLEPPLPEEEKEGSDLRPVVIDGSNVAMSHGNKEVFSCRGILLAVNWFLERGHTDITVFP
PSWRKEQPRPDVPITDQHILRELEKKKILVFTPSRRVGGKRVVCYDDRFIVKLAYESDGI
VVSNDTYRDLQGERQEWKRFIEERLLMYSFVNDKFMPPDDPLGRHGPSLDNFLRKKPL
TLEHRKQPCPYGRKCTYGIKCRFFHPERPSCPQRSVADELARANALLSPPRAPSKDKNGR
PSPSSQSSLLTESEQCSLDGKKGGAQASPGSRQEGLTQTYAPSGRSLAPSGGSGSSFGPT
DWLPQTLDSLPHYVSQDCLDSGIGSLESQMSELWGVRGGGPGEPGPPRAPPYTGYSYGSE
LPATAAFSAFGRAMGAGHFSVPADYPPAPPAPPPREYWSEPYPLPPPTSVLQEPPVQSPG
AGRSPWGRAGSLAKEQASVYTKLCGVFPPHLVEAVMGRFPQLLDPQQLAAEILSYKSQ
HPSE (SEQ ID NO: 43).

[0250] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Reactive Intermediate Imine Deaminase A (RIDA) polypeptide. In some embodiments, the RIDA polypeptide comprises or consists of:

SSLIRR VISTAKAPGAIGPYSQAVLVDR TIYISGQIGMDPSSGQLVSGGVAEEAKQALKN
MGEILKAAGCDFTNVVKTTVLLADINDFNTVNEIYKQYFKSNFPARAAYQVAALPKGS
RIEIEAVAIQGPLTTASL (SEQ ID NO: 44).

[0251] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Phospholipase D Family Member 6 (PDL6) polypeptide. In some embodiments, the PDL6 polypeptide comprises or consists of:

EALFFPSQVTCTEALLRAPGAELAELPEGCPCGLPHGESALSRLLRALLAARASLDLCLF
AFSSPQLGRAVQLLHQRGVRVRVVTDCDYMALNGSQIGLLRKAGIQVRHDQDPGYMH
HKFAIVDKRVLITGSLNWTTQAIQNNRENVLITEDDEYVRLFLEEFERIWEQFNPTKYTF
FPPKSHGSCAPPVSRAGGRLLSWHRTC GTSSSESQT (SEQ ID NO: 126).

[0252] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a mitochondrial ribonuclease P catalytic subunit (KIAA0391) polypeptide. In some embodiments, the KIAA0391 polypeptide comprises or consists of:

KARYKTLEPRGYSLLIRGLIHSDRWREALLLLEDIKKVITPSKKNYNDICIQGALLHQDVN
TAWNLYQELLGHDIVPMLETLKAFFDFGKDIKDDNYSNKLLDILSYLRNNQLYPGESFA
HSIKTWFESVPGKQWKQGF TTVRKSGQCSGCGKTIESIQLSPEEYECLKGKIMRDVIDGG
DQYRK TTPQELKRFENFIKSRPPFDVVIDGLNVAKMFPKVRESQLLLNVVSQLAKRNLR
LLVLGRKHMLRRSSQWSRDEMEEVQKQASCFFADDISEDDPFLLYATLHSGNHCRFITR
DLMRDHKACL PDAKTQRLFFKWQQGHQLAIVNRFPGSKLTFQRILSYDTVVQTTGDSW
HIPYDEDLVERCSCEVPTKWLC LHQKT (SEQ ID NO: 127).

[0253] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an argonaute 2 (AGO2) polypeptide.

In some embodiments of the compositions of the disclosure, the AGO2 polypeptide comprises or consists of:

SVEPMFRHLKNTYAGLQLVVVILPGKTPVYAEVKRVGDTV LGMATQCVQMKNVQRTT
PQTL SNLCLKINVKLGGVNNILLPQGRPPVFQQPVIFLGADVTHPPAGDGKKPSIAAVVG
SMDAHPNRYCATVRVQQHRQEIIQDLAAMVRELLIQFYKSTRFKPTRIIFYRDGVSEGQF
QQVLHHELLAIREACIKLEKDYQPGITFIVVQKRHHTRLFCTDKNERVGKSGNIPAGTTV
DTKITHPTEFD FYLC SHAGIQGTSRPSHYHVLWDDNRFSSDELQILTYQLCHTYVRCTRS

VSIPAPAYY AHLVAFRARYHLVDKEHDSAEGSHTSGQSNGRDHQALAKAVQVHQDTL
RTMYFA (SEQ ID NO: 128).

[0254] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a mitochondrial nuclease EXOG (EXOG) polypeptide. In some embodiments, the EXOG polypeptide comprises or consists of:

QGAEGALTGKQPDGSAEKA VLEQFGFPLTGTEARCYTNHALSYDQAKRVPRWVLEHIS
KSKIMGDADRKHCKFKPDPNIPPTFSAFNEDYVGSWSRGHMAPAGNNKFSSKAMAET
FYLSNIVPQDFDNNSGYWNRIEMYCRELTERFEDVWVVSGLTLPQTRGDGKKIVSYQV
IGEDNVAVPSHLYKVILARRSSVSTEPLALGAFVVPNEAIGFQPQLTEFQVSLQDLEKLSG
LVFFPHLDRTSDIRNICSVDTCCKLLDFQEFTLYLSTRKIEGARSVLRLEKIMENLKNAEIEP
DDYFMSRYEKKLEELKAKEQSGTQIRKPS (SEQ ID NO: 129).

[0255] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Zinc Finger CCCH-Type Containing 12D (ZC3H12D) polypeptide. In some embodiments, the ZC3H12D polypeptide comprises or consists of:

EHPSKMEFFQKLG YDREDVLRVLGKLGEGALVNDVLQELIRTGSRPGALEHPAAPRLVP
RGSCGVPDSAQRGPGTAL EEDFRTLASSLRPIVIDGSNVAMSHGNKETFSCRGIKLA VD
WFRDRGHTYIKVFVPSWRKDP PRADTPIREQHVLAE LERQAVLVYTPSRKVHGKRLVC
YDDRYIVKVA YEQDGVIVSNDNYRDLQSENPEWKWFIEQRLLMFSFVNDRFMPPDDPL
GRHGPSLSNFLSRKPKPPEPSWQHCPYGGKCTYGIKCKFYHPERPHHAQLA VADELRAK
TGARPGAGAE EQRPPRAPGGSAGARAAPREPF AHSLPPARGSPDLAALRGSF SRLAFSD
DLGPLGPPLPVPACSLTPRLGGPDWVSAGGRVPGPLSLSPESQFSPGDLPPPPGLQLQPR
GEHRPRDLHGDLLSPRRPPDDPW ARPPRSDFPGRSVWAEP AWGDGATGGLSVYATED
DEGDARARARIALYSVFPRDQVDRVMAAFPELSDLARLILLVQRCQSAGAPLGKP (SEQ
ID NO: 130).

[0256] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an endoplasmic reticulum to nucleus signaling 2 (ERN2) polypeptide. In some embodiments, the ERN2 polypeptide comprises or consists of:

RQQQPQVVEKQQETPLAPADFAHISQDAQSLHSGASRRSQKRLQSPSKQAQPLDDPEAE
QLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRAVAVKRLRECFGLVRREVQLLQES
DRHPNVLR YFCTERGPQFH YIALELCRASLQEYVENPDLDRGGLEPEVVLQQLMSGLAH

LHSLHIVHRDLKPGNILITGPDSQGLGRVVLSDFGGLCKKLPAGRCSFSLHSGIPGTEGWM
 APELLQLLPPDSPTSAVDIFSAGCVFYVLSGGSHPFGDSL YRQANILTGAPCLAHLEEEV
 HDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSRAKQLQFFQDVSDWLEKESEQEP
 LVRALEAGGCAVVRDNWHEHISMPLQTDLRKFRSYKGTSVRDLLRAVRNKKHHYREL
 PVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASESLFLPYPPDSEARRPCPG
 ATGR (SEQ ID NO: 131).

[0257] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a pelota mRNA surveillance and ribosome rescue factor (PELO) polypeptide. In some embodiments, the PELO polypeptide comprises or consists of:

KLVRKNIEKDNAGQVTLVPEEPEDMWHTYNLVQVGDSLRASTIRKVQTESSTGSGVGSN
 RVRTTLTLCVEAIDFDSQACQLRVKGTNIQENEYVKMGAYHTIELEPNRQFTLAKKQW
 DSVVLERIEQACDPAWSADVAAVVMQEGLAHICLVTPSMTLTRAKVEVNIPRKRKGNC
 SQHDRALERFYEQVVQAIQRHIFDVVKCILVASPGFVREQFCDYLFQQA VKTDNKLLL
 ENRSKFLQVHASSGHKYSLKEALCDPTVASRLSDTKAAGEVKALDDFYKMLQHEPDRA
 FYGLKQVEKANEAMAIDTLLISDELFRHQDVATR SRYVRLVDSVKENAGTVRIFSSLHV
 SGEQLS QLTGVAAILRFPVPELSDQEGDSSSEED (SEQ ID NO: 132).

[0258] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a YBEY metalloproteinase (YBEY) polypeptide. In some embodiments, the YBEY polypeptide comprises or consists of:

SLVIRNLQRVIPRRAPLRSKIEIVRRILGVQKFDLGIICVDNKNIQHINRIYRDRNVPTDVL
 SFPFHEHLKAGEFPQPDFDDYNLGDIFLGVEYIFHQCKENEDYNDVLTVTATHGLCHLL
 GFTHGTEAEWQQMFQKEKAVLDELGRRTGTRLQPLTRGLFGGS (SEQ ID NO: 133).

[0259] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a cleavage and polyadenylation specific factor 4 like (CPSF4L) polypeptide. In some embodiments, the CPSF4L polypeptide comprises or consists of:

QEVIAGLERFTFAFEKDVEMQKGTGLLPFQGMDKSASAVCNFFTKGLCEKGKLCPRRH
 DRGKMMVVCKHWLRGLCKKGDHCKFLHQYDLTRMPECYFYSKFGDCSNKECSFLHVK
 PAFKSQDCPWYDQGFCKDGPLCKYRHVPRIMCLNYLVGFCPEGPKCQFAQKIREFKLLP
 GSKI (SEQ ID NO: 134).

[0260] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an hCG_2002731 polypeptide. In some embodiments, the hCG_2002731 polypeptide comprises or consists of:

KLVRKNIEKDNAGQVTLVPEEPEDMWHTYNLVQVGDSLRASTIRKVQTESSTGSVGSN
RVRTTLTLCVEAIDFDSQACQLRVKGTNIQENEYVKMGAYHTIELEPNRQFTLAKKQW
DSVVLERIEQACDPAWSADVAAVVMQEGLAHICLVTPSMTLTRAKVEVNIPRKRKGNC
SQHDRALERFYEQVVQAIQRHIFDVVKCILVASPGFVREQFCDYMFQQAVKTDNKLLL
ENRSKFLQVHASSGHKYSLKEALCDPTVASRLSDTKAAGEVKALDDFYKMLQHEPDRA
FYGLKQVEKANEAMAIDTLLISDELFRHQDVATRERYVRLVDSVKENAGTVRIFSSLHV
SGEQLSQLTGVAAILRFPVPELSDQEGDSSSEED (SEQ ID NO: 135).

[0261] In some embodiments, the hCG_2002731 polypeptide comprises or consists of:

DPAWSADVAAVVMQEGLAHICLVTPSMTLTRAKVEVNIPRKRKGNC
SQHDRALERFYEQVVQAIQRHIFDVVKCILVASPGFVREQFCDYMFQQAVKTDNKLLLENRSKFLQVHAS
SGHKYSLKEALCDPTVASRLSDTKAAGEVKALDDFYKMLQHEPDRAFYGLKQVEKAN
EAMAIDTLLISDELFRHQDVATRERYVRLVDSVKENAGTVRIFSSLHVS
SGEQLSQLTGVAAILRFPVPELSDQEGDSSSEED (SEQ ID NO: 136).

[0262] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of an Excision Repair Cross-Complementation Group 1 (ERCC1) polypeptide. In some embodiments, the ERCC1 polypeptide comprises or consists of:

MDPGKDKEGVPQPSGPPARKKFVIPLDEDEVPPGVRGNPVLKFVRNVPWFEFGDVIPDYV
LGQSTCALFLSLRYHNLHPDYIHGRLQSLGKNFALRVLLVQVDVKDPQQALKELAKMC
ILADCTLILAWSPEEAGRYLETYKAYEQKPADLLMEKLEQDFVSRVTECLTTVKSVNKT
DSQTLTTFGSLEQLIAASREDLALCPGLGPQK (SEQ ID NO: 137).

[0263] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a ras-related C3 botulinum toxin substrate 1 isoform (RAC1) polypeptide. In some embodiments, the RAC1 polypeptide comprises or consists of:

KESRAKKFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNV
CFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYV
PVHFDASVEDST (SEQ ID NO: 138).

[0264] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Ribonuclease A A1 (RAA1) polypeptide. In some embodiments, the RAA1 polypeptide comprises or consists of:

QDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGKNKRSIKAICENK
NGNPHRENLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVVACENGLPVHLDQSI
FRRP (SEQ ID NO: 139).

[0265] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Ras Related Protein (RAB1) polypeptide. In some embodiments, the RAB1 polypeptide comprises or consists of:

GLGLVQPSYGQDGMVQRFLRQHVHPEETGGSDRYCNLMMQRRKMTLYHCKRFNTFIH
EDIWNIRSICSTTNIQCKNGKMNCHEGVVKVTDCRDTGSSRAPNCRYRAIASTRRVVIAC
EGNPQVPVHFDG (SEQ ID NO: 140).

[0266] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a DNA Replication Helicase/Nuclease 2 (DNA2) polypeptide. In some embodiments, the DNA2 polypeptide comprises or consists of:

XSAVDNILLKLAKFKIGFLRLGQIQKVHPAIQQFTEQEICRSKSIKSLALLEELYNSQLIVA
TTCMGINHPHIFSRKIFDFCIVDEASQISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARA
LGMSESLFKRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEKLECGSDKVANAVINL
RHFKDVKLELEFYADYSDNPWLMGVFEPNPNVCFLNTDKVPAPEQVEKGGVSNVTEA
KLIVFLTSIFVKAGCSPDIGIIPYRQQLKIINDLLARSIGMVEVNTVDKYQGRDKSIVLV
SFVRSNKDGTVGELLKDWRLNVAITRAKHKLILLGCVPSLNCYPPLEKLLNHLNSEKLI
SFFFCIWSHLIALL (SEQ ID NO: 141).

[0267] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a FLJ35220 polypeptide. In some embodiments, the FLJ35220 polypeptide comprises or consists of:

MALRSHDRSTRPLYISVGHMSLEAAVRLTCCCCRFRIPEPVRQADICSREHIRKSLGLP
GPPTPRSPKAQRPVACPKGDSGESSALC (SEQ ID NO: 142).

[0268] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a FLJ13173 polypeptide. In some embodiments, the FLJ13173 polypeptide comprises or consists of:

CYTNHALSYDQAKRVPRWVLEHISKSKIMGDADRKHCKFKPDPNIPPTFSAFNEDYVGS
 GWSRGHMAPAGNNKFSSKAMAETFYLSNIVPQDFDNNSGYWNRIEMYCRELTERFEDV
 WVVSGLTLPQTRGDGKKIVSYQVIGEDNVAVPSHLYKVLARRSSVSTEPLALGAFVV
 PNEAIGFQPQLTEFQVSLQDLEKLSGLVFFPHLDRT (SEQ ID NO: 143).

[0269] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein (TENM) polypeptide. In some embodiments, the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein 1 (TENM1) polypeptide. In some embodiments, the TENM1 polypeptide comprises or consists of:

VTVSQMTSVLNGKTRRFADIQLQHGCALCFNIRYGTVEEEKNHVLEIARQRAVAQAWT
 KEQRRLQEGEEGIRAWTEGEKQQLSTGRVQGYDGYFVLSVEQYLELSDSANNIHFMR
 QSEIGRR (SEQ ID NO: 144).

In some embodiments, the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein 2 (TENM2) polypeptide. In some embodiments, the TENM2 polypeptide comprises or consists of:

TVSQPTLLVNGKTRRFTNIEFQYSTLLLSIRYGLTPDTLDEEKARVLDQARQRALGTAW
 AKEQQKARDGREGSRLWTEGEKQQLSTGRVQGYEGYYVLPVEQYPELADSSSNIQFL
 RQNEMGKR (SEQ ID NO: 145).

In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a Ribonuclease Kappa (RNaseK) polypeptide. In some embodiments, the RNaseK polypeptide comprises or consists of:

MGWLRPGPRPLCPPARASWAFSHRFPSPAPRRSPTPFMASLLCCGPKLAACGIVLSA
 WGVIMLIMLGIFNVHSAVLIEDVPFTEKDFENGPNQNIYNLYEQVSYNCFIAAGLYLLLG
 GFSFCQVRLNKRKEYMVR (SEQ ID NO: 204).

[0270] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a transcription activator-like effector nuclease (TALEN) polypeptide or a nuclease domain thereof. In some embodiments, the TALEN polypeptide comprises or consists of:

1	MRIGKSSGWL	NESVSLEYEH	VSPPTPRDRT	RRRPRAAGDG	GLAHLHRRLA	VGYAEDTPRT
61	EARSPAPRRP	LPVAPASAPP	APSLVPEPPM	PVSLPAVSSP	RFSAGSSAAI	TDFPFSLPPT
121	PVLYAMAREL	EALSDATWQP	AVPLPAEPPT	DARRGNTVFD	EASASSPVIA	SACPQAFASP
181	PRAPRSARAR	RARTGGDAWP	APTFLSRPSS	SRIGRDVFGK	LVALGYSREQ	IRKLKQESLS

241 EIAKYHTTTLT GQGFTHADIC RISRRRQSLR VVARNYPELA AALPELTRAH IVDIARQRSR
 301 DLALQALLPV ATALTAAPLR LSASQIATVA QYGERPAIQA LYRLRRKLTR APLHLTPQQV
 361 VAIASNTGGK RALEAVCVQL PVLRAAPYRL STEQVVAIAS NKGGKQALEA VKAHLDDLGLG
 421 APYVLDTEQV VAIASHNGGK QALEAVKADL LDLRGAPYAL STEQVVAIAS HNGGKQALEA
 481 VKADLLELRG APYALSTEQV VAIASHNGGK QALEAVKAHL LDLRGVPYAL STEQVVAIAS
 541 HNGGKQALEA VKAQLLDLRG APYALSTAQV VAIASNGGGK QALEGIGEQL LKLRTAPYGL
 601 STEQVVAIAS HDGGKQALEA VGAQLVALRA APYALSTEQV VAIASNKGGK QALEAVKAQL
 661 LELRGAPYAL STAQVVAIAS HDGGNQALEA VGTQLVALRA APYALSTEQV VAIASHDGGK
 721 QALEAVGAQL VALRAAPYAL NTEQVVAIAS SHGGKQALEA VRALFPDLRA APYALSTAQL
 781 VAIASNPGGK QALEAVRALF RELRAAPYAL STEQVVAIAS NHGGKQALEA VRALFRGLRA
 841 APYGLSTAQV VAIASSNGGK QALEAVWALL VTLRATPYDL NTAQIVAIAS HDGGKPALEA
 901 VWAKLPVLRG APYALSTAQV VAIACISGQQ ALEAIEAHMP TLRQASHSLR PERVAIACI
 961 GGRSAVEAVR QGLPVKAIRR IRREKAPVAG PPPASLGPTP QELVAVLHFF RAHQQPRQAF
 1021 VDALAAFQAT RPALLRLLSS VGVTEIEALG GTIPDATERW QRLGLRGLGFR PATGAAAPSP
 1081 DSLQGFAQSL ERTLGSFGMA GQSACSPHRK RPAETAIAPR SIRRSPNNAG QPSEPWPDQL
 1141 AWLQRRKRTA RSHIRADSAA SVPANLHLGT RAQFTPDRLR AEPGPIMQAH TSPASVSFGS
 1201 HVAFEPGLPD PGTPTSADLA SFEAEPFGVG PLDFHLDWLL QILET (SEQ ID NO: 205).

In some embodiments, the TALEN polypeptide comprises or consists of:

1 mdpirsrtps parellpgpq pdrvqptadr ggappaggl dglparrtms rtrlpsppap
 61 spafsagsfs dllrqfdpsl ldtslldsmp avgtphtaaa paecdevqsg lraaddpppt
 121 vrvavtaarp prakparr r aaqpsdaspa aqvdlrtlgy sqqqqekikp kvgstvaqhh
 181 ealvghgfth ahivalsrhp aalgtvavky qdmiaalpea thedivgvvk qwsgaralea
 241 lltvagelrg pplqldtgql vkiakrggvt aveavhasrn altgaplnlt paqvvaian
 301 nggkqaletv qrllpvlcqa hgltpaqvva iashdggkqa letmqrllpv lcqahglppd
 361 qvvaianig gkqaletvqr llpvlcqhah ltpdqvvaia shgggkqale tvqrllpvlc
 421 qahgltpdqv vaiashdggk qaletvqrll pvlcqhahgt pdqvvaian gggkqaletv
 481 qrllpvlcqa hgltpdqvva iasnggkqal etvqrllpvl cqahgltpdq vvaiashdgg
 541 kqaletvqrl lpvlcqhthgl tpaqvvaian hdggkqalet vqqlpvlcqh ahgltpdqvv
 601 aianiggkq alatvqrllp vlcqhahgltp dqvvaian gggkqaletv rllpvlcqhah
 661 gltpdqvvai asnggkqal etvqrllpvl cqahgltpdq vvaiianigg kqaletvqrl
 721 lpvlcqhahgl tpaqvvaian hdggkqalet vqrllpvlcqh ahgltpdqvv aianiggkq
 781 aletvqrllp vlcqhahgltp eqvvaian gggkqaletv rllpvlcqhah gltpdqvvai
 841 asnggkqal etvqrllpvl cqahgltpaq vvaiianigg kqaletvqrl lpvlcqhahgl
 901 tlaqvvaian niggkqalet vqrllpvlcqh ahgltpdqvv aianiggkq aletvqrllp
 961 vlcdhgltp dqvvaian gggkqaletv rllpvlcqhah gltdqvvaian asnggkqale
 1021 tvqrllpvlc qdhgltpdqv vaiannggk qaletvqrll pvlcqhahgl pnqvvaian
 1081 gkqaletv qdhdgltpdqv aalndhlva laclggrpam davkkgqlpha pelirrvnrr
 1141 igertshrva dyaqvrvle ffqchshpay afdeamtqfg msrnlvqlf rrvgvtelea
 1201 rggtlppasq rdvdrilqasg mkrakpspts aqtpdqaslh afadslerdl dapsmhegd
 1261 qtgassrkrs rsdravtgps aqhsfevrp eqrdahlpl swrvkrprtr igggldpdpgt
 1321 piaadlaass tvmweqdaap fagaaddfpa fneelawlm ellpqsgsvg gti (SEQ ID
 NO: 206).

[0271] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists a zinc finger nuclease polypeptide or a nuclease domain thereof. In some embodiments, the second RNA binding protein comprises or consists of a ZNF638 polypeptide or a nuclease domain thereof. In some embodiments, the ZNF638 polypeptide comprises or consists of:

1 MSRPRFNPRG DFPLQRPRAP NPSGMRPPGP FMRPGSMGLP RFYPAGRARG IPHRFAGHES
 61 YQNMGPQRMN VQVTQHRTPD RLTKEKLDLFH EAQQKKGKPH GSRWDDEPHI SASVAVKQSS

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121 VTQVTEQSPK VQSRYTKESA SSILASFGLS NEDLEELSRV PDEQLTPENM PLILRDIRMR
181 KMGRRLPNLP SQSRNKETLG SEAVSSNVID YGHASKYGYT EDPLEVRIYD PEIPTDEVEN
241 EFQSQQNISA SVPNPNVICN SMFPVEDVFR QMDFPGESSN NRSFFSVESG TKMSGHLHISG
301 GQSVLEPIKS VNQSINQTVS QTMSQSLIPP SMNQPFSSSE LISSVSQQER IPHEPVINSS
361 NVHVGSRGSK KNYQSQADIP IRSPFGIVKA SWLPKFSHAD AQKMKRLPTP SMMNDYYAAS
421 PRIFPHLCSL CNVECSHLKD WIQHONTSTH IESCRQLRQQ YPDWNPEILP SRRNEGNRKE
481 NETPRRRSHS PSPRRSRRSS SSHRFRRSRS PMHYMYRPRS RSPRICHRFI SRYRSRSRSR
541 SPYRIRNPFGR GSPKCFRSVS PERMSRRSVR SDRKKALED VVQSRGHGTE FNKQKHLEAA
601 DKGHSPAQKP KTSSGKPSV KPTSATKSDS NLGGHSIRCK SKNLEDDTLS ECKQVSDKAV
661 SLQRKLRKEQ SLHYGSVLLI TELPEDGCTE EDVRKLFQPF GKVNDVLIVP YRKEAYLEME
721 FKEAITAIMK YIETTPLTIK GKSVKICVPG KKAQNKEVK KKTLESKKVS ATSLKRDADA
781 SKAVEIVTST SAAKTGQAKA SVAKVNKSTG KSASSVKS SV TVAVKGNKAS IKTAKSGGKK
841 SLEAKKTGNV KNKDSNKPVT IPENSEIKTS IEVKATENCA KEAISDAALE ATENEPLNKE
901 TEEMCVMLVS NLPNKGYSVE EVYDLAKPFG GLKDILILSS HKKAYIEINR KAAESMKVYF
961 TCFPVLMDGN QLSISMAPEN MNIKDEEAI F ITLVKENDPE ANIDTIYDRF VHLDNLPEDG
1021 LQCVLCVGLQ FGKVDHVF I SNRNKAILQL DSPESAQSMY SFLKQNPQNI GDHMLTCSLS
1081 PKIDLPEVQI EHDPELEKES PGLKNSPIDE SEVQTATDSP SVKPNELEEE STPSIQTTETL
1141 VQQEEPCEEE AEKATCDSDF AVETLELETQ GEEVKEEIP L VASASVSIEQ FTENAEBCAL
1201 NQQMFNSDLE KKGAEIINPK TALLPSDSVF AEERNLKGIL EESPSEADF ISGITQTMVE
1261 AVAEVEKNET VSEILPSTCI VTLVPGIPTG DEKTVDKKNI SEKKGNMDEK EEKEFNTKET
1321 RMDLQIGTEK AEKNEGRMDA EKVEKMAAMK EKPAENTL FK AYPNKGVGQA NKPDETSKTS
1381 ILAVSDVSSS KPSIKAVIVS SPKAKATVSK TENQKSFPKS VPRDQINA EK KLSAKEFGLL
1441 KPTSARSGLA ESSSKFKPTQ SSLTRGGSGR ISALQGKLSK LDYRDITKQS QETEARPSIM
1501 KRDDSNNKTL AEQNTKNPKS TTGRSSKSKE EPLFPFNLDE FVTVDEVIEE VNPSQAKQNP
1561 LKGKRKETLK NVPFSELNLK KKKGKTSTPR GVEGELSFTV LDEIGEEEDA AAHLAQALVT
1621 VDEVIDEEL NMEEMVKNSN SLFTLDELID QDDCISHSEP KDVTVLSVAE EQDLLKQERL
1681 VTVDEIGEVE ELPLNESADI TFATLNTKGN EGDTVRDSIG FISSQVPEDP STLVTVDEIQ
1741 DDSSDLHLVT LDEVTEDED SLADFNNLKE ELNFVTVDEV GEEEDGDNDL KVELAQSKND
1801 HPTDKKGRNK KRAVDTKKTK LESLSQVGPV NENVMEEDLK TMIERHLTAK TPTKRVRI GK
1861 TLPSEKAVVT EPAKGEEAFQ MSEVDEESGL KDSEPERK RK KTEDSSSGKS VASDVPEELD
1921 FLVPKAGFFC PICSLFYSGE KAMTNHCKST RHKQNTKFM AKQRKEKEQN EAEERSSR
(SEQ ID NO: 207) .

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[0272] In some embodiments of the compositions of the disclosure, the second RNA binding protein comprises or consists of a PIN domain derived from the human SMG6 protein, also commonly known as telomerase-binding protein EST1A isoform 3, NCBI Reference Sequence: NP_001243756.1. In some embodiments, the PIN from hSMG6 is used herein in the form of a Cas fusion protein and as an internal control, for example, and without limitation, see Figure 9, which shows PIN-dSauCas9, PIN-dSauCas9dHNH, PIN-dSPCas9, and dcjeCas9-PIN.

[0273] In some embodiments of the compositions of the disclosure, the composition further comprises (a) a sequence comprising a gRNA that specifically binds within an RNA molecule and (b) a sequence encoding a nuclease. In some embodiments, a nuclease comprises a sequence isolated or derived from a CRISPR/Cas protein. In some embodiments, the CRISPR/Cas protein is isolated or derived from any one of a type I, a type IA, a type IB, a type IC, a type ID, a type IE, a type IF, a type IU, a type III, a type IIIA, a type IIIB, a type IIIC, a type IIID, a type IV, a

type IVA, a type IVB, a type II, a type IIA, a type IIB, a type IIC, a type V, or a type VI CRISPR/Cas protein. In some embodiments, a nuclease comprises a sequence isolated or derived from a TALEN or a nuclease domain thereof. In some embodiments, a nuclease comprises a sequence isolated or derived from a zinc finger nuclease or a nuclease domain thereof.

Fusion Proteins

[0274] In some embodiments of the compositions and methods of the disclosure, the composition comprises a sequence encoding a target RNA-binding fusion protein comprising (a) a sequence encoding a first RNA-binding polypeptide or portion thereof; and (b) a sequence encoding a second RNA-binding polypeptide, wherein the first RNA-binding polypeptide binds a target RNA, and wherein the second RNA-binding polypeptide comprises RNA-nuclease activity.

[0275] In some embodiments, a target RNA-binding fusion protein is an RNA-guided target RNA-binding fusion protein. RNA-guided target RNA-binding fusion proteins comprise at least one RNA-binding polypeptide which corresponds to a gRNA which guides the RNA-binding polypeptide to target RNA. RNA-guided target RNA-binding fusion proteins include without limitation, RNA-binding polypeptides which are CRISPR/Cas-based RNA-binding polypeptides or portions thereof.

[0276] In some embodiments, a target RNA-binding fusion protein is not an RNA-guided target RNA-binding fusion protein and as such comprises at least one RNA-binding polypeptide which is capable of binding a target RNA without a corresponding gRNA sequence. Such non-guided RNA-binding polypeptides include, without limitation, at least one RNA-binding protein or RNA-binding portion thereof which is a PUF (Pumilio and FBF homology family). This type RNA-binding polypeptide can be used in place of a gRNA-guided RNA binding protein such as CRISPR/Cas. The unique RNA recognition mode of PUF proteins (named for *Drosophila* Pumilio and *C. elegans* fem-3 binding factor) that are involved in mediating mRNA stability and translation are well known in the art. The PUF domain of human Pumilio1, also known in the art, binds tightly to cognate RNA sequences and its specificity can be modified. It contains eight PUF repeats that recognize eight consecutive RNA bases with each repeat recognizing a single base. Since two amino acid side chains in each repeat recognize the Watson-Crick edge of the

corresponding base and determine the specificity of that repeat, a PUF domain can be designed to specifically bind most 8-nt RNA. Wang et al., Nat Methods. 2009; 6(11): 825-830. See also WO2012/068627 which is incorporated by reference herein in its entirety.

[0277] In some embodiments of the non-guided RNA-binding fusion proteins of the disclosure, the fusion protein comprises at least one RNA-binding protein or RNA-binding portion thereof which is a PUMBY (Pumilio-based assembly) protein. RNA-binding protein PumHD (Pumilio homology domain, a member of the PUF family), which has been widely used in native and modified form for targeting RNA, has been engineered to yield a set of four canonical protein modules, each of which targets one RNA base. These modules (i.e., Pumby, for Pumilio-based assembly) can be concatenated in chains of varying composition and length, to bind desired target RNAs. The specificity of such Pumby–RNA interactions is high, with undetectable binding of a Pumby chain to RNA sequences that bear three or more mismatches from the target sequence. Katarzyna et al., PNAS, 2016; 113(19): E2579-E2588. See also US 2016/0238593 which is incorporated by reference herein in its entirety.

[0278] In some embodiments of the compositions of the disclosure, the first RNA binding protein comprises a Pumilio and FBF (PUF) protein. In some embodiments, the first RNA binding protein comprises a Pumilio-based assembly (PUMBY) protein. In some embodiments, a PUF1 protein of the disclosure comprises or consists of the amino acid sequence of

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MDKSKQMNIN NLSNIPEVID PGITIPYEE EYENNGESNS QLQQQPQKLG SYRSRAGKFS 60
NTLSNLLPSI SAKLHHSKKN SHGKNGAEFS SSNNSSQSTV ASKTPRASPS RSKMMESSID 120
GVTMDRPGSL TPPQDMEKLV HFPDSSNNFL IPAPRGSSDS FNLPHQISRT RNNTMSSQIT 180
SISSIAPKPR TSSGIWSSNA SANDPMQQHL LQQLQPTTSN NTTNSNTLND YSTKTAYFDN 240
MVSTSGSQMA DNKMNTNLA IPNSVWSNTR QRSQSNASSI YTDAPLYEQP ARASISSHYT 300
IPTQESPLIA DEIDPQSINW VTMDPTVPSI NQISNLLPTN TISISNVFPL QHQQPQLNNA 360
INLTSTSLAT LCKYGEVIS ARTLRNLNMA LVEFSSVESA VKALDSLOGK EVSMIGAPSK 420
ISFAKILPMH QQPPQFLNS QGLPLGLENN NLQPQLLQE QLFNGAVTFQ QQGNVSI PVF 480
NQSQSQSQHQ NHSSGSAGFS NVLHGYNMNN SMHGNNNSA NEKEQCPFPL PPNVNEKED 540
LLREIIELEF ANSDEYQINS LIKKSLNHKG TSDTQNFGL PEPLSGREFD PPKLRELKRS 600
IDSNAFSDLE IEQLAIAMLD ELPELSSDYL GNTIVQKLF E HSSDIKDIM LRKTSKYLTS 660
MGVHKNGTWA CQKMITMAHT PRQIMQVTQG VKDYCTPLIN DQFGNYVIQC VLKFGFPWNQ 720
FIFESIINF WVIQNRGGA RAVRACLEAH DIVTPEQSIV LSAMIVTYAE YLSTNSNGAL 780
LVTWFLDTSV LPNRHSILAP RLTKRIVELC GHRLASLTIL KVLNYRGDDN ARKIILDSLF 840
GNVNAHDSSP PKELTKLLCE TNYGPTFVHK VLAMPLLEDD LRAHIIKQVR KVLTDSTQIQ 900
PSRRLLEEVG LASPSSTHNK TKQQQQQHHN SSISHMFATP DTSGQHMRGL SVSSVKSGGS 960
KHTMNTTTT NGSSASTLSP GQPLNANSNS SMGYFSYPGV FVSGFSGNA SNGYAMNDD 1020
LSSQFDMLNF NNGTRLSLPQ LSLTNHNNNT MELVNVGSS QPHTNNNNNN NNTNYNDNT 1080
VFETLTLHSA N 1091
(SEQ ID NO: 209).

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In some embodiments, a PUF3 protein of the disclosure comprises or consists of the amino acid sequence of

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1 MEMNMDMDMD MELASIVSSL SALSHSNNNG GQAAAAGIVN GGAAGSQQIG GFRRSSFTTA
61 NEVDSEILLL HGSSESSPIF KKTALSVGTA PPFSTNSKKF FGNGGNYQY RSTDTASLSS
121 ASYNNYHTHH TAANLGKNNK VNHLGQYSA SIAGPVYNG NDNNSGGEG FFEKFGKSLI
181 DGTRELESQD RPDVNTQSQ FISKSVSNAS LDTQNTFEQN VESDKNFNKL NRNTTNSGSL
241 YHSSNSGSS ASLESENAHY PKRNIWNVAN TPVFRPSNNP AAVGATNVAL PNQODGPANN
301 NFPYMGFFP PNQFHQGPY QNFPNYLIGS PSNFISQMS VQIPANEDTE DSNGKKKKKA
361 NRPSSVSSPS SPPNNSPFPF AYPNPMFMP FPPLSAPQQ QQQQQQQQQE DQQQQQQQEN
421 PYIYPTPNP IPVKMPKDEK TFKKRNKNH PANNSNNANK QANPYLENSI PTKNTSKKNA
481 SSKSNESTAN NHKSHSHSH HSQSLQQQQQ TYHRSPLEEQ LRNSSSDKNS NSNMSLKDIF
541 GHSLEFCKDQ HGSRFIQREL ATSPASEKEV IFNEIRDDAI ELSNDVFGNY VIQKFFEFGS
601 KIQKNTLVDQ FKGNMKQLSL QMYACRVIQK ALEYIDSNQR IELVLELSDS VLQMIKDQNG
661 NHVIQKAIET IPIEKLFPIL SSLTGHYHL STHSYGCRVI QRLLEFGSSE DQESILNELK
721 DFIPYLIQDQ YGNYVIQYVL QQDQFTNKEM VDIKQEIET VANNVVEYSK HKFASNVVEK
781 SILYGSKNQK DLIISKILPR DKNHALNLED DSPMILMIK QFANYVIQKL VNVSEGEK
841 LIVIAIRAYL DKLKNSNSLG NRHLASVEKL AALVENAEV (SEQ ID NO: 210). In some

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embodiments, a PUF4 protein of the disclosure comprises or consists of the amino acid sequence of

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1 MSTKGLKEEI DDVPSVDFVV SETVNSALEQ LQLDDPEENA TSNAFANKVS QDSQFANGPP
61 SQMFFHPQMM GGMGFMPYSQ MMQVPHNCP FFPFDFNDP TAPLSSSPLN AGGPPMLFKN
121 DSLPFQMLSS GAAVATQGGQ NLNPLINDNS MKVLPASAD PLWTHSNVPG SASVAIEETT
181 ATLQESLPSK GRESNNKASS FRRQTFHALS PTDLINAANN VTLSKDFQSD MQNFSKAKKP
241 SVGANNTAKT RTQSISFDNT PSSTSFIPPT NSVSEKLSDF KIETSKEDLI NKTAPAKKES
301 PTTYGAAYPY GGPLLQPNPI MPGHPHNISS PIYGIRSPFP NSYEMGAQFQ PFSPILNPTS
361 HSLNANSPIP LTQSPIHLAP VLNPSNSVA FSDMKNDGGK PTTDNDKAGP NVRMDLINPN
421 LGPSMPPFHI LPPQQNTPPP PWLYSTPPP NAMVPPHLLA QNHMPLMNSA NKKHHGRNNN
481 SSSHNDNDN IGNSNYNNKD TGRSNVGMK NMKNSYHGY NNNNNNNNNN NNNNSNATN
541 SNSAEKQRKI EESSRFADAV LDQYIGSIHS LCKDQHGCRF LQKQLDILGS KAADAFEET
601 KDYTVELMTD SFGNYLIQKL LEEVTTEQRI VLTKISSPHF VEISLNPHGT RALQKLIETI
661 KTDEEAQIVV DSLRPYTVQL SKDLNGNHVI QKCLQRLKPE NFQFIFDAIS DSCIDIATHR
721 HGCCVLQRCL DHGTTEQCDN LCDKLLALVD KLTLDPFQNY VVQYIITKEA EKNKYDYTHK
781 IVHLLKPRAI ELSIHKFGSN VIEKILKTAI VSEPMILEIL NNGGETGIQS LLNDSYGNV
841 LQTALDISHK QNDYLYKRLS EIVAPLLVGP IRNTPHGKRI IGMLHLDS (SEQ ID NO:

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211).

In some embodiments, a PUF5 protein of the disclosure comprises or consists of the amino acid sequence of

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1 MSDSTGRINS KASDSSSISD HQTADLSIFN GSFDDGAFSS SNIPLFNFMG TGNQRFQYSP
61 HPEAKSSDPC RLAALTPSTP KGPLNLTPAD FGLADFSVGN ESFADFTANN TSFVGNVQSN
121 VRSTRLLPAW AVDNSGNIRD DLTLQDVVSN GSLIDFAMDR TGVKFLERHF PEDHDNEMHF
181 VLFDKLTEQG AVFTSLCRSA AGNFIIQKFV EHATLDEQER LVRKMCDNGL IEMCLDKFAC
241 RVVQMSIQKF DVSIAMKLVE KISSLDFLPL CTDQCAIHVL QKVVKLLPIS AWSFFVKFLC
301 RDDNLMFVCQ DKYGCRLVQQ TIDKLSDNPK LHCFNTRLQL LHGLMTSVAR NCFRLSSNEF
361 ANYVVQYVIK SSGVMEMYRD TIEKCLLRN ILSMSQDKYA SHVVEGAFLF APPLLLSEMM
421 DEIFDGYVKD QETNRDALDI LLFHQYGNV VQQMISICIS ALLGKEERKM VASEMRLYAK
481 WFDRIKNRVN RHSGRLERFS SGKKIIESLQ KLNVPMTMTN EPMPYWAMPT PLMDISAHFM
541 NKLNFQKNSV FDE (SEQ ID NO: 212). In some embodiments, a PUF6 protein of

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the disclosure comprises or consists of the amino acid sequence of

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1 MTPNRRSTDS YNMLGASFDF DPDFSLLSNK THKNKNPKPP VKLLPYRHGS NTTSSDLNDY

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61 IFNSGSGSSD DETPPPAAPI FISLEEVLLN GLLIDFAIDP SGVKFLEANY PLDSEDQIRK
 121 AVFEKLTST TLFVGLCHSR NGNFIVQKLV ELATPAEQRE LLRQIMDGGL LVMCKDKFAC
 181 RVVQLALQKF DHSNVFQLIQ ELSTFDLAAM CTDQISIHVI QRVVKQLPVD MWTFFVHFLS
 241 SGDSLMAVCQ DKYGCRLVQQ VIDRLAENPK LPCFKFRIQL LHSLMTCIVR NCYRLSSNEF
 301 ANYVIQYVIK SSGIMEMYRD TIIDKCLLRN LLSMSQDKYA SHVIEGAFLF APPALLHEMM
 361 EEIFSGYVKD VELNRDALDI LLFHQYGNV VQQMISICTA ALIGKEERQL PPAILLLYSG
 421 WYEKMKQVRL QHASRLERFS SGKKIIDSVM RHGVPTAAAI NAQAAPSLME LTAQFDAMFP
 481 SFLAR (SEQ ID NO: 213). In some embodiments, a PUF7 protein of the

disclosure comprises or consists of the amino acid sequence of

1 MTPNRRSTDS YNMLGASFDF DPDFSLLSNK THKNKNPKPP VKLLPYRHGS NTTSSDSDSY
 61 IFNSGSGSSD AETPAPVAPI FISLEDVLLN GQLIDFAIDP SGVKFLEANY PLDSEDQIRK
 121 AVFEKLTST TLFVGLCHSR NGNFIVQKLV ELATPAEQRE LLRQIMDGGL LAMCKDKFAC
 181 RVVQLALQKF DHSNVFQLIQ ELSTFDLAAM CTDQISIHVI QRVVKQLPVD MWTFFVHFLS
 241 SGDSLMAVCQ DKYGCRLVQQ VIDRLAENPK LPCFKFRIQL LHSLMTCIVR NCYRLSSNEF
 301 ANYVIQYVIK SSGIMEMYRD TIIDKCLLRN LLSMSQDKYA SHVIEGAFLF APPALLHEMM
 361 EEIFSGYVKD VESNRDALDI LLFHQYGNV VQQMISICTA ALIGKEEREL PPAILLLYSG
 421 WYEKMKQVRL QHASRLERFS SGKKIIDSVM RHGVPTAAAV NAQAAPSLME LTAQFDAMFP
 481 SFLAR (SEQ ID NO: 214). In some embodiments, a PUF8 protein of the

disclosure comprises or consists of the amino acid sequence of

1 MSRPISIGNT CTFDPSASPI ESLGRSIGAQ KIVDSVCGSP IRSYGRHIST NPKNERLPDT
 61 PEFQFATYMH QGGKVIQNT LHMFGTTPSC YCAQENIPIS SNVGHVLSTI NNNYMNHQYN
 121 GSNMFSNQMF QMLQAQAYND LQMHOAHSQS IRVPVQPSAT GIFSNPYREP TTTDDLTRY
 181 RANPAMMKNL KLSDIRGALL KFAKDQVGRS FTQQELASSK DRFEKDSIFD EVVSNADDELV
 241 DDI FGNVYVQ KFFEYGEERH WARLVDALID RVPEYAFQMY ACRVLQKALE KINEPLQIKI
 301 LSQIRHVIHR CMKDQNGNHV VQKAIEKVSP QYVQFIVDTL LESSNTIYEM SVDPYGCRRV
 361 QRCLEHCSPS QTKFVIGQIH KRFDEIANNQ YGNYVVQHV I EHGSEEDRMV IVTRVSNNFL
 421 EFATHKYSSN VIEKCLEQGA VYHKSMIVGA ACHHQEGSVP IVVQMMKDQY ANYVVQKMF
 481 QVTSEQRREL ILTVRPHIPV LRQFPHGKHI LAKLEKYFQK PAVMSYPYQD MQGSH (SEQ

ID NO: 215). In some embodiments, a PUF9 protein of the disclosure comprises or consists of the amino acid sequence of

1 MADPNWAYAP PTNYYADHSI AKPIMISGGH PSQDQGHSPK SESFGQSVTT AFNGMVDNLV
 61 GSPSSSVQQR NYFTTTPFPI SRSPNDRNDD KIMGNQSYGV PIPVQDQVVP QGTPDFQMT
 121 FLQGGHLLIG GSPNGPVQVS GNWYSGGAGI FSTMQQADPS NGMPGMAAEF VNNENGMPPG
 181 NGMHQAMIS GSPFFPYQNM MNLTSFSGAM GLGPQQIQQR DPQMFQQPIL HEPIQGMQON
 241 GFGQVFFFTQ MQNQHPQGG AQQQLOQLAQ QHQQQNSQQ FFGQGNMG NGGVMNDWSQ
 301 RSFGMPQQA QNGLPFPNS QNPPRRRGPE DPNGQTPKTL QDIKNNVIEF AKDQHGSRFI
 361 QKLERASLR DKAEIFTPVL ENAEELMTDV FGNYVIQKFF EFGNNEQRNQ LVGTIRGNVM
 421 KLALQMYGCR VIQKALEYVE EKYQHEILGE MEGQVLKCVK DQNGNHVIQK VIERVEPERL
 481 QFIIDAFKTN NSDNVYTLV HPYGCRIQR VLEYCNEEQK QPVLDAQIH LKQLVLDQYG
 541 NYVIQHVIEH GSPSDKEQIV QDVISDDLK FAQHKEASNV IEKCLTFGGH AERNLIIDKV
 601 CGDPNDPSP LLQMMKDPFA NYVVQKMLDV ADPQHRKKIT LTIKPHIATL RKNYFGKHIL
 661 LKLEKYFAKQ APANSSNSSS NDQIYHSFP DIPLGADFSN HPF (SEQ ID NO:

216).

[0279] In some embodiments of the compositions of the disclosure, at least one of the RNA-binding proteins or RNA-binding portions thereof is a PPR protein. PPR proteins (proteins with pentatricopeptide repeat (PPR) motifs derived from plants) are nuclear-encoded and exclusively

controlled at the RNA level organelles (chloroplasts and mitochondria), cutting, translation, splicing, RNA editing, genes specifically acting on RNA stability. PPR proteins are typically a motif of 35 amino acids and have a structure in which a PPR motif is about 10 contiguous amino acids. The combination of PPR motifs can be used for sequence-selective binding to RNA. PPR proteins are often comprised of PPR motifs of about 10 repeat domains. PPR domains or RNA-binding domains may be configured to be catalytically inactive. WO 2013/058404 incorporated herein by reference in its entirety.

[0280] In some embodiments, the fusion protein disclosed herein comprises a linker between the at least two RNA-binding polypeptides. In some embodiments, the linker is a peptide linker. In some embodiments, the peptide linker comprises one or more repeats of the tri-peptide GGS. In other embodiments, the linker is a non-peptide linker. In some embodiments, the non-peptide linker comprises polyethylene glycol (PEG), polypropylene glycol (PPG), co-poly(ethylene/propylene) glycol, polyoxyethylene (POE), polyurethane, polyphosphazene, polysaccharides, dextran, polyvinyl alcohol, polyvinylpyrrolidones, polyvinyl ethyl ether, polyacryl amide, polyacrylate, polycyanoacrylates, lipid polymers, chitins, hyaluronic acid, heparin, or an alkyl linker.

[0281] In some embodiments, the at least one RNA-binding protein does not require multimerization for RNA-binding activity. In some embodiments, the at least one RNA-binding protein is not a monomer of a multimer complex. In some embodiments, a multimer protein complex does not comprise the RNA binding protein. In some embodiments, the at least one of RNA-binding protein selectively binds to a target sequence within the RNA molecule. In some embodiments, the at least one RNA-binding protein does not comprise an affinity for a second sequence within the RNA molecule. In some embodiments, the at least one RNA-binding protein does not comprise a high affinity for or selectively bind a second sequence within the RNA molecule. In some embodiments, the at least one RNA-binding protein comprises between 2 and 1300 amino acids, inclusive of the endpoints.

[0282] In some embodiments, the at least one RNA-binding protein of the fusion proteins disclosed herein further comprises a sequence encoding a nuclear localization signal (NLS). In some embodiments, a nuclear localization signal (NLS) is positioned 3' to the RNA binding protein. In some embodiments, the at least one RNA-binding protein comprises an NLS at a C-

terminus of the protein. In some embodiments, the at least one RNA-binding protein further comprises a first sequence encoding a first NLS and a second sequence encoding a second NLS. In some embodiments, the first NLS or the second NLS is positioned 3' to the RNA-binding protein. In some embodiments, the at least one RNA-binding protein comprises the first NLS or the second NLS at a C-terminus of the protein. In some embodiments, the at least one RNA-binding protein further comprises an NES (nuclear export signal) or other peptide tag or secretory signal.

[0283] In some embodiments, a fusion protein disclosed herein comprises the at least one RNA-binding protein as a first RNA-binding protein together with a second RNA-binding protein comprising or consisting of a nuclease domain.

[0284] In some embodiments, the second RNA-binding polypeptide is operably configured to the first RNA-binding polypeptide at the C-terminus of the first RNA-binding polypeptide. In some embodiments, the second RNA-binding polypeptide is operably configured to the first RNA-binding polypeptide at the N-terminus of the first RNA-binding polypeptide. For example, one such exemplary fusion protein is E99 which is configured so that RNase1(R39D, N67D, N88A, G89D, R19D, H119N, K41R) is located at the N-terminus of SpyCas9 whereas another exemplary fusion protein, E100, is configured so that RNase1(R39D, N67D, N88A, G89D, R19D, H119N, K41R) is located at the C-terminus of SpyCas9. See Figure 6.

Vectors

[0285] In some embodiments of the compositions and methods of the disclosure, a vector comprises a guide RNA of the disclosure. In some embodiments, the vector comprises at least one guide RNA of the disclosure. In some embodiments, the vector comprises one or more guide RNA(s) of the disclosure. In some embodiments, the vector comprises two or more guide RNAs of the disclosure. In some embodiments, the vector further comprises a fusion protein of the disclosure. In some embodiments, the fusion protein comprises a first RNA binding protein and a second RNA binding protein.

[0286] In some embodiments of the compositions and methods of the disclosure, a first vector comprises a guide RNA of the disclosure and a second vector comprises a fusion protein of the disclosure. In some embodiments, the first vector comprises at least one guide RNA of the disclosure. In some embodiments, the first vector comprises one or more guide RNA(s) of the

disclosure. In some embodiments, the first vector comprises two or more guide RNA(s) of the disclosure. In some embodiments, the fusion protein comprises a first RNA binding protein and a second RNA binding protein. In some embodiments, the first vector and the second vector are identical. In some embodiments, the first vector and the second vector are not identical.

[0287] In some embodiments of the compositions and methods of the disclosure, the vector is or comprises a component of a “2-component RNA targeting system” comprising (a) nucleic acid sequence encoding a RNA-targeted fusion protein of the disclosure; and (b) a single guide RNA (sgRNA) sequence comprising: on its 5’ end, an RNA sequence (or spacer sequence) that hybridizes to or binds to a target RNA sequence; and on its 3’ end, an RNA sequence (or scaffold sequence) capable of binding to or associating with the CRISPR/Cas protein of the fusion protein; and wherein the 2-component RNA targeting system recognizes and alters the target RNA in a cell in the absence of a PAMmer. In some embodiments, the sequences of the 2-component system are in a single vector. In some embodiments, the spacer sequence of the 2-component system targets a repeat sequence selected from the group consisting of CUG, CCUG, CAG, and GGGGCC.

[0288] In some embodiments of the compositions and methods of the disclosure, a vector of the disclosure is a viral vector. In some embodiments, the viral vector comprises a sequence isolated or derived from a retrovirus. In some embodiments, the viral vector comprises a sequence isolated or derived from a lentivirus. In some embodiments, the viral vector comprises a sequence isolated or derived from an adenovirus. In some embodiments, the viral vector comprises a sequence isolated or derived from an adeno-associated virus (AAV). In some embodiments, the viral vector is replication incompetent. In some embodiments, the viral vector is isolated or recombinant. In some embodiments, the viral vector is self-complementary.

[0289] In some embodiments of the compositions and methods of the disclosure, the viral vector comprises a sequence isolated or derived from an adeno-associated virus (AAV). In some embodiments, the viral vector comprises an inverted terminal repeat sequence or a capsid sequence that is isolated or derived from an AAV of serotype AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11 or AAV12. In some embodiments, the viral vector is replication incompetent. In some embodiments, the viral vector is isolated or recombinant (rAAV). In some embodiments, the viral vector is self-complementary (scAAV).

[0290] In some embodiments of the compositions and methods of the disclosure, a vector of the disclosure is a non-viral vector. In some embodiments, the vector comprises or consists of a nanoparticle, a micelle, a liposome or lipoplex, a polymersome, a polyplex or a dendrimer. In some embodiments, the vector is an expression vector or recombinant expression system. As used herein, the term “recombinant expression system” refers to a genetic construct for the expression of certain genetic material formed by recombination.

[0291] In some embodiments of the compositions and methods of the disclosure, an expression vector, viral vector or non-viral vector provided herein, includes without limitation, an expression control element. An “expression control element” as used herein refers to any sequence that regulates the expression of a coding sequence, such as a gene. Exemplary expression control elements include but are not limited to promoters, enhancers, microRNAs, post-transcriptional regulatory elements, polyadenylation signal sequences, and introns. Expression control elements may be constitutive, inducible, repressible, or tissue-specific, for example. A “promoter” is a control sequence that is a region of a polynucleotide sequence at which initiation and rate of transcription are controlled. It may contain genetic elements at which regulatory proteins and molecules may bind such as RNA polymerase and other transcription factors. In some embodiments, expression control by a promoter is tissue-specific. Non-limiting exemplary promoters include CMV, CBA, CAG, Cbh, EF-1a, PGK, UBC, GUSB, UCOE, hAAT, TBG, Desmin, MCK, C5-12, NSE, Synapsin, PDGF, MecP2, CaMKII, mGluR2, NFL, NFH, n β 2, PPE, ENK, EAAT2, GFAP, MBP, and U6 promoters. An “enhancer” is a region of DNA that can be bound by activating proteins to increase the likelihood or frequency of transcription. Non-limiting exemplary enhancers and posttranscriptional regulatory elements include the CMV enhancer and WPRE.

[0292] In some embodiments of the compositions and methods of the disclosure, an expression vector, viral vector or non-viral vector provided herein, includes without limitation, vector elements such as an IRES or 2A peptide sites for configuration of “multicistronic” or “polycistronic” or “bicistronic” or tricistronic” constructs, i.e., having double or triple or multiple coding areas or exons, and as such will have the capability to express from mRNA two or more proteins from a single construct. Multicistronic vectors simultaneously express two or more separate proteins from the same mRNA. The two strategies most widely used for

constructing multicistronic configurations are through the use of an IRES or a 2A self-cleaving site. An “IRES” refers to an internal ribosome entry site or portion thereof of viral, prokaryotic, or eukaryotic origin which are used within polycistronic vector constructs. In some embodiments, an IRES is an RNA element that allows for translation initiation in a cap-independent manner. The term “self-cleaving peptides” or “sequences encoding self-cleaving peptides” or “2A self-cleaving site” refer to linking sequences which are used within vector constructs to incorporate sites to promote ribosomal skipping and thus to generate two polypeptides from a single promoter, such self-cleaving peptides include without limitation, T2A, and P2A peptides or sequences encoding the self-cleaving peptides.

[0293] In some embodiments, the vector is a viral vector. In some embodiments, the vector is an adenoviral vector, an adeno-associated viral (AAV) vector, or a lentiviral vector. In some embodiments, the vector is a retroviral vector, an adenoviral/retroviral chimera vector, a herpes simplex viral I or II vector, a parvoviral vector, a reticuloendotheliosis viral vector, a polioviral vector, a papillomaviral vector, a vaccinia viral vector, or any hybrid or chimeric vector incorporating favorable aspects of two or more viral vectors. In some embodiments, the vector further comprises one or more expression control elements operably linked to the polynucleotide. In some embodiments, the vector further comprises one or more selectable markers. In some embodiments, the AAV vector has low toxicity. In some embodiments, the AAV vector does not incorporate into the host genome, thereby having a low probability of causing insertional mutagenesis. In some embodiments, the AAV vector can encode a range of total polynucleotides from 4.5 kb to 4.75 kb. In some embodiments, exemplary AAV vectors that may be used in any of the herein described compositions, systems, methods, and kits can include an AAV1 vector, a modified AAV1 vector, an AAV2 vector, a modified AAV2 vector, an AAV3 vector, a modified AAV3 vector, an AAV4 vector, a modified AAV4 vector, an AAV5 vector, a modified AAV5 vector, an AAV6 vector, a modified AAV6 vector, an AAV7 vector, a modified AAV7 vector, an AAV8 vector, an AAV9 vector, an AAV.rh10 vector, a modified AAV.rh10 vector, an AAV.rh32/33 vector, a modified AAV.rh32/33 vector, an AAV.rh43 vector, a modified AAV.rh43 vector, an AAV.rh64R1 vector, and a modified AAV.rh64R1 vector and any combinations or equivalents thereof. In some embodiments, the lentiviral vector is an integrase-competent lentiviral vector (ICLV). In some embodiments, the

lentiviral vector can refer to the transgene plasmid vector as well as the transgene plasmid vector in conjunction with related plasmids (e.g., a packaging plasmid, a rev expressing plasmid, an envelope plasmid) as well as a lentiviral-based particle capable of introducing exogenous nucleic acid into a cell through a viral or viral-like entry mechanism. Lentiviral vectors are well-known in the art (see, e.g., Trono D. (2002) *Lentiviral vectors*, New York: Springer-Verlag Berlin Heidelberg and Durand et al. (2011) *Viruses* 3(2):132-159 doi: 10.3390/v3020132). In some embodiments, exemplary lentiviral vectors that may be used in any of the herein described compositions, systems, methods, and kits can include a human immunodeficiency virus (HIV) 1 vector, a modified human immunodeficiency virus (HIV) 1 vector, a human immunodeficiency virus (HIV) 2 vector, a modified human immunodeficiency virus (HIV) 2 vector, a sooty mangabey simian immunodeficiency virus (SIV_{SM}) vector, a modified sooty mangabey simian immunodeficiency virus (SIV_{SM}) vector, a African green monkey simian immunodeficiency virus (SIV_{AGM}) vector, a modified African green monkey simian immunodeficiency virus (SIV_{AGM}) vector, an equine infectious anemia virus (EIAV) vector, a modified equine infectious anemia virus (EIAV) vector, a feline immunodeficiency virus (FIV) vector, a modified feline immunodeficiency virus (FIV) vector, a Visna/maedi virus (VNV/VMV) vector, a modified Visna/maedi virus (VNV/VMV) vector, a caprine arthritis-encephalitis virus (CAEV) vector, a modified caprine arthritis-encephalitis virus (CAEV) vector, a bovine immunodeficiency virus (BIV), or a modified bovine immunodeficiency virus (BIV).

Nucleic Acids

[0294] Provided herein are the nucleic acid sequences encoding the fusion proteins disclosed herein for use in gene transfer and expression techniques described herein. It should be understood, although not always explicitly stated that the sequences provided herein can be used to provide the expression product as well as substantially identical sequences that produce a protein that has the same biological properties. These “biologically equivalent” or “biologically active” or “equivalent” polypeptides are encoded by equivalent polynucleotides as described herein. They may possess at least 60%, or alternatively, at least 65%, or alternatively, at least 70%, or alternatively, at least 75%, or alternatively, at least 80%, or alternatively at least 85%, or alternatively at least 90%, or alternatively at least 95% or alternatively at least 98%, identical primary amino acid sequence to the reference polypeptide when compared using sequence

identity methods run under default conditions. Specific polypeptide sequences are provided as examples of particular embodiments. Modifications to the sequences to amino acids with alternate amino acids that have similar charge. Additionally, an equivalent polynucleotide is one that hybridizes under stringent conditions to the reference polynucleotide or its complement or in reference to a polypeptide, a polypeptide encoded by a polynucleotide that hybridizes to the reference encoding polynucleotide under stringent conditions or its complementary strand. Alternatively, an equivalent polypeptide or protein is one that is expressed from an equivalent polynucleotide.

[0295] The nucleic acid sequences (e.g., polynucleotide sequences) disclosed herein may be codon-optimized which is a technique well known in the art. In some embodiments disclosed herein, exemplary Cas sequences, such as e.g., SEQ ID NO: 46 (Cas13d), are codon optimized for expression in human cells. Codon optimization refers to the fact that different cells differ in their usage of particular codons. This codon bias corresponds to a bias in the relative abundance of particular tRNAs in the cell type. By altering the codons in the sequence to match with the relative abundance of corresponding tRNAs, it is possible to increase expression. It is also possible to decrease expression by deliberately choosing codons for which the corresponding tRNAs are known to be rare in a particular cell type. Codon usage tables are known in the art for mammalian cells, as well as for a variety of other organisms. Based on the genetic code, nucleic acid sequences coding for, e.g., a Cas protein, can be generated. In some embodiments, such a sequence is optimized for expression in a host or target cell, such as a host cell used to express the Cas protein or a cell in which the disclosed methods are practiced (such as in a mammalian cell, e.g., a human cell). Codon preferences and codon usage tables for a particular species can be used to engineer isolated nucleic acid molecules encoding a Cas protein (such as one encoding a protein having at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to its corresponding wild-type protein) that takes advantage of the codon usage preferences of that particular species. For example, the Cas proteins disclosed herein can be designed to have codons that are preferentially used by a particular organism of interest. In one example, an Cas nucleic acid sequence is optimized for expression in human cells, such as one having at least 70%, at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, at least 98%, or at least

99% sequence identity to its corresponding wild-type or originating nucleic acid sequence. In some embodiments, an isolated nucleic acid molecule encoding at least one Cas protein (which can be part of a vector) includes at least one Cas protein coding sequence that is codon optimized for expression in a eukaryotic cell, or at least one Cas protein coding sequence codon optimized for expression in a human cell. In one embodiment, such a codon optimized Cas coding sequence has at least 80%, at least 85%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to its corresponding wild-type or originating sequence. In another embodiment, a eukaryotic cell codon optimized nucleic acid sequence encodes a Cas protein having at least 85%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to its corresponding wild-type or originating protein. In another embodiment, a variety of clones containing functionally equivalent nucleic acids may be routinely generated, such as nucleic acids which differ in sequence but which encode the same Cas protein sequence. Silent mutations in the coding sequence result from the degeneracy (i.e., redundancy) of the genetic code, whereby more than one codon can encode the same amino acid residue. Thus, for example, leucine can be encoded by CTT, CTC, CTA, CTG, TTA, or TTG; serine can be encoded by TCT, TCC, TCA, TCG, AGT, or AGC; asparagine can be encoded by AAT or AAC; aspartic acid can be encoded by GAT or GAC; cysteine can be encoded by TGT or TGC; alanine can be encoded by GCT, GCC, GCA, or GCG; glutamine can be encoded by CAA or CAG; tyrosine can be encoded by TAT or TAC; and isoleucine can be encoded by ATT, ATC, or ATA. Tables showing the standard genetic code can be found in various sources (see, for example, Stryer, 1988, Biochemistry, 3rd Edition, W.H. Freeman and Co., NY).

[0296] “Hybridization” refers to a reaction in which one or more polynucleotides react to form a complex that is stabilized via hydrogen bonding between the bases of the nucleotide residues. The hydrogen bonding may occur by Watson-Crick base pairing, Hoogsteen binding, or in any other sequence-specific manner. The complex may comprise two strands forming a duplex structure, three or more strands forming a multi-stranded complex, a single self-hybridizing strand, or any combination of these. A hybridization reaction may constitute a step in a more extensive process, such as the initiation of a PCR reaction, or the enzymatic cleavage of a polynucleotide by a ribozyme.

[0297] Examples of stringent hybridization conditions include: incubation temperatures of about 25°C to about 37°C; hybridization buffer concentrations of about 6x SSC to about 10x SSC; formamide concentrations of about 0% to about 25%; and wash solutions from about 4x SSC to about 8x SSC. Examples of moderate hybridization conditions include: incubation temperatures of about 40°C to about 50°C; buffer concentrations of about 9x SSC to about 2x SSC; formamide concentrations of about 30% to about 50%; and wash solutions of about 5x SSC to about 2x SSC. Examples of high stringency conditions include: incubation temperatures of about 55°C to about 68°C; buffer concentrations of about 1x SSC to about 0.1x SSC; formamide concentrations of about 55% to about 75%; and wash solutions of about 1x SSC, 0.1x SSC, or deionized water. In general, hybridization incubation times are from 5 minutes to 24 hours, with 1, 2, or more washing steps, and wash incubation times are about 1, 2, or 15 minutes. SSC is 0.15 M NaCl and 15 mM citrate buffer. It is understood that equivalents of SSC using other buffer systems can be employed.

[0298] “Homology” or “identity” or “similarity” refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are homologous at that position. A degree of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. An “unrelated” or “non-homologous” sequence shares less than 40% identity, or alternatively less than 25% identity, with one of the sequences of the present invention.

Cells

[0299] In some embodiments of the compositions and methods of the disclosure, a cell of the disclosure is a prokaryotic cell.

[0300] In some embodiments of the compositions and methods of the disclosure, a cell of the disclosure is a eukaryotic cell. In some embodiments, the cell is a mammalian cell. In some embodiments, the cell is a bovine, murine, feline, equine, porcine, canine, simian, or human cell. In some embodiments, the cell is a non-human mammalian cell such as a non-human primate cell.

[0301] In some embodiments, a cell of the disclosure is a somatic cell. In some embodiments, a cell of the disclosure is a germline cell. In some embodiments, a germline cell of the disclosure is not a human cell.

[0302] In some embodiments of the compositions and methods of the disclosure, a cell of the disclosure is a stem cell. In some embodiments, a cell of the disclosure is an embryonic stem cell. In some embodiments, an embryonic stem cell of the disclosure is not a human cell. In some embodiments, a cell of the disclosure is a multipotent stem cell or a pluripotent stem cell. In some embodiments, a cell of the disclosure is an adult stem cell. In some embodiments, a cell of the disclosure is an induced pluripotent stem cell (iPSC). In some embodiments, a cell of the disclosure is a hematopoietic stem cell (HSC).

[0303] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is an immune cell. In some embodiments, an immune cell of the disclosure is a lymphocyte. In some embodiments, an immune cell of the disclosure is a T lymphocyte (also referred to herein as a T-cell). Exemplary T-cells of the disclosure include, but are not limited to, naïve T cells, effector T cells, helper T cells, memory T cells, regulatory T cells (Tregs) and Gamma delta T cells. In some embodiments, an immune cell of the disclosure is a B lymphocyte. In some embodiments, an immune cell of the disclosure is a natural killer cell. In some embodiments, an immune cell of the disclosure is an antigen-presenting cell.

[0304] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is a muscle cell. In some embodiments, a muscle cell of the disclosure is a myoblast or a myocyte. In some embodiments, a muscle cell of the disclosure is a cardiac muscle cell, skeletal muscle cell or smooth muscle cell. In some embodiments, a muscle cell of the disclosure is a striated cell.

[0305] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is an epithelial cell. In some embodiments, an epithelial cell of the disclosure forms a squamous cell epithelium, a cuboidal cell epithelium, a columnar cell epithelium, a stratified cell epithelium, a pseudostratified columnar cell epithelium or a transitional cell epithelium. In some embodiments, an epithelial cell of the disclosure forms a gland including, but not limited to, a pineal gland, a thymus gland, a pituitary gland, a thyroid gland, an adrenal gland, an apocrine gland, a holocrine gland, a merocrine gland, a serous gland,

a mucous gland and a sebaceous gland. In some embodiments, an epithelial cell of the disclosure contacts an outer surface of an organ including, but not limited to, a lung, a spleen, a stomach, a pancreas, a bladder, an intestine, a kidney, a gallbladder, a liver, a larynx or a pharynx. In some embodiments, an epithelial cell of the disclosure contacts an outer surface of a blood vessel or a vein.

[0306] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is a neuronal cell. In some embodiments, a neuron cell of the disclosure is a neuron of the central nervous system. In some embodiments, a neuron cell of the disclosure is a neuron of the brain or the spinal cord. In some embodiments, a neuron cell of the disclosure is a neuron of the retina. In some embodiments, a neuron cell of the disclosure is a neuron of a cranial nerve or an optic nerve. In some embodiments, a neuron cell of the disclosure is a neuron of the peripheral nervous system. In some embodiments, a neuron cell of the disclosure is a neuroglial or a glial cell. In some embodiments, a glial of the disclosure is a glial cell of the central nervous system including, but not limited to, oligodendrocytes, astrocytes, ependymal cells, and microglia. In some embodiments, a glial of the disclosure is a glial cell of the peripheral nervous system including, but not limited to, Schwann cells and satellite cells.

[0307] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is a primary cell.

[0308] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is a cultured cell.

[0309] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is in vivo, in vitro, ex vivo or in situ.

[0310] In some embodiments of the compositions and methods of the disclosure, a somatic cell of the disclosure is autologous or allogeneic.

Methods of Use

[0311] The disclosure provides a method of modifying level of expression of an RNA molecule of the disclosure or a protein encoded by the RNA molecule comprising contacting the composition and the RNA molecule under conditions suitable for binding of one or more of the guide RNA or the fusion protein (or a portion thereof) to the RNA molecule.

[0312] The disclosure provides a method of modifying an activity of a protein encoded by an RNA molecule comprising contacting the composition and the RNA molecule under conditions suitable for binding of one or more of the guide RNA or the fusion protein (or a portion thereof) to the RNA molecule.

[0313] The disclosure provides a method of modifying level of expression of an RNA molecule of the disclosure or a protein encoded by the RNA molecule comprising contacting the composition and a cell comprising the RNA molecule under conditions suitable for binding of one or more of the guide RNA or the fusion protein (or a portion thereof) to the RNA molecule. In some embodiments, the cell is in vivo, in vitro, ex vivo or in situ. In some embodiments, the composition comprises a vector comprising composition comprising a guide RNA of the disclosure and a fusion protein of the disclosure. In some embodiments, the vector is an AAV.

[0314] The disclosure provides a method of modifying an activity of a protein encoded by an RNA molecule comprising contacting the composition and a cell comprising the RNA molecule under conditions suitable for binding of one or more of the guide RNA or the fusion protein (or a portion thereof) to the RNA molecule. In some embodiments, the cell is in vivo, in vitro, ex vivo or in situ. In some embodiments, the composition comprises a vector comprising composition comprising a guide RNA or a single guide RNA of the disclosure and a fusion protein of the disclosure. In some embodiments, the vector is an AAV.

[0315] The disclosure provides a method of modifying level of expression of an RNA molecule of the disclosure or a protein encoded by the RNA molecule comprising contacting the composition and the RNA molecule under conditions suitable for RNA nuclease activity wherein the fusion protein induces a break in the RNA molecule.

[0316] The disclosure provides a method of modifying an activity of a protein encoded by an RNA molecule comprising contacting the composition and the RNA molecule under conditions suitable for RNA nuclease activity wherein the fusion protein induces a break in the RNA molecule.

[0317] The disclosure provides a method of modifying a level of expression of an RNA molecule of the disclosure or a protein encoded by the RNA molecule comprising contacting the composition and a cell comprising the RNA molecule under conditions suitable for RNA nuclease activity wherein the fusion protein induces a break in the RNA molecule. In some

embodiments, the cell is in vivo, in vitro, ex vivo or in situ. In some embodiments, the composition comprises a vector comprising composition comprising a guide RNA of the disclosure and a fusion protein of the disclosure. In some embodiments, the vector is an AAV.

[0318] The disclosure provides a method of modifying an activity of a protein encoded by an RNA molecule comprising contacting the composition and a cell comprising the RNA molecule under conditions suitable for RNA nuclease activity wherein the fusion protein induces a break in the RNA molecule. In some embodiments, the cell is in vivo, in vitro, ex vivo or in situ. In some embodiments, the composition comprises a vector comprising composition comprising a guide RNA or a single guide RNA of the disclosure and a fusion protein of the disclosure. In some embodiments, the vector is an AAV.

[0319] The disclosure provides a method of treating a disease or disorder comprising administering to a subject a therapeutically effective amount of a composition of the disclosure.

[0320] The disclosure provides a method of treating a disease or disorder comprising administering to a subject a therapeutically effective amount of a composition of the disclosure, wherein the composition comprises a vector comprising composition comprising a guide RNA of the disclosure and a fusion protein of the disclosure and wherein the composition modifies a level of expression of an RNA molecule of the disclosure or a protein encoded by the RNA molecule.

[0321] The disclosure provides a method of treating a disease or disorder comprising administering to a subject a therapeutically effective amount of a composition of the disclosure, wherein the composition comprises a vector comprising composition comprising a guide RNA of the disclosure and a fusion protein of the disclosure and wherein the composition modifies an activity of a protein encoded by an RNA molecule.

[0322] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, a genetic disease or disorder. In some embodiments, the genetic disease or disorder is a single-gene disease or disorder. In some embodiments, the single-gene disease or disorder is an autosomal dominant disease or disorder, an autosomal recessive disease or disorder, an X-chromosome linked (X-linked) disease or disorder, an X-linked dominant disease or disorder, an X-linked recessive disease or disorder, a Y-linked disease or disorder or a mitochondrial disease or disorder. In some embodiments, the

genetic disease or disorder is a multiple-gene disease or disorder. In some embodiments, the genetic disease or disorder is a multiple-gene disease or disorder. In some embodiments, the single-gene disease or disorder is an autosomal dominant disease or disorder including, but not limited to, Huntington's disease, neurofibromatosis type 1, neurofibromatosis type 2, Marfan syndrome, hereditary nonpolyposis colorectal cancer, hereditary multiple exostoses, Von Willebrand disease, and acute intermittent porphyria. In some embodiments, the single-gene disease or disorder is an autosomal recessive disease or disorder including, but not limited to, Albinism, Medium-chain acyl-CoA dehydrogenase deficiency, cystic fibrosis, sickle-cell disease, Tay-Sachs disease, Niemann-Pick disease, spinal muscular atrophy, and Roberts syndrome. In some embodiments, the single-gene disease or disorder is X-linked disease or disorder including, but not limited to, muscular dystrophy, Duchenne muscular dystrophy, Hemophilia, Adrenoleukodystrophy (ALD), Rett syndrome, and Hemophilia A. In some embodiments, the single-gene disease or disorder is a mitochondrial disorder including, but not limited to, Leber's hereditary optic neuropathy.

[0323] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, an immune disease or disorder. In some embodiments, the immune disease or disorder is an immunodeficiency disease or disorder including, but not limited to, B-cell deficiency, T-cell deficiency, neutropenia, asplenia, complement deficiency, acquired immunodeficiency syndrome (AIDS) and immunodeficiency due to medical intervention (immunosuppression as an intended or adverse effect of a medical therapy). In some embodiments, the immune disease or disorder is an autoimmune disease or disorder including, but not limited to, Achalasia, Addison's disease, Adult Still's disease, Agammaglobulinemia, Alopecia areata, Amyloidosis, Anti-GBM/Anti-TBM nephritis, Antiphospholipid syndrome, Autoimmune angioedema, Autoimmune dysautonomia, Autoimmune encephalomyelitis, Autoimmune hepatitis, Autoimmune inner ear disease (AIED), Autoimmune myocarditis, Autoimmune oophoritis, Autoimmune orchitis, Autoimmune pancreatitis, Autoimmune retinopathy, Autoimmune urticaria, Axonal & neuronal neuropathy (AMAN), Baló disease, Behcet's disease, Benign mucosal pemphigoid, Bullous pemphigoid, Castleman disease (CD), Celiac disease, Chagas disease, Chronic inflammatory demyelinating polyneuropathy (CIDP), Chronic recurrent multifocal osteomyelitis (CRMO), Churg-Strauss

Syndrome (CSS) or Eosinophilic Granulomatosis (EGPA), Cicatricial pemphigoid, Cogan's syndrome, Cold agglutinin disease, Congenital heart block, Coxsackie myocarditis, CREST syndrome, Crohn's disease, Dermatitis herpetiformis, Dermatomyositis, Devic's disease (neuromyelitis optica), Discoid lupus, Dressler's syndrome, Endometriosis, Eosinophilic esophagitis (EoE), Eosinophilic fasciitis, Erythema nodosum, Essential mixed cryoglobulinemia, Evans syndrome, Fibromyalgia, Fibrosing alveolitis, Giant cell arteritis (temporal arteritis), Giant cell myocarditis, Glomerulonephritis, Goodpasture's syndrome, Granulomatosis with Polyangiitis, Graves' disease, Guillain-Barre syndrome, Hashimoto's thyroiditis, Hemolytic anemia, Henoch-Schonlein purpura (HSP), Herpes gestationis or pemphigoid gestationis (PG), Hidradenitis Suppurativa (HS) (Acne Inversa), Hypogammaglobulinemia, IgA Nephropathy, IgG4-related sclerosing disease, Immune thrombocytopenic purpura (ITP), Inclusion body myositis (IBM), Interstitial cystitis (IC), Juvenile arthritis, Juvenile diabetes (Type 1 diabetes), Juvenile myositis (JM), Kawasaki disease, Lambert-Eaton syndrome, Leukocytoclastic vasculitis, Lichen planus, Lichen sclerosus, Ligneous conjunctivitis, Linear IgA disease (LAD), Lupus, Lyme disease chronic, Meniere's disease, Microscopic polyangiitis (MPA), Mixed connective tissue disease (MCTD), Mooren's ulcer, Mucha-Habermann disease, Multifocal Motor Neuropathy (MMN) or MMNCB, Multiple sclerosis, Myasthenia gravis, Myositis, Narcolepsy, Neonatal Lupus, Neuromyelitis optica, Neutropenia, Ocular cicatricial pemphigoid, Optic neuritis, Palindromic rheumatism (PR), PANDAS, Paraneoplastic cerebellar degeneration (PCD), Paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, Pars planitis (peripheral uveitis), Parsonnage-Turner syndrome, Pemphigus, Peripheral neuropathy, Perivenous encephalomyelitis, Pernicious anemia (PA), POEMS syndrome, Polyarteritis nodosa, Polyglandular syndromes type I, II, III, Polymyalgia rheumatica, Polymyositis, Postmyocardial infarction syndrome, Postpericardiotomy syndrome, Primary biliary cirrhosis, Primary sclerosing cholangitis, Progesterone dermatitis, Psoriasis, Psoriatic arthritis, Pure red cell aplasia (PRCA), Pyoderma gangrenosum, Raynaud's phenomenon, Reactive Arthritis, Reflex sympathetic dystrophy, Relapsing polychondritis, Restless legs syndrome (RLS), Retroperitoneal fibrosis, Rheumatic fever, Rheumatoid arthritis, Sarcoidosis, Schmidt syndrome, Scleritis, Scleroderma, Sjögren's syndrome, Sperm & testicular autoimmunity, Stiff person syndrome (SPS), Subacute bacterial endocarditis (SBE), Susac's syndrome, Sympathetic ophthalmia (SO), Takayasu's

arteritis, Temporal arteritis/Giant cell arteritis, Thrombocytopenic purpura (TTP), Tolosa-Hunt syndrome (THS), Transverse myelitis, Type 1 diabetes, Ulcerative colitis (UC), Undifferentiated connective tissue disease (UCTD), Uveitis, Vasculitis, Vitiligo, Vogt-Koyanagi-Harada Disease, or Wegener's granulomatosis.

[0324] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, an inflammatory disease or disorder.

[0325] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, a metabolic disease or disorder.

[0326] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, a degenerative or a progressive disease or disorder. In some embodiments, the degenerative or a progressive disease or disorder includes, but is not limited to, amyotrophic lateral sclerosis (ALS), Huntington's disease, Alzheimer's disease, and aging.

[0327] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, an infectious disease or disorder.

[0328] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, a pediatric or a developmental disease or disorder.

[0329] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, a cardiovascular disease or disorder.

[0330] In some embodiments of the compositions and methods of the disclosure, a disease or disorder of the disclosure includes, but is not limited to, a proliferative disease or disorder. In some embodiments, the proliferative disease or disorder is a cancer. In some embodiments, the cancer includes, but is not limited to, Acute Lymphoblastic Leukemia (ALL), Acute Myeloid Leukemia (AML), Adrenocortical Carcinoma, AIDS-Related Cancers, Kaposi Sarcoma (Soft Tissue Sarcoma), AIDS-Related Lymphoma (Lymphoma), Primary CNS Lymphoma (Lymphoma), Anal Cancer, Appendix Cancer, Gastrointestinal Carcinoid Tumors, Astrocytomas, Atypical Teratoid/Rhabdoid Tumor, Central Nervous System (Brain Cancer), Basal Cell Carcinoma, Bile Duct Cancer, Bladder Cancer, Bone Cancer, Ewing Sarcoma, Osteosarcoma, Malignant Fibrous Histiocytoma, Brain Tumors, Breast Cancer, Burkitt

Lymphoma, Carcinoid Tumor, Carcinoma, Cardiac (Heart) Tumors, Embryonal Tumors, Germ Cell Tumor, Primary CNS Lymphoma, Cervical Cancer, Cholangiocarcinoma, Chordoma, Chronic Lymphocytic Leukemia (CLL), Chronic Myelogenous Leukemia (CML), Chronic Myeloproliferative Neoplasms, Colorectal Cancer, Craniopharyngioma, Cutaneous T-Cell Lymphoma, Ductal Carcinoma In Situ, Embryonal Tumors, Endometrial Cancer (Uterine Cancer), Ependymoma, Esophageal Cancer, Esthesioneuroblastoma (Head and Neck Cancer), Ewing Sarcoma (Bone Cancer), Extracranial Germ Cell Tumor, Extragonadal Germ Cell Tumor, Eye Cancer, Childhood Intraocular Melanoma, Intraocular Melanoma, Retinoblastoma, Fallopian Tube Cancer, Fibrous Histiocytoma of Bone, Malignant, and Osteosarcoma, Gallbladder Cancer, Gastric (Stomach) Cancer, Gastrointestinal Carcinoid Tumor, Gastrointestinal Stromal Tumors (GIST) (Soft Tissue Sarcoma), Childhood Gastrointestinal Stromal Tumors, Germ Cell Tumors, Childhood Extracranial Germ Cell Tumors, Extragonadal Germ Cell Tumors, Ovarian Germ Cell Tumors, Testicular Cancer, Gestational Trophoblastic Disease, Hairy Cell Leukemia, Head and Neck Cancer, Heart Tumors, Hepatocellular (Liver) Cancer, Histiocytosis, Hodgkin Lymphoma, Hypopharyngeal Cancer (Head and Neck Cancer), Intraocular Melanoma, Islet Cell Tumors, Pancreatic Neuroendocrine Tumors, Kaposi Sarcoma (Soft Tissue Sarcoma), Kidney (Renal Cell) Cancer, Langerhans Cell Histiocytosis, Laryngeal Cancer (Head and Neck Cancer), Leukemia, Lip and Oral Cavity Cancer (Head and Neck Cancer), Liver Cancer, Lung Cancer (Non-Small Cell and Small Cell), Childhood Lung Cancer, Lymphoma, Male Breast Cancer, Malignant Fibrous Histiocytoma of Bone and Osteosarcoma, Melanoma, Merkel Cell Carcinoma (Skin Cancer), Mesothelioma, Metastatic Squamous Neck Cancer with Occult Primary (Head and Neck Cancer), Midline Tract Carcinoma With NUT Gene Changes, Mouth Cancer (Head and Neck Cancer), Multiple Endocrine Neoplasia Syndromes, Multiple Myeloma/Plasma Cell Neoplasms, Mycosis Fungoides (Lymphoma), Myelodysplastic Syndromes, Myelodysplastic/Myeloproliferative Neoplasms, Nasal Cavity and Paranasal Sinus Cancer (Head and Neck Cancer), Nasopharyngeal Cancer (Head and Neck Cancer), Neuroblastoma, Non-Hodgkin Lymphoma, Non-Small Cell Lung Cancer, Oral Cancer, Lip and Oral Cavity Cancer and Oropharyngeal Cancer, Osteosarcoma and Malignant Fibrous Histiocytoma of Bone, Ovarian Cancer, Pancreatic Cancer, Pancreatic Neuroendocrine Tumors (Islet Cell Tumors), Papillomatosis, Paraganglioma, Parathyroid Cancer, Penile Cancer,

Pharyngeal Cancer (Head and Neck Cancer), Pheochromocytoma , Plasma Cell Neoplasm/Multiple Myeloma, Pleuropulmonary Blastoma, Pregnancy and Breast Cancer, Primary Central Nervous System (CNS) Lymphoma, Primary Peritoneal Cancer, Prostate Cancer, Rectal Cancer, Recurrent Cancer, Renal Cell (Kidney) Cancer, Retinoblastoma, Rhabdomyosarcoma, Childhood (Soft Tissue Sarcoma), Salivary Gland Cancer (Head and Neck Cancer), Sarcoma, Childhood Rhabdomyosarcoma (Soft Tissue Sarcoma), Childhood Vascular Tumors (Soft Tissue Sarcoma), Ewing Sarcoma (Bone Cancer), Kaposi Sarcoma (Soft Tissue Sarcoma), Osteosarcoma (Bone Cancer), Uterine Sarcoma, Sézary Syndrome, Lymphoma, Skin Cancer, Small Cell Lung Cancer, Small Intestine Cancer, Soft Tissue Sarcoma, Squamous Cell Carcinoma of the Skin, Squamous Neck Cancer, Stomach (Gastric) Cancer, T-Cell Lymphoma, Testicular Cancer, Throat Cancer (Head and Neck Cancer), Nasopharyngeal Cancer, Oropharyngeal Cancer, Hypopharyngeal Cancer, Thymoma and Thymic Carcinoma , Thyroid Cancer, Transitional Cell Cancer of the Renal Pelvis and Ureter, Renal Cell Cancer, Urethral Cancer, Uterine Sarcoma, Vaginal Cancer, Vascular Tumors (Soft Tissue Sarcoma), Vulvar Cancer, Wilms Tumor and Other Childhood Kidney Tumors.

[0331] In some embodiments of the methods of the disclosure, a subject of the disclosure has been diagnosed with the disease or disorder. In some embodiments, the subject of the disclosure presents at least one sign or symptom of the disease or disorder. In some embodiments, the subject has a biomarker predictive of a risk of developing the disease or disorder. In some embodiments, the biomarker is a genetic mutation.

[0332] In some embodiments of the methods of the disclosure, a subject of the disclosure is female. In some embodiments of the methods of the disclosure, a subject of the disclosure is male. In some embodiments, a subject of the disclosure has two XX or XY chromosomes. In some embodiments, a subject of the disclosure has two XX or XY chromosomes and a third chromosome, either an X or a Y.

[0333] In some embodiments of the methods of the disclosure, a subject of the disclosure is a neonate, an infant, a child, an adult, a senior adult, or an elderly adult. In some embodiments of the methods of the disclosure, a subject of the disclosure is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 days old. In some embodiments of the methods of the disclosure, a subject of the disclosure is at least 1, 2, 3, 4, 5,

6, 7, 8, 9, 10, 11 or 12 months old. In some embodiments of the methods of the disclosure, a subject of the disclosure is at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or any number of years or partial years in between of age.

[0334] In some embodiments of the methods of the disclosure, a subject of the disclosure is a mammal. In some embodiments, a subject of the disclosure is a non-human mammal.

[0335] In some embodiments of the methods of the disclosure, a subject of the disclosure is a human.

[0336] In some embodiments of the methods of the disclosure, a therapeutically effective amount comprises a single dose of a composition of the disclosure. In some embodiments, a therapeutically effective amount comprises a therapeutically effective amount comprises at least one dose of a composition of the disclosure. In some embodiments, a therapeutically effective amount comprises a therapeutically effective amount comprises one or more dose(s) of a composition of the disclosure.

[0337] In some embodiments of the methods of the disclosure, a therapeutically effective amount eliminates a sign or symptom of the disease or disorder. In some embodiments, a therapeutically effective amount reduces a severity of a sign or symptom of the disease or disorder.

[0338] In some embodiments of the methods of the disclosure, a therapeutically effective amount eliminates the disease or disorder.

[0339] In some embodiments of the methods of the disclosure, a therapeutically effective amount prevents an onset of a disease or disorder. In some embodiments, a therapeutically effective amount delays the onset of a disease or disorder. In some embodiments, a therapeutically effective amount reduces the severity of a sign or symptom of the disease or disorder. In some embodiments, a therapeutically effective amount improves a prognosis for the subject.

[0340] In some embodiments of the methods of the disclosure, a composition of the disclosure is administered to the subject systemically. In some embodiments, the composition of the disclosure is administered to the subject by an intravenous route. In some embodiments, the composition of the disclosure is administered to the subject by an injection or an infusion.

[0341] In some embodiments of the methods of the disclosure, a composition of the disclosure is administered to the subject locally. In some embodiments, the composition of the disclosure is administered to the subject by an intraosseous, intraocular, intracerebrospinal or intraspinal route. In some embodiments, the composition of the disclosure is administered directly to the cerebral spinal fluid of the central nervous system. In some embodiments, the composition of the disclosure is administered directly to a tissue or fluid of the eye and does not have bioavailability outside of ocular structures. In some embodiments, the composition of the disclosure is administered to the subject by an injection or an infusion.

[0342] In some embodiments, the compositions comprising the RNA-binding fusion proteins disclosed herein are formulated as pharmaceutical compositions. Briefly, pharmaceutical compositions for use as disclosed herein may comprise a fusion protein(s) or a polynucleotide encoding the fusion protein(s), optionally comprised in an AAV, which is optionally also immune orthogonal, in combination with one or more pharmaceutically or physiologically acceptable carriers, diluents or excipients. Such compositions may comprise buffers such as neutral buffered saline, phosphate buffered saline and the like; carbohydrates such as glucose, mannose, sucrose or dextrans, mannitol; proteins; polypeptides or amino acids such as glycine; antioxidants; chelating agents such as EDTA or glutathione; adjuvants (e.g., aluminum hydroxide); and preservatives. Compositions of the disclosure may be formulated for oral, intravenous, topical, enteral, intraocular, and/or parenteral administration. In certain embodiments, the compositions of the present disclosure are formulated for intravenous administration.

Example Embodiments:

[0343] Embodiment 1. A composition comprising:

- (a) a sequence comprising a guide RNA (gRNA) that specifically binds a target sequence within an RNA molecule and
- (b) a sequence encoding a fusion protein, the sequence comprising a sequence encoding a first RNA-binding polypeptide and a sequence encoding a second RNA-binding polypeptide, wherein neither the first RNA-binding polypeptide nor the second RNA-binding polypeptide comprises a significant DNA-nuclease activity,

wherein the first RNA-binding polypeptide and the second RNA-binding polypeptide are not identical, and

wherein the second RNA-binding polypeptide comprises an RNA-nuclease activity;

or

a composition comprising nucleic acid sequence encoding a fusion protein, the fusion protein comprising a first RNA-binding polypeptide and a second RNA-binding polypeptide, wherein the first RNA-binding polypeptide is not a guided RNA-binding polypeptide, wherein the first RNA-binding polypeptide and the second RNA-binding polypeptide are not identical, and wherein the second RNA-binding polypeptide comprises an RNA-nuclease activity.

Embodiment 2. The composition of embodiment 1, wherein the target sequence comprises at least one repeated sequence.

Embodiment 3. The composition of embodiment 1 or 2, wherein the sequence comprising the gRNA comprises a promoter capable of expressing the gRNA in a eukaryotic cell.

Embodiment 4. The composition of embodiment 3, wherein the eukaryotic cell is an animal cell.

Embodiment 5. The composition of embodiment 4, wherein the animal cell is a mammalian cell.

Embodiment 6. The composition of embodiment 5, wherein the animal cell is a human cell.

Embodiment 7. The composition of any one of embodiments 1-6, wherein the promoter is a constitutively active promoter.

Embodiment 8. The composition of any one of embodiments 1-7, wherein the promoter is isolated or derived from a promoter capable of driving expression of an RNA polymerase.

Embodiment 9. The composition of embodiment 8, wherein the promoter is isolated or derived from a U6 promoter.

Embodiment 10. The composition of any one of embodiments 1-7, wherein the promoter is isolated or derived from a promoter capable of driving expression of a transfer RNA (tRNA).

Embodiment 11. The composition of embodiment 10, wherein the promoter is isolated or derived from an alanine tRNA promoter, an arginine tRNA promoter, an asparagine tRNA promoter, an aspartic acid tRNA promoter, a cysteine tRNA promoter, a glutamine tRNA promoter, a glutamic acid tRNA promoter, a glycine tRNA promoter, a histidine tRNA promoter, an isoleucine tRNA promoter, a leucine tRNA promoter, a lysine tRNA promoter, a methionine tRNA promoter, a phenylalanine tRNA promoter, a proline tRNA promoter, a serine tRNA promoter, a threonine tRNA promoter, a tryptophan tRNA promoter, a tyrosine tRNA promoter, or a valine tRNA promoter.

Embodiment 12. The composition of embodiment 10, wherein the promoter is isolated or derived from a valine tRNA promoter.

Embodiment 13. The composition of any one of embodiments 1-12, wherein the sequence comprising the gRNA comprises a spacer sequence that specifically binds to the target RNA sequence.

Embodiment 14. The composition of embodiment 13, wherein the spacer sequence has at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 87%, 90%, 95%, 97%, 99% or any percentage in between of complementarity to the target RNA sequence.

Embodiment 15. The composition of embodiment 13, wherein the spacer sequence has 100% complementarity to the target RNA sequence.

Embodiment 16. The composition of any one of embodiments 13-15, wherein the spacer sequence comprises or consists of 20 nucleotides.

Embodiment 17. The composition of any one of embodiments 13-15, wherein the spacer sequence comprises or consists of 21 nucleotides.

Embodiment 18. The composition of embodiment 17, wherein the spacer sequence comprises the sequence UGGAGCGAGCAUCCCCAAA (SEQ ID NO: 1), GUUUGGGGAUGCUCGCUCCA (SEQ ID NO: 2), CCCUCACUGCUGGGGAGUCC (SEQ ID NO: 3), GGACUCCCCAGCAGUGAGGG (SEQ ID NO: 4), GCAACUGGAUCAAUUUGCUG (SEQ ID NO: 5), GCAGCAAUUGAUCCAGUUGC (SEQ ID NO: 6), GCAUUCUUAUCUGGUCAGUGC (SEQ ID NO: 7), GCACUGACCAGAUAAAGAAUG (SEQ ID NO: 8), GAGCAGCAGCAGCAGCAGCAG (SEQ ID NO: 9), GCAGGCAGGCAGGCAGGCAGG (SEQ ID NO: 10), GCCCCGGCCCCGGCCCCGGC (SEQ ID NO: 11), or GCTGCTGCTGCTGCTGCTGC (SEQ ID NO: 12), GGGGCCGGGGCCGGGGCCGG (SEQ ID NO: 74), GGGCCGGGGCCGGGGCCGGG (SEQ ID NO: 75), GGCCGGGGCCGGGGCCGGGG (SEQ ID NO: 76), GCCGGGGCCGGGGCCGGGGC (SEQ ID NO: 77), CCGGGGCCGGGGCCGGGGCC (SEQ ID NO: 78), CGGGGCCGGGGCCGGGGCCG (SEQ ID NO: 79).

Embodiment 19. The composition of any one of embodiments 1-18, wherein the sequence comprising the gRNA comprises a scaffold sequence that specifically binds to the first RNA binding protein.

Embodiment 20. The composition of embodiment 19, wherein the scaffold sequence comprises a stem-loop structure.

Embodiment 21. The composition of embodiment 19 or 20, wherein the scaffold sequence comprises or consists of 90 nucleotides.

Embodiment 22. The composition of embodiment 19 or 20, wherein the scaffold sequence comprises or consists of 93 nucleotides.

Embodiment 23. The composition of embodiment 22, wherein the scaffold sequence comprises the sequence

GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUU
AUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 13).

Embodiment 24. The composition of embodiment 16, wherein the spacer sequence comprises the sequence GUGAUAAGUGGAAUGCCAUG (SEQ ID NO: 14),
CUGGUGAACUCCGAUAGUG (SEQ ID NO: 15), or GAGATATAGCCTGGTGGTTC
(SEQ ID NO: 16).

Embodiment 25. The composition of embodiment 19 or 24, wherein the scaffold sequence comprises a step-loop structure.

Embodiment 26. The composition of embodiment 25, wherein the scaffold sequence comprises or consists of 85 nucleotides.

Embodiment 27. The composition of embodiment 26, wherein the scaffold sequence comprises the sequence

GGACAGCAUAGCAAGUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG
CACCGAGUCGGUGCUUUUU (SEQ ID NO: 17).

Embodiment 28. The composition of embodiment 16, wherein the spacer sequence comprises the sequence at least 1, 2, 3, 4, 5, 6, or 7 repeats of the sequence CUG (SEQ ID NO: 18), CCUG (SEQ ID NO: 19), CAG (SEQ ID NO: 80), GGGGCC (SEQ ID NO: 81) or any combination thereof.

Embodiment 29. The composition of embodiment 28, wherein the sequence comprising the gRNA comprises a scaffold sequence that specifically binds to the first RNA binding protein.

Embodiment 30. The composition of embodiment 29, wherein the scaffold sequence comprises a stem-loop structure.

Embodiment 31. The composition of embodiment 29 or 30, wherein the scaffold sequence comprises or consists of 90 nucleotides.

Embodiment 32. The composition of embodiment 30 or 31, wherein the scaffold sequence comprises or consists of 93 nucleotides.

Embodiment 33. The composition of embodiment 32, wherein the scaffold sequence comprises the sequence
GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUU
AUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 82) or
GUUUUAGAGCUAGAAAUAAGCAAGUUAAAUAAGGCUAGUCCGUUAUCAACUUGA
AAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 83).

Embodiment 34. The composition of any one of embodiments 1-33, wherein the gRNA does not bind or does not selectively bind to a second sequence within the RNA molecule.

Embodiment 35. The composition of embodiment 34, wherein an RNA genome or an RNA transcriptome comprises the RNA molecule.

Embodiment 36. The composition of any one of embodiments 1-35, wherein the first RNA binding protein comprises a CRISPR-Cas protein.

Embodiment 37. The composition of embodiment 36, wherein the CRISPR-Cas protein is a Type II CRISPR-Cas protein.

Embodiment 38. The composition of embodiment 37, wherein the first RNA binding protein comprises a Cas9 polypeptide or an RNA-binding portion thereof.

Embodiment 39. The composition of embodiment 36, wherein the CRISPR-Cas protein is a Type V CRISPR-Cas protein.

Embodiment 40. The composition of embodiment 39, wherein the first RNA binding protein comprises a Cpf1 polypeptide or an RNA-binding portion thereof.

Embodiment 41. The composition of embodiment 36, wherein the CRISPR-Cas protein is a Type VI CRISPR-Cas protein.

Embodiment 42. The composition of embodiment 41, wherein the first RNA binding protein comprises a Cas13 polypeptide or an RNA-binding portion thereof.

Embodiment 43. The composition of any one of embodiments 36-42, wherein the CRISPR-Cas protein comprises a native RNA nuclease activity.

Embodiment 44. The composition of embodiment 43, wherein the native RNA nuclease activity is reduced or inhibited.

Embodiment 45. The composition of embodiment 43, wherein the native RNA nuclease activity is increased or induced.

Embodiment 46. The composition of any one of embodiments 36-45, wherein the CRISPR-Cas protein comprises a native DNA nuclease activity and wherein the native DNA nuclease activity is inhibited.

Embodiment 47. The composition of embodiment 46, wherein the CRISPR-Cas protein comprises a mutation.

Embodiment 48. The composition of embodiment 47, wherein a nuclease domain of the CRISPR-Cas protein comprises the mutation.

Embodiment 49. The composition of embodiment 47, wherein the mutation occurs in a nucleic acid encoding the CRISPR-Cas protein.

Embodiment 50. The composition of embodiment 47, wherein the mutation occurs in an amino acid encoding the CRISPR-Cas protein.

Embodiment 51. The composition of any one of embodiments 47-50, wherein the mutation comprises a substitution, an insertion, a deletion, a frameshift, an inversion, or a transposition.

Embodiment 52. The composition of any one of embodiments 47-50, wherein the mutation comprises a deletion of a nuclease domain, a binding site within the nuclease domain, an active site within the nuclease domain, or at least one essential amino acid residue within the nuclease domain.

Embodiment 53. The composition of any one of embodiments 1-35, wherein the first RNA binding protein comprises a Pumilio and FBF (PUF) protein.

Embodiment 54. The composition of embodiment 53, wherein the first RNA binding protein comprises a Pumilio-based assembly (PUMBY) protein.

Embodiment 55. The composition of any one of embodiments 1-54, wherein the first RNA binding protein does not require multimerization for RNA-binding activity.

Embodiment 56. The composition of embodiment 55, wherein the first RNA binding protein is not a monomer of a multimer complex

Embodiment 57. The composition of embodiment 55, wherein a multimer protein complex does not comprise the first RNA binding protein.

Embodiment 58. The composition of any one of embodiments 1-57, wherein the first RNA binding protein selectively binds to a target sequence within the RNA molecule.

Embodiment 59. The composition of embodiment 58, wherein the first RNA binding protein does not comprise an affinity for a second sequence within the RNA molecule.

Embodiment 60. The composition of embodiment 58 or 59, wherein the first RNA binding protein does not comprise a high affinity for or selectively bind a second sequence within the RNA molecule.

Embodiment 61. The composition of embodiment 60, wherein an RNA genome or an RNA transcriptome comprises the RNA molecule.

Embodiment 62. The composition of any one of embodiments 1-61, wherein the first RNA binding protein comprises between 2 and 1300 amino acids, inclusive of the endpoints.

Embodiment 63. The composition of any one of embodiments 1-62, wherein the sequence encoding the first RNA binding protein further comprises a sequence encoding a nuclear localization signal (NLS).

Embodiment 64. The composition of embodiment 63, wherein the sequence encoding a nuclear localization signal (NLS) is positioned 3' to the sequence encoding the first RNA binding protein.

Embodiment 65. The composition of embodiment 64, wherein the first RNA binding protein comprises an NLS at a C-terminus of the protein.

Embodiment 66. The composition of any one of embodiments 1-62, wherein the sequence encoding the first RNA binding protein further comprises a first sequence encoding a first NLS and a second sequence encoding a second NLS.

Embodiment 67. The composition of embodiment 66, wherein the sequence encoding the first NLS or the second NLS is positioned 3' to the sequence encoding the first RNA binding protein.

Embodiment 68. The composition of embodiment 67, wherein the first RNA binding protein comprises the first NLS or the second NLS at a C-terminus of the protein.

Embodiment 69. The composition of any one of embodiments 1-68, wherein the second RNA binding protein comprises or consists of a nuclease domain.

Embodiment 70. The composition of embodiment 69, wherein the sequence encoding the second RNA binding protein comprises or consists of an RNase.

Embodiment 71. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase1.

Embodiment 72. The composition of embodiment 71, wherein the RNase1 protein comprises or consists of SEQ ID NO: 20.

Embodiment 73. The composition of embodiment 72, wherein the second RNA binding protein comprises or consists of an RNase4.

Embodiment 74. The composition of embodiment 73, wherein the RNase4 protein comprises or consists of: (SEQ ID NO: 21.

Embodiment 75. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase6.

Embodiment 76. The composition of embodiment 75, wherein the RNase6 protein comprises or consists of SEQ ID NO: 22.

Embodiment 77. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase7.

Embodiment 78. The composition of embodiment 77, wherein the RNase7 protein comprises or consists of SEQ ID NO: 23.

Embodiment 79. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase8.

Embodiment 80. The composition of embodiment 79, wherein the RNase8 protein comprises or consists of SEQ ID NO: 24.

Embodiment 81. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase2.

Embodiment 82. The composition of embodiment 81, wherein the RNase2 protein comprises or consists of SEQ ID NO: 25.

Embodiment 83. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase6PL.

Embodiment 84. The composition of embodiment 83, wherein the RNase6PL protein comprises or consists of SEQ ID NO: 26.

Embodiment 85. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNaseL.

Embodiment 86. The composition of embodiment 85, wherein the RNaseL protein comprises or consists of SEQ ID NO: 27.

Embodiment 87. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNaseT2.

Embodiment 88. The composition of embodiment 87, wherein the RNaseT2 protein comprises or consists of SEQ ID NO: 28.

Embodiment 89. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNase11.

Embodiment 90. The composition of embodiment 89, wherein the RNase11 comprises or consists of SEQ ID NO: 29.

Embodiment 91. The composition of embodiment 70, wherein the second RNA binding protein comprises or consists of an RNaseT2-like.

Embodiment 92. The composition of embodiment 91, wherein the RNaseT2-like protein comprises or consists of SEQ ID NO: 30.

Embodiment 93. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a NOB1 polypeptide.

Embodiment 94. The composition of embodiment 93, wherein the NOB1 polypeptide comprises or consists of SEQ ID NO: 31.

Embodiment 95. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an endonuclease.

Embodiment 96. The composition of embodiment 95, wherein the second RNA binding protein comprises or consists of an endonuclease V (ENDOV).

Embodiment 97. The composition of embodiment 96, wherein the ENDOV protein comprises or consists of SEQ ID NO: 32.

Embodiment 98. The composition of embodiment 95, wherein the second RNA binding protein comprises or consists of an endonuclease G (ENDOG).

Embodiment 99. The composition of embodiment 98, wherein the ENDOG protein comprises or consists of SEQ ID NO: 33.

Embodiment 100. The composition of embodiment 95, wherein the second RNA binding protein comprises or consists of an endonuclease D1 (ENDOD1).

Embodiment 101. The composition of embodiment 100, wherein the ENDOD1 protein comprises or consists of SEQ ID NO: 34.

Embodiment 102. The composition of embodiment 95, wherein the second RNA binding protein comprises or consists of a Human flap endonuclease-1 (hFEN1).

Embodiment 103. The composition of embodiment 102, wherein the hFEN1 protein comprises or consists of SEQ ID NO: 35.

Embodiment 104. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a human Schlafen 14 (hSLFN14) polypeptide.

Embodiment 105. The composition of embodiment 104, wherein the hSLFN14 polypeptide comprises or consists of SEQ ID NO: 36.

Embodiment 106. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a human beta-lactamase-like protein 2 (hLACTB2) polypeptide.

Embodiment 107. The composition of embodiment 106, wherein the hLACTB2 polypeptide comprises or consists of SEQ ID NO: 37.

Embodiment 108. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an apurinic/apyrimidinic (AP) endodeoxyribonuclease (APEX2) polypeptide.

Embodiment 109. The composition of embodiment 108, wherein the APEX2 polypeptide comprises or consists of SEQ ID NO: 38.

Embodiment 110. The composition of embodiment 108, wherein the APEX2 polypeptide comprises or consists of: SEQ ID NO: 39.

Embodiment 111. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an angiogenin (ANG) polypeptide.

Embodiment 112. The composition of embodiment 111, wherein the ANG polypeptide comprises or consists of SEQ ID NO: 40.

Embodiment 113. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a heat responsive protein 12 (HRSP12) polypeptide.

Embodiment 114. The composition of embodiment 113, wherein the HRSP12 polypeptide comprises or consists of SEQ ID NO: 41.

Embodiment 115. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Zinc Finger CCCH-Type Containing 12A (ZC3H12A) polypeptide.

Embodiment 116. The composition of embodiment 115, wherein the ZC3H12A polypeptide comprises or consists of SEQ ID NO: 42.

Embodiment 117. The composition of embodiment 115, wherein the ZC3H12A polypeptide comprises or consists of SEQ ID NO: 43.

Embodiment 118. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Reactive Intermediate Imine Deaminase A (RIDA) polypeptide.

Embodiment 119. The composition of embodiment 118, wherein the RIDA polypeptide comprises or consists of SEQ ID NO: 44.

Embodiment 120. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Phospholipase D Family Member 6 (PDL6) polypeptide.

Embodiment 121. The composition of embodiment 120, wherein the PDL6 polypeptide comprises or consists of: (SEQ ID NO: 126).

Embodiment 122. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Endonuclease III-like **protein 1** (NTHL) polypeptide.

Embodiment 123. The composition of embodiment 122, wherein the NTHL polypeptide comprises or consists of SEQ ID NO: 123.

Embodiment 124. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Mitochondrial ribonuclease P catalytic subunit (KIAA0391) polypeptide.

Embodiment 125. The composition of embodiment 124, wherein the KIAA0391 polypeptide comprises or consists of SEQ ID NO: 127.

Embodiment 126. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an apurinic or apyrimidinic site lyase (APEX1) polypeptide.

Embodiment 127. The composition of embodiment 126, wherein the APEX1 polypeptide comprises or consists of SEQ ID NO: 125.

Embodiment 128. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an argonaute 2 (AGO2) polypeptide.

Embodiment 129. The composition of embodiment 128, wherein the AGO2 polypeptide comprises or consists of SEQ ID NO: 128.

Embodiment 130. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mitochondrial nuclease EXOG (EXOG) polypeptide.

Embodiment 131. The composition of embodiment 130, wherein the EXOG polypeptide comprises or consists of SEQ ID NO: 129.

Embodiment 132. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Zinc Finger CCCH-Type Containing 12D (ZC3H12D) polypeptide.

Embodiment 133. The composition of embodiment 132, wherein the ZC3H12D polypeptide comprises or consists of SEQ ID NO: 130.

Embodiment 134. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an endoplasmic reticulum to nucleus signaling 2 (ERN2) polypeptide.

Embodiment 135. The composition of embodiment 134, wherein the ERN2 polypeptide comprises or consists of SEQ ID NO: 131.

Embodiment 136. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a pelota mRNA surveillance and ribosome rescue factor (PELO) polypeptide.

Embodiment 137. The composition of embodiment 136, wherein the PELO polypeptide comprises or consists of SEQ ID NO: 132.

Embodiment 138. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a YBEY metallopeptidase (YBEY) polypeptide.

Embodiment 139. The composition of embodiment 138, wherein the YBEY polypeptide comprises or consists of SEQ ID NO: 133.

Embodiment 140. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a cleavage and polyadenylation specific factor 4 like (CPSF4L) polypeptide.

Embodiment 141. The composition of embodiment 140, wherein the CPSF4L comprises or consists of SEQ ID NO: 134.

Embodiment 142. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an hCG_2002731 polypeptide.

Embodiment 143. The composition of embodiment 142, wherein the hCG_2002731 polypeptide comprises or consists of SEQ ID NO: 135.

Embodiment 144. The composition of embodiment 142, wherein the hCG_2002731 polypeptide comprises or consists of SEQ ID NO: 136.

Embodiment 145. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of an Excision Repair Cross-Complementation Group 1 (ERCC1) polypeptide.

Embodiment 146. The composition of embodiment 145, wherein the ERCC1 polypeptide comprises or consists of SEQ ID NO: 137.

Embodiment 147. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a ras-related C3 botulinum toxin substrate 1 isoform (RAC1) polypeptide.

Embodiment 148. The composition of embodiment 147, wherein the RAC1 polypeptide comprises or consists of SEQ ID NO: 138.

Embodiment 149. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Ribonuclease A A1 (RAA1) polypeptide.

Embodiment 150. The composition of embodiment 149, wherein the RAA1 polypeptide comprises or consists of SEQ ID NO: 139.

Embodiment 151. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a Ras Related Protein (RAB1) polypeptide.

Embodiment 152. The composition of embodiment 151, wherein the RAB1 polypeptide comprises or consists of SEQ ID NO: 140.

Embodiment 153. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a DNA Replication Helicase/Nuclease 2 (DNA2) polypeptide.

Embodiment 154. The composition of embodiment 153, wherein the DNA2 polypeptide comprises or consists of SEQ ID NO: 141.

Embodiment 155. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a FLJ35220 polypeptide.

Embodiment 156. The composition of embodiment 155, wherein the FLJ35220 polypeptide comprises or consists of SEQ ID NO: 142.

Embodiment 157. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a FLJ13173 polypeptide.

Embodiment 158. The composition of embodiment 157, wherein the FLJ13173 polypeptide comprises or consists of: (SEQ ID NO: 143).

Embodiment 159. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a DNA repair endonuclease XPF (ERCC4) polypeptide.

Embodiment 160. The composition of embodiment 159, wherein the ERCC4 polypeptide comprises or consists of SEQ ID NO: 64.

Embodiment 161. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R)) polypeptide.

Embodiment 162. The composition of embodiment 161, wherein the Rnase1(K41R) polypeptide comprises or consists of SEQ ID NO: 116.

Embodiment 163. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R, D121E)) polypeptide.

Embodiment 164. The composition of embodiment 163, wherein the Rnase1 (Rnase1(K41R, D121E)) polypeptide comprises or consists of SEQ ID NO: 117.

Embodiment 165. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(K41R, D121E, H119N)) polypeptide.

Embodiment 166. The composition of embodiment 165, wherein the Rnase1 (Rnase1(K41R, D121E, H119N)) polypeptide comprises or consists of SEQ ID NO: 118.

Embodiment 167. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(H119N)) polypeptide.

Embodiment 168. The composition of embodiment 167, wherein the Rnase1 (Rnase1(H119N)) polypeptide comprises or consists of SEQ ID NO: 119.

Embodiment 169. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide.

Embodiment 170. The composition of embodiment 169, wherein the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide comprises or consists of SEQ ID NO: 120.

Embodiment 171. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide.

Embodiment 172. The composition of embodiment 171, wherein the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N, K41R, D121E)) polypeptide comprises or consists of SEQ ID NO: 121.

Embodiment 173. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of a mutated Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D, H119N)) polypeptide.

Embodiment 174. The composition of embodiment 173, wherein the Rnase1 (Rnase1(R39D, N67D, N88A, G89D, R91D)) polypeptide comprises or consists of SEQ ID NO: 122.

Embodiment 175. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein 1 (TENM1) polypeptide.

Embodiment 176. The composition of embodiment 175, wherein the TENM1 polypeptide comprises or consists of SEQ ID NO: 144.

Embodiment 177. The composition of embodiment 69, wherein the second RNA binding protein comprises or consists of Teneurin Transmembrane Protein 2 (TENM2) polypeptide.

Embodiment 178. The composition of embodiment 177, wherein the TENM2 polypeptide comprises or consists of SEQ ID NO: 145.

Embodiment 179. A composition comprising a sequence encoding a target RNA-binding fusion protein comprising (a) a sequence encoding a first RNA-binding polypeptide or portion thereof; and (b) a sequence encoding a second RNA-binding polypeptide, wherein the first RNA-binding polypeptide binds a target RNA not guided by a gRNA sequence, and wherein the second RNA-binding polypeptide comprises RNA-nuclease activity.

Embodiment 180. The composition of embodiment 179, wherein the first RNA-binding polypeptide or portion thereof is a PUF, PUMBY, or PPR polypeptide or portion thereof.

Embodiment 181. A method for modifying the level of expression of an RNA molecule or a protein encoded by the RNA molecule, the method comprising contacting the composition of embodiments 1 or 179 and the RNA molecule under conditions suitable for binding of the fusion protein or a portion thereof to the RNA molecule.

EXAMPLES

Example 1: Methods

[0344] HEK-293 cells were cultured in DMEM with 10% FBS and 1% penicillin/streptomycin (GIBCO) and passaged at 90%–100% confluency. Cells were seeded at 1×10^5 cells per well of a 24-well plate for RNA isolation or $.5 \times 10^5$ cells per well of a 96-well plate for luciferase assays. RNA isolations were carried out with RNAeasy columns (Qiagen) according to the manufacturer's protocol. RNA quality and concentrations were estimated using the Nanodrop spectrophotometer. cDNA preparation was done using Superscript III (Thermo) with random primers according to the manufacturer's protocol. qPCR was carried out with primers in a sequence adjacent to the CTG repeat in the reporter plasmid using the following primers:

Forward Primer	TetCTG DMPK E15 F	TCGGAGCGGTTGTGAACT	SEQ ID NO: 83
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Reverse Primer	TetCTG DMPK E15 R	GTTCCGCCGTTGTTCTGTC	SEQ ID NO: 84
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[0345] Relative abundance of the CTG repeat reporter was determined by normalization to GAPDH. Next, levels of the CTG-targeting sgRNA were normalized to a non-targeting sgRNA to generate a final value reported in the associated data package.

CTG-targeting spacer	AGCAGCAGCAGCAGCAGCAG	SEQ ID NO: 85
Non-targeting control spacer (λ 2)	GTGATAAGTGGAATGCCATG	SEQ ID NO: 86
sgRNA scaffold (N's indicate spacer)	GNNNNNNNNNNNNNNNNNNNNNNNGUUUAAGAGCUAUGCUG GAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUA UCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUUUUU	SEQ ID NO: 87

[0346] Luciferase assays were conducted with the Promega Dual Luciferase kit according to manufacturer’s directions. Reported values are a ratio of firefly and renilla luciferase luminescence readings.

Example 2: RNA-guided cleavage of repetitive RNA molecules and mRNA molecules

[0347] Experimental Design: Various fusions of human proteins with annotated RNA endonuclease activity and Cas9 (*Streptococcus pyogenes* or *Campylobacter jejuni*) were constructed. Plasmids encoding the above fusions were co-transfected with either a repeat-containing plasmid or a luciferase assay plasmid (comprising an mRNA sequence encoding a luciferase protein). A level of CTG repeat-containing RNA was measured with qPCR in the condition in which an RNA endonuclease/Cas9 fusion was co-transfected with a repetitive RNA. A level of luciferase protein was measured using a luminescence assay in the condition in which an RNA endonuclease/Cas9 fusion was co-transfected with a luciferase assay plasmid. All measurements were normalized to a non-targeting sgRNA control construct (Figures 3A-5 and Figure 9).

Example 3: RNA-guided cleavage of Viral RNA Molecules

[0348] A549 cells were cultured in DMEM with 10% FBS and 1% penicillin/streptomycin (GIBCO) and passaged at 90%–100% confluency. Cells were seeded at 1×10^5 cells per well of a 24-well plate for RNA isolation or $.5 \times 10^5$ cells per well. Cells were transfected with plasmids encoding *Campylobacter jejuni* Cas9 (CjeCas9) fused to the gene NTHL1 (residues 31-312, E43) or CPSF4L (full length, E67) with plasmids encoding one of four sites in Zika NS5 RNA. CjeCas9 was driven by an EFS promoter while the guide RNAs were driven by U6 promoter. The sequences of the sgRNAs are presented in Table 1. The sequences of the constructs used in this study are presented below.

[0349] RNA isolations were carried out with RNeasy columns (Qiagen) according to the manufacturer's protocol. RNA quality and concentrations were estimated using the Nanodrop spectrophotometer. cDNA preparation was done using Superscript III (Thermo) with random primers according to the manufacturer's protocol. qPCR was carried out with the following primers as listed in Table 2.

[0350] Figure 7 shows expression levels of Zika NS5 assessed in the presence of both E43 and E67 endonucleases with sgRNAs containing the various NS5-targeting spacer sequences as indicated in Table 2. Zika NS5 expression is displayed as fold change relative to the endonuclease loaded with an sgRNA containing a control (Lambda) spacer sequence.

[0351] Immunofluorescence microscopy was used to visualize Zika NS5 expression in the presence of E43 or E67 endonucleases fused to CjeCas9. Figure 8A shows a fluorescence microscopy image of cells transfected with CjeCas9-endonuclease fusions loaded with an sgRNA containing a Zika NS5-targeting spacer sequence. Expression of Zika NS5 is markedly decreased in the presence of CjeCas9-endonuclease fusions loaded with the appropriate Zika NS5-targeting sgRNA as compared to CjeCas9-endonuclease fusions loaded with a non-Zika NS5 targeting sgRNA (Figures 8A and 8B). Figure 6 is a list of exemplary endonucleases for use in the compositions of the disclosure.

[0352] **Table 1:** qPCR primers

GAPDH_F	CAGCCTCAAGATCATCAGCAA (SEQ ID NO: 192)
GAPDH_R	TGTGGTCATGAGTCCTTCCA (SEQ ID NO: 193)
NS5_F	GAGGAGAGTGCCAGAGTTGT (SEQ ID NO: 194)

NS5_R	TCTCTCTCCCCATCCAGTGA (SEQ ID NO: 195)
-------	---------------------------------------

[0353] Table 2: sgRNA sequences

NS5-targeting spacer 1	gcaatgatcttcatgttgggagc (SEQ ID NO: 196)
NS5-targeting spacer 2	gaaccttggtgatgaactcttc (SEQ ID NO: 197)
NS5-targeting spacer 3	gttggtgattagagcttcattc (SEQ ID NO: 198)
NS5-targeting spacer 4	gagtgatcctcgttcaagaatcc (SEQ ID NO: 199)
Non-targeting control spacer (λ 2)	GTGATAAGTGGAATGCCATG (SEQ ID NO: 200)
sgRNA scaffold (N's indicate spacer)	GNNNNNNNNNNNNNNNNNNNNNGUUUAAAGAGCUAUG CUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGU CCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGU GCUUUUUUU (SEQ ID NO: 201)

[0354] A E43-CjeCas9 and sgRNA plasmid may comprise or consist of the sequence (U6: N's=sgRNA spacer, E43, CjeCas9):

gtttattacagggacagcagagatccagtttggttaattaaggtaccgagggcctatttcccatgattccttcatatttgcataacgatacaagg
ctgttagagagataaattagaattaattgactgtaaacacaaagatattagtacaaaatacgtgacgtagaaagtaataattcttgggtagtttg
cagttttaaattatgttttaaattggactatcatatgcttaccgtaacttgaagattttcgatttcttgctttatatatcttGTGGAAAGG
ACGAAACACCNNNNNNNNNNNNNNNNNNNNGTTTTAGTCCCTGAAGGGACTAAAAT
AAAGAGTTTGCGGGACTCTGCGGGGTACAATCCCCTAAAACCGCTTTTTTTTCCTGC
AGCCCGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAGCTT
TTGTTCCCTTTAGTGAGGGTTAATTGCGCGAATTCGCTAGCTAGGTCTTGAAAGGAG
TGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
GAGAAGTTGGGGGGAGGGGTCGGCAATTGATCCGGTGCCTAGAGAAGGTGGCGCG
GGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCCGAGGGTGGGG
GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCGCAACGGGTTTG
CCGCCAGAACACAGGACCGGTTCTAGAGCGCTATTTAGAACCatgTGTTCTCCCCAA
GAATCTGGCATGACCGCTCTTTCAGCGAGGATGTTGACGCGAAGCAGATCCCT
GGGACCTGGGGCCGGGCCACGAGGGTGTGCGGGAAGAACCAGGACCGTTGCGA
CGGAGGGAAGCAGCAGCGGAAGCTCGGAAATCCCATTCTCCGGTTAAACGACC
CCGCAAGGCACAACGGCTCAGGGTTGCTTACGAGGGGAGCGATTCCGAAAAGG
GTGAAGGAGCAGAGCCCTTGAAGGTTCCAGTATGGGAACCCAGGATTGGCAG
CAGCAGCTTGTAACATCCGAGCAATGAGGAACAAAAAAGATGCACCTGTTGA
TCACCTCGGAACCGAACATTGTTATGATTCTAGTGCGCCGCCAAAAGTCCGCC
GGTATCAGGTTCTGTTGAGTTTGATGCTGAGTAGTCAGACTAAGGACCAGGTT
ACGGCCGGAGCAATGCAACGGCTTCGGGCACGGGGACTCACGGTTCGATAGCAT
TTTGCAGACCGATGACGCAACATTGGGTAACTCATATATCCAGTTGGCTTCTG
GCGGAGCAAAGTGAAGTACATCAAGCAGACCTCAGCCATTCTCCAACAACATT
ACGGAGGTGATATACCCGCAAGCGTAGCTGAACTGGTAGCACTGCCGGGCGTC
GGTCCCAAAATGGCACATCTGGCTATGGCGGTTGCTTGGGGAACGGTGTCTGG
TATCGCAGTTGATACGCATGTCCACCGCATCGCCAATCGGCTGAGGTGGACTA

AAAAAGCCACTAAGTCTCCTGAAGAAACACGGGCTGCTCTGGAAGAGTGGCTT
CCACGAGAGCTGTGGCATGAAATCAATGGATTGCTGGTTGGTTTCGGGCAGCA
GACATGCTTGCCCGTGCACCCCCGGTGTTCATGCTTGCTTGAACCAGGCTTTGT
GCCCAGCTGCCCAGGGCCTGAGTGGAAGTGAGACACCGGGAACATCTGAGTCTGC
GACCCCGGAGAGCacaaacGCGCGAATCCTGGCCTTCGcgATTGGCATTAGCAGCAT
CGGCTGGGCATTCTCTGAAAACGACGAACTGAAGGATTGCGGCCGTGCGAATTT
TCACTAAGGTCGAAAATCCCAAACACTGGTGAATCACTCGCTCTCCCTAGACGAC
TGGCACGCTCCGCACGAAAGAGGCTTGCCCGCCGCAAGGCACGCTTGAACCAT
CTTAAACACCTTATTGCAAATGAGTTTAAACTGAATTATGAGGACTACCAATCC
TTTGACGAGTCTCTTGCTAAAGCCTACAAAGGGAGCCTTATATCCCCGTATGAG
CTCCGGTTCAGAGCACTCAACGAACTGCTGTCCAACAGGATTTTGCTCGCGT
GATTCTCCACATAGCGAAGAGGGCGAGGATACGATGACATTA AAAACAGTGATG
ATAAGGAAAAAGGGGCCATACTCAAAGCGATTAAGCAAATGAAGAGAAGCTC
GCTAACTATCAATCAGTAGGGGAGTATCTCTATAAAGAGTACTTCCAGAAGTTC
AAAGAAAATAGCAAGGAATTTACTAATGTCCGGAATAAAAAGGAGTCTTACGA
AAGATGTATTGCGCAATCTTTCCTCAAGGACGAGCTCAAATTTGATTTTCAAGAA
ACAAAGGGAATTTGGGTTCACTTCTCAAAAAAATTTGAGGAAGAGGTTCTGA
GCGTTGCCTTTTACAAACGCGCCCTTAAGGACTTCTCACATCTCGTAGGGAATT
GTAGTTTCTTACCGATGAAAACGGGCGCCAAAAAATAGCCCTTTGGCTTTTA
TGTTTGTGCTCTGACTCGCATCATTAACTGCTCAACAACCTTAAAAACACGG
AAGGGATTCTGTACACAAAGGATGATCTGAACGCTCTGCTTAAACGAAGTTTGA
AGAACGGGACTTTGACCTACAAACAAACCAAAAAGCTTCTTGGTCTCAGTGATG
ACTACGAATTC AAGGGAGAAAAAGGGACATATTT CATCGAATTC AAGAAGTATA
AGGAGTTCATCAAAGCCTTGGGCGAGCACAACTTGTCTCAAGATGATCTCAAC
GAAATTGCTAAGGATATCACTCTGATTAAGACGAGATCAAGCTCAAAAAGGC
GTTGGCGAAGTATGACCTTAAACCAAACCAAATAGATAGCCTCAGCAAGTTGG
AATTTAAAGATCACTTGAATATAAGTTTCAAGGCCCTTAAGTTGGTCACCCCT
TGATGCTTGAAGGAAAGAAATATGATGAGGCATGTAATGAGCTGAATCTCAAG
GTTGCTATTAACGAAGACAAAAAAGATTTCTCCAGCTTTCAATGAGACTTAC
TATAAGGACGAGGTTACCAATCCTGTGGTGCTCCGAGCCATCAAAGAGTATCG
AAAGGTCCTGAATGCTTTGCTCAAAAAATACGGTAAGGTACACAAAAATAAATAT
TGAGCTCGCAAGGGAGGTCGGTAAGAACCACTCCCAGCGCGCCAAAAATAGAAA
AGGAACAGAATGAAAATTACAAAGCGAAAAAGGACGCCGAGCTCGAGTGCGAA
AAGCTGGGCCTGAAAATAAACAGCAAGAACATTCTCAAACCTCCGCCTCTTCAA
GAACAAAAAGAATTTTGTGCTTATAGTGGTGAGAAAAATAAAAATCTCCGATCTT
CAAGACGAGAAGATGCTCGAAATAGACcgATATATCCATATAGCAGGTCTTTTG
ACGATTCTTACATGAATAAAGTGCTTGTTTTCACTAAGCAGAATCAGGAAAAGT
TGAATCAGACCCCTTTGAGGCCTTTGGCAACGACTCAGCAAAGTGGCAGAAG
ATCGAGGTCTTGGCTAAGAATCTTCTACTAAGAAACAGAAAAGGATATTGGAT
AAGA ACTATAAAGACAAAGAACAAAAGA ACTTTAAAGACCGCAACCTCAATGA
CACCAGATACATAGCAAGATTGGTTCTGAACTACACAAAAGATTATTTGGACTT
CTTGCCGCTGTCTGATGATGAGAACACGAACTCAACGACACGCAAAAAGGGGT
CTAAAGTCCACGTCGAAGCTAAATCTGGGATGCTCACCTCAGCATTGAGGCAT
ACGTGGGGATTCTCAGCAAAGGACCGAAACAATCACCTGCACCATGCCATTGA
CGCAGTTATCATAGCGTATGCCAATAATTCAATAGTAAAAGCGTTTAGCGACTT

CAAGAAGGAACAAGAGTCCAACAGCGCCGAGCTCTACGCAAAAAAGATTAGTG
AACTCGACTACAAAACAAAGAAAATTCTTTGAGCCGTTTCAGCGGATTTCGAC
AGAAGGTATTGGATAAAATAGATGAAATTTTCGTGAGCAAACCCGAAAGGAAA
AAGCCCTCAGGCGCCTTGCACGAAGAGACTTTCAGGAAGGAAGGAATTCTA
CCAAAGCTACGGCGGAAAAGAGGGAGTTTTGAAGGCTCTCGAACTTGGAAGA
TTAGGAAGGTGAACGGCAAGATAGTGAAAAACGGCGATATGTTCCGGGTGAT
ATCTTCAAACATAAAAAACGAATAAATTTTATGCTGTGCCTATATACACTATG
GACTTCGCACTTAAGGTCCTGCCGAATAAGGCGGTAGCCCGATCTAAAAAAGG
CGAAATTAAGGACTGGATTTTGATGGATGAAAATTACGAGTTCTGCTTTTCTCT
CTACAAGGATTCCTTATATTGATACAGACGAAAGATATGCAGGAACCGGAATT
CGTGTATTACAACGCTTTTACTTCCTCTACGGTATCTTTGATTGTCTCCAAACAT
GACAACAAATTCGAAACACTCAGTAAAAACCAAAGATTCTCTTTAAAAATGCG
AACGAGAAAGAAGTAATTGCAAATCAATTGGCATCCAAAATTTGAAAGTTTTT
GAAAAATATATAGTATCTGCCCTCGGAGAGGTTACTAAAGCGGAATTTAGACA
GCGAGAGGACTTCAAAAAATCAGGTCCACCCAAGAAAAAACGCAAGGTGGAAGA
 TCCGAAGAAAAAGCGAAAAGTGGATGT^{Gtaa}CGTTTTCCGGGACGCCGGCTGGATGA
 TCCTCCAGCGCGGGGATCTCATGCTGGAGTCTTCGCCACCCCAACTTGTTTATTGC
 AGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCAT
 TTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTC
 TGTATACCG (SEQ ID NO: 202).

[0355] A E67-CjeCas9 and sgRNA plasmid may comprise or consist of the sequence (U6: N's=sgRNA spacer, E67, CjeCas9):

gtttattacagggacagcagagatccagtttggttaattaaggtaccgagggcctatttcccatgattccttcatatttgcatacagatacaagg
ctgttagagagataattagaattaattgactgtaaacacaaagatattagtacaaaatcgtgacgtagaaagtaataatttctgggtagttg
cagttttaaattatgttttaaattggactatcatatgcttaccgtaactgaaagtatttcgatttcttgctttatatatcttGTGGAAAGG
 ACGAAACACCNNNNNNNNNNNNNNNNNNGTTTTAGTCCCTGAAGGGACTAAAAT
 AAAGAGTTTGCGGGACTCTGCGGGGTTACAATCCCCTAAAACCGCTTTTTTTTCCTGC
 AGCCCGGGGATCCACTAGTTCTAGAGCGGCCGCCACCGCGGTGGAGCTCCAGCTT
 TTGTTCCCTTTAGTGAGGGTTAATTGCGCGAATTCGCTAGCTAGGTCTTGAAAGGAG
 TGGGAATTGGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCC
 GAGAAGTTGGGGGGAGGGGTGCGCAATTGATCCGGTGCCTAGAGAAGGTGGCGCG
 GGGTAAACTGGGAAAGTGTGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGG
 GAGAACCGTATAAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCGCAACGGGTTTG
 CCGCCAGAACACAGGACCGGTTCTAGAGCGCTATTTAGAACC^{atg}CAGGAGGTAATA
 GCGGGGCTTGAGCGATTTACCTTTGCCTTCGAAAAAGACGTAGAGATGCAGAA
 GGGAACCGGCCTGCTCCCATTTCAAGGTATGGACAAATCAGCATCTGCCGTGT
 GCAATTTTTTACCAAGGGTCTGTGTGAAAAGGGGAAGCTCTGTCCATTTCCGCC
 ATGATCGCGGAGAGAAGATGGTGGTGTGTAAGCACTGGCTGAGAGGGCTTTGC
 AAAAAAGGCGACCACTGCAAATTTCTTACCAATATGACCTGACTCGAATGCCT
 GAGTGTTATTTTTACAGTAAGTTCGGTGACTGTAGCAACAAAGAATGCAGCTTC
 TTGCATGTCAAACCAGCATTCAAGTCACAGGATTGCCCGTGGTACGATCAGGG
 TTTTTGCAAGGACGGTCCCCTCTGCAAATATCGACACGTACCCAGAATTATGTG
 CCTTAATTACCTGGTTCGGCTTCTGTCTGAAAGGGCCAAAATGTCAGTTTGCTCA

AAAAATTCGCGAGTTCAAATTGCTCCCTGGGTCTAAAATTTGGGAACCCAGGA
TTGGCAGCAGCAGCTTGTAACATCCGAGCAATGAGGAACAAAAAGATGCAC
CTGTTGATCACCTCGGAACCGAACATTGTTATGATTCTAGTGCGCCGCCAAAAG
TCCGCCGGTATCAGGTTCTGTTGAGTTTGTATGCTGAGTAGTCAGACTAAGGAC
CAGGTTACGGCCGGAGCAATGCAACGGCTTCGGGCACGGGGACTCACGGTCG
ATAGCATTTTGCAGACCGATGACGCAACATTGGGTAACTCATATATCCAGTTG
GCTTCTGGCGGAGCAAAGTGAAGTACATCAAGCAGACCTCAGCCATTCTCCAA
CAACATTACGGAGGTGATATACCCGCAAGCGTAGCTGAACTGGTAGCACTGCC
GGGCGTTCGGTCCCAAATGGCACATCTGGCTATGGCGGTTGCTTGGGGAACGG
TGTCTGGTATCGCAGTTGATACGCATGTCCACCGCATCGCCAATCGGCTGAGG
TGGACTAAAAAGCCACTAAGTCTCCTGAAGAAACACGGGCTGCTCTGGAAGA
GTGGCTTCCACGAGAGCTGTGGCATGAAATCAATGGATTGCTGGTTGGTTTCG
GGCAGCAGACATGCTTGCCCGTGCACCCCGGTGTCATGCTTGAACCAG
GCTTTGTGCCAGCTGCCAGGGCCTGAGTGGAAGTGAGACACCGGGAACATCT
GAGTCTGCGACCCCGGAGAGCacaacGCGCGAATCCTGGCCTTCGcgATTGGCATT
AGCAGCATCGGCTGGGCATTCTCTGAAAACGACGAACTGAAGGATTGCGGGCGT
GCGAATTTTCACTAAGGTCGAAAATCCCAAACCTGGTGAATCACTCGCTCTCCC
TAGACGACTGGCACGCTCCGCACGAAAGAGGCTTGCCCGCCGCAAGGCACGCT
TGAACCATCTTAAACACCTTATTGCAAATGAGTTTAAACTGAATTATGAGGACT
ACCAATCCTTTGACGAGTCTCTTGCTAAAGCCTACAAAGGGAGCCTTATATCCC
CGTATGAGCTCCGGTTCAGAGCACTCAACGAACTGCTGTCCAAACAGGATTTT
GCTCGCGTGATTCTCCACATAGCGAAGAGGGCGAGGATACGATGACATTA AAAA
CAGTGATGATAAGGAAAAAGGGGCCATACTCAAAGCGATTAAGCAAATGAAG
AGAAGCTCGCTAACTATCAATCAGTAGGGGAGTATCTCTATAAAGAGTACTTCC
AGAAGTTCAAAGAAAAATAGCAAGGAATTTACTAATGTCCGGAATAAAAAGGAG
TCTTACGAAAGATGTATTGCGCAATCTTTCCTCAAGGACGAGCTCAAATTGATT
TTCAAGAAACAAAGGGAATTTGGGTTTCAGCTTCTCAAAAAAATTTGAGGAAGA
GGTTCTGAGCGTTGCCTTTTACAAACGCGCCCTTAAGGACTTCTCACATCTCGT
AGGGAATTGTAGTTTCTTACCAGATGAAAACGGGCGCCAAAAAATAGCCCTTT
GGCTTTTATGTTTGTGCTCTGACTCGCATCATTAACTGCTCAACAACCTTAA
AAACACGGAAGGATTCTGTACACAAAGGATGATCTGAACGCTCTGCTTAAACG
AAGTTTTGAAGAACGGGACTTTGACCTACAAACAAACCAAAAAGCTTCTTGGTC
TCAGTGATGACTACGAATTCAAGGGAGAAAAAGGGACATATTCATCGAATTCA
AGAAGTATAAGGAGTTCATCAAAGCCTTGGGCGAGCACA ACTTGTCTCAAGAT
GATCTCAACGAAATTGCTAAGGATATCACTCTGATTAAAGACGAGATCAAGCTC
AAAAAGGCGTTGGCGAAGTATGACCTTAACCAAAACCAAATAGATAGCCTCAG
CAAGTTGGAATTTAAAGATCACTTGAATATAAGTTTCAAGGCCCTTAAGTTGGT
CACCCCTTGATGCTTGAAGGAAAGAAATATGATGAGGCATGTAATGAGCTGA
ATCTCAAGGTTGCTATTAACGAAGACAAAAAAGATTTCTCCAGCTTTCAATG
AGACTTACTATAAGGACGAGGTTACCAATCCTGTGGTGCTCCGAGCCATCAA
GAGTATCGAAAGGTCCTGAATGCTTTGCTCAAAAAATACGGTAAGGTACACAA
AATAAATATTGAGCTCGCAAGGGAGGTTCGGTAAGAACCCTCCAGCGCGCCA
AAATAGAAAAGGAACAGAATGAAAATTACAAAGCGAAAAAGGACGCCGAGCTC
GAGTGCGAAAAGCTGGGCCTGAAAATAAACAGCAAGAACATTCTCAA ACTCCG
CCTCTTCAAAGAACAAAAAGAATTTTGTGCTTATAGTGGTGAGAAAAATAAAAAT

CTCCGATCTTCAAGACGAGAAGATGCTCGAAATAGACgcgATATATCCATATAGC
AGGTCCTTTTGACGATTCTTACATGAATAAAGTGCTTGTTCCTACTAAGCAGAAT
CAGGAAAAGTTGAATCAGACCCCTTTGAGGCCTTTGGCAACGACTCAGCAAA
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AAGATTAGTGAAGTCTGACTACAAAAACAAAAGAAAATTCTTTGAGCCGTTCAGC
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GAAAGGAAAAAGCCCTCAGGCGCCTTGACAGAAAGAGACTTTCAGGAAGGAAGA
GGAATTCTACCAAAGCTACGGCGGAAAAGAGGGAGTTTTGAAGGCTCTCGAAC
TTGGAAGATTAGGAAGGTGAACGGCAAGATAGTGAAAACGGCGATATGTTC
CGGGTTGATATCTTCAAACATAAAAAACGAATAAATTTTATGCTGTGCCTATA
TACACTATGGACTTCGCACTTAAGGTCTGCGCAATAAGGCGGTAGCCCGATC
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CTTTTCTCTCTACAAGGATTCCTTATATTGATACAGACGAAAGATATGCAGGA
ACCGGAATTCGTGTATTACAACGCTTTTACTTCTCTACGGTATCTTTGATTGT
CTCCAAACATGACAACAAATTCGAAACACTCAGTAAAAACCAAAAGATTCTCTT
TAAAAATGCGAACGAGAAAGAAGTAATTGCAAAATCAATTGGCATCCAAAATTT
GAAAGTTTTTGAAAAATATATAGTATCTGCCCTCGGAGAGGTTACTAAAGCGGA
ATTTAGACAGCGAGAGGACTTCAAAAAATCAGGTCCACCCAAGAAAAAACGCAA
GGTGAAGATCCGAAGAAAAAGCGAAAAGTGATGTGtaaCGTTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACT
TGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTCACAA
ATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATC
TTATCATGTCTGTATACCG (SEQ ID NO: 203).

INCORPORATION BY REFERENCE

[0356] Every document cited herein, including any cross referenced or related patent or application is hereby incorporated herein by reference in its entirety unless expressly excluded or otherwise limited. The citation of any document is not an admission that it is prior art with respect to any invention disclosed or embodied herein or that it alone, or in any combination with any other reference or references, teaches, suggests or discloses any such invention. Further, to the extent that any meaning or definition of a term in this document conflicts with any meaning or definition of the same term in a document incorporated by reference, the meaning or definition assigned to that term in this document shall govern.

OTHER EMBODIMENTS

[0357] While particular embodiments of the disclosure have been illustrated and described, various other changes and modifications can be made without departing from the spirit and scope of the disclosure. The scope of the appended claims includes all such changes and modifications that are within the scope of this disclosure.

CLAIMS

What is claimed is:

1. A composition comprising a nucleic acid sequence encoding an RNA-guided target RNA-binding fusion protein comprising (a) a first RNA-binding polypeptide or portion thereof; and (b) a second RNA-binding polypeptide, wherein the first RNA-binding polypeptide binds a target RNA when guided by a gRNA sequence, and wherein the second RNA-binding polypeptide comprises RNA-nuclease activity.
2. The composition of claim 1, wherein the first RNA-binding polypeptide or portion thereof is a CRISPR/Cas polypeptide or portion thereof.
3. The composition of claim 2, wherein the CRISPR/Cas polypeptide or portion thereof is selected from the group consisting of Cas9, Cpf1, Cas13a, Cas13b, Cas13c and CasRX/Cas13d, wherein the CRISPR/Cas polypeptide has native, reduced or null activity.
4. The composition of claim 1, wherein the second RNA-binding polypeptide binds RNA in a manner in which it associates with RNA.
5. The composition of claim 4, wherein the second RNA-binding polypeptide associates with RNA in a manner in which it cleaves RNA.
6. The composition of claim 1, wherein the nucleic acid sequence comprises a promoter.
7. The composition of claim 6, wherein the promoter is a constitutive promoter or a tissue-specific promoter.
8. The composition of claim 1, wherein the nucleic acid sequence further comprises a gRNA sequence, wherein the gRNA sequence comprises a spacer sequence that specifically binds a target sequence within an RNA molecule and a scaffold sequence that specifically binds to the first RNA-binding polypeptide.
9. The composition of claim 8, wherein the spacer sequence comprises a sequence comprising at least 1, 2, 3, 4, 5, 6, or 7 repeats of a sequence selected from the group consisting of: CUG (SEQ ID NO: 18), CCUG (SEQ ID NO: 19), CAG (SEQ ID NO: 80), GGGGCC (SEQ ID NO: 81), and a combination thereof.

10. The composition of claim 8, wherein the nucleic acid sequence comprises a promoter which drives expression of the gRNA sequence.
11. The composition of claim 9, wherein the promoter is a polymerase III promoter.
12. The composition of claim 10, wherein the polymerase III promoter is a U6 promoter.
13. The composition of claims 1 or 9, wherein the promoter is a tRNA promoter.
14. The composition of claims 1 or 9, wherein the fusion protein comprises an NLS, NES or tag.
15. A vector comprising the composition of claim 1 or 8.
16. The vector of claim 15, wherein the vector is selected from the group consisting of: adeno-associated virus, retrovirus, lentivirus, adenovirus, nanoparticle, micelle, liposome, lipoplex, polymersome, polyplex, and dendrimer.
17. A cell comprising the vector of claim 15.
18. The composition of claim 1, wherein the second RNA-binding polypeptide is selected from the group consisting of: RNase1, RNase4, RNase6, RNase7, RNase8, RNase2, RNase6PL, RNaseL, RNaseT2, RNase11, RNaseT2-like, NOB1, ENDOV, ENDOG, ENDOD1, hFEN1, hSLFN14, hLACTB2, APEX2, ANG, HRSP12, ZC3H12A, RIDA, PDL6, NTHL, KIAA0391, APEX1, AGO2, EXOG, ZC3H12D, ERN2, PELO, YBEY, CPSF4L, hCG_2002731, ERCC1, RAC1, RAA1, RAB1, DNA2, FLJ35220, FLJ13173, ERCC4, Rnase1(K41R), Rnase1(K41R, D121E), Rnase1(K41R, D121E, H119N), Rnase1(H119N), Rnase1(R39D, N67D, N88A, G89D, R91D, H119N), Rnase1(R39D, N67D, N88A, G89D, R91D, H119N, K41R, D121E), Rnase1(R39D, N67D, N88A, G89D, R91D), TENM1, TENM2, RNaseK, TALEN, and ZNF638.
19. A composition comprising:
 - (a) a guide RNA (gRNA) sequence comprising a spacer sequence that specifically binds a target sequence within an RNA molecule and a scaffold sequence that specifically binds to the first RNA-binding polypeptide;
 - (b) a nucleic acid sequence encoding a fusion protein, the fusion protein comprising a first RNA-binding polypeptide and a sequence encoding a second RNA-binding polypeptide,

wherein neither the first RNA-binding polypeptide nor the second RNA-binding polypeptide comprises a significant DNA-nuclease activity,

wherein the first RNA-binding polypeptide and the second RNA-binding polypeptide are not identical, and

wherein the second RNA-binding polypeptide comprises an RNA-nuclease activity.

20. A method for modifying the level of expression of a target RNA molecule or a protein encoded by the RNA molecule, the method comprising contacting the composition of claims 19 and the RNA molecule under conditions suitable for binding of the fusion protein or a portion thereof to the RNA molecule.

FIGURE 1

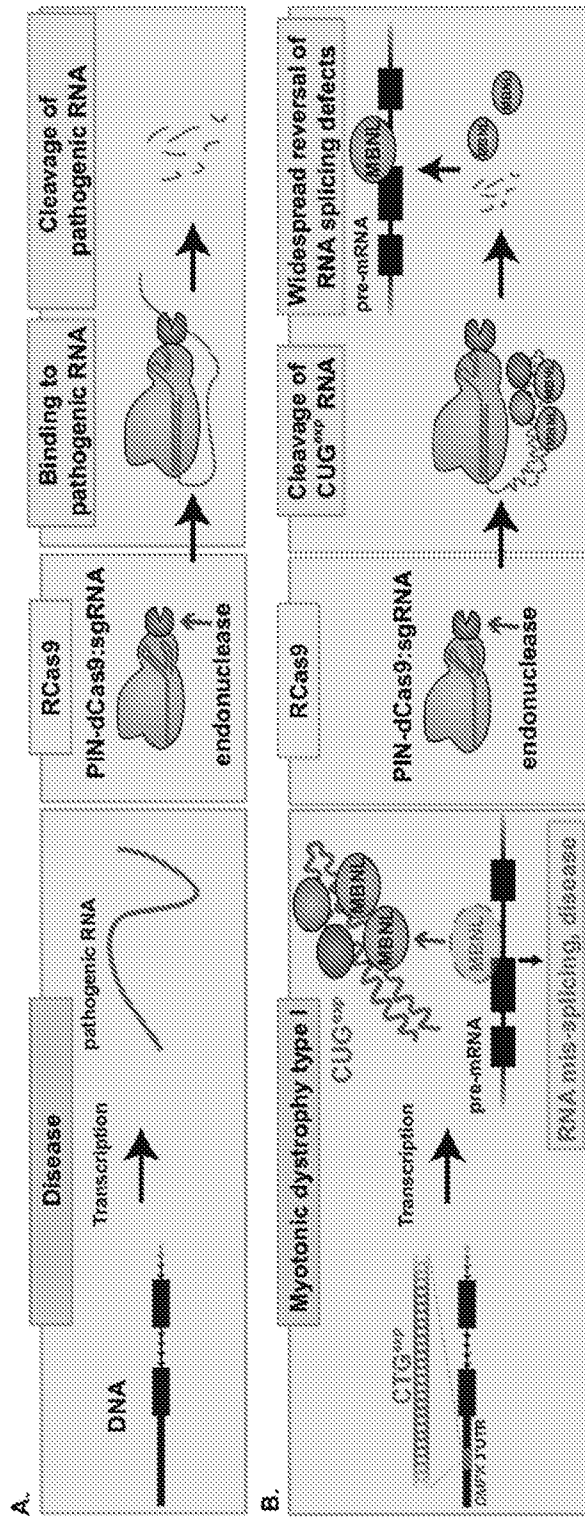


FIGURE 2

A Modular Therapeutic Platform

Genetic disease is most safely and in many cases most effectively addressed on the level of RNA

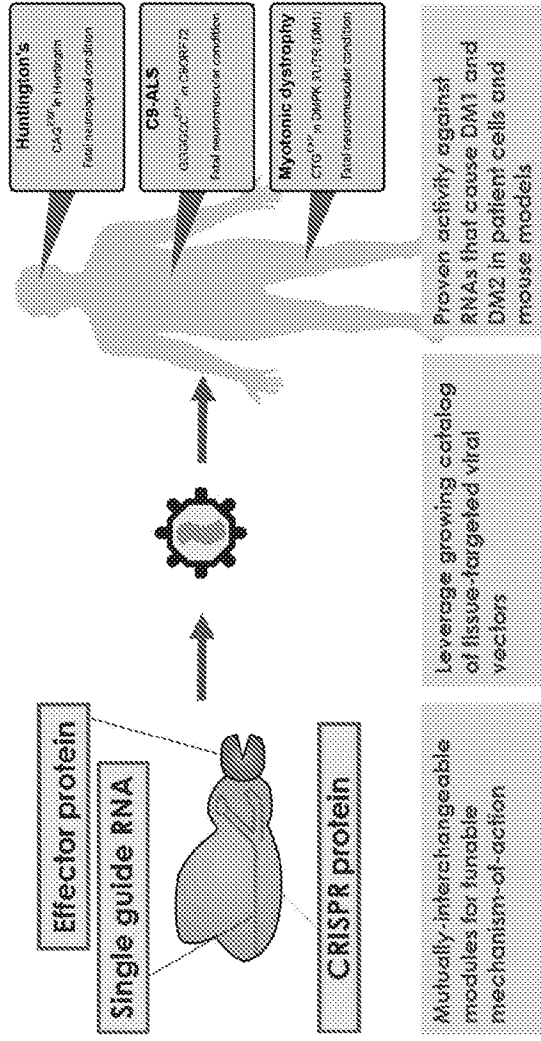


FIGURE 3A

High expression positive control: "pos control"

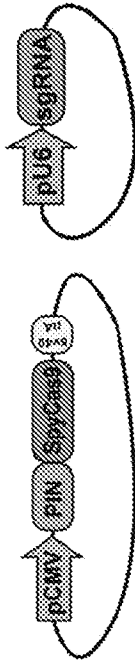
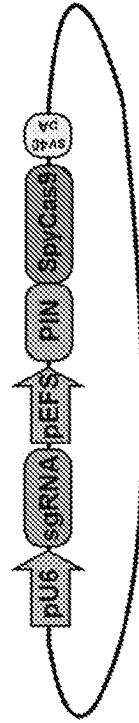
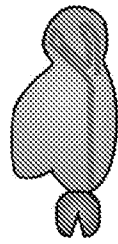


FIGURE 3B

Low expression positive control: "P13"



CjeCas9 with N-terminal endonuclease: activity against CTG repeats



Endonuclease-C. jejuni Cas9 (nuclease inactive)

FIGURE 4A

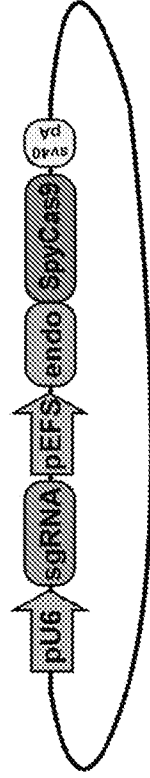


FIGURE 4B

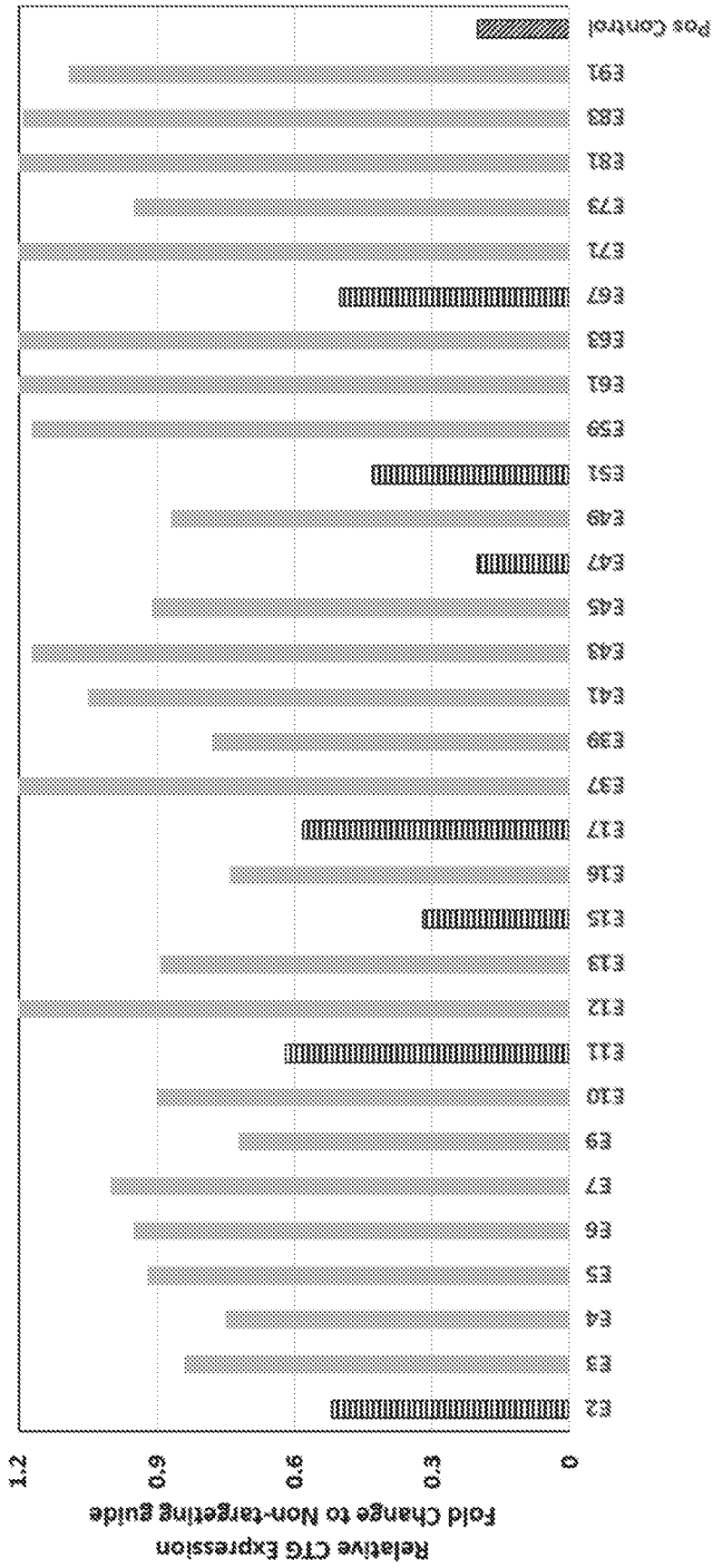


FIGURE 5A

SpyCas9 with N-terminal endonuclease: activity against luciferase mRNA



Endonuclease-C. jejuni Cas9 (nuclease inactive)

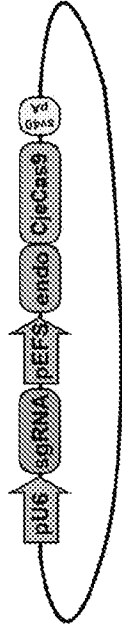


FIGURE 5B

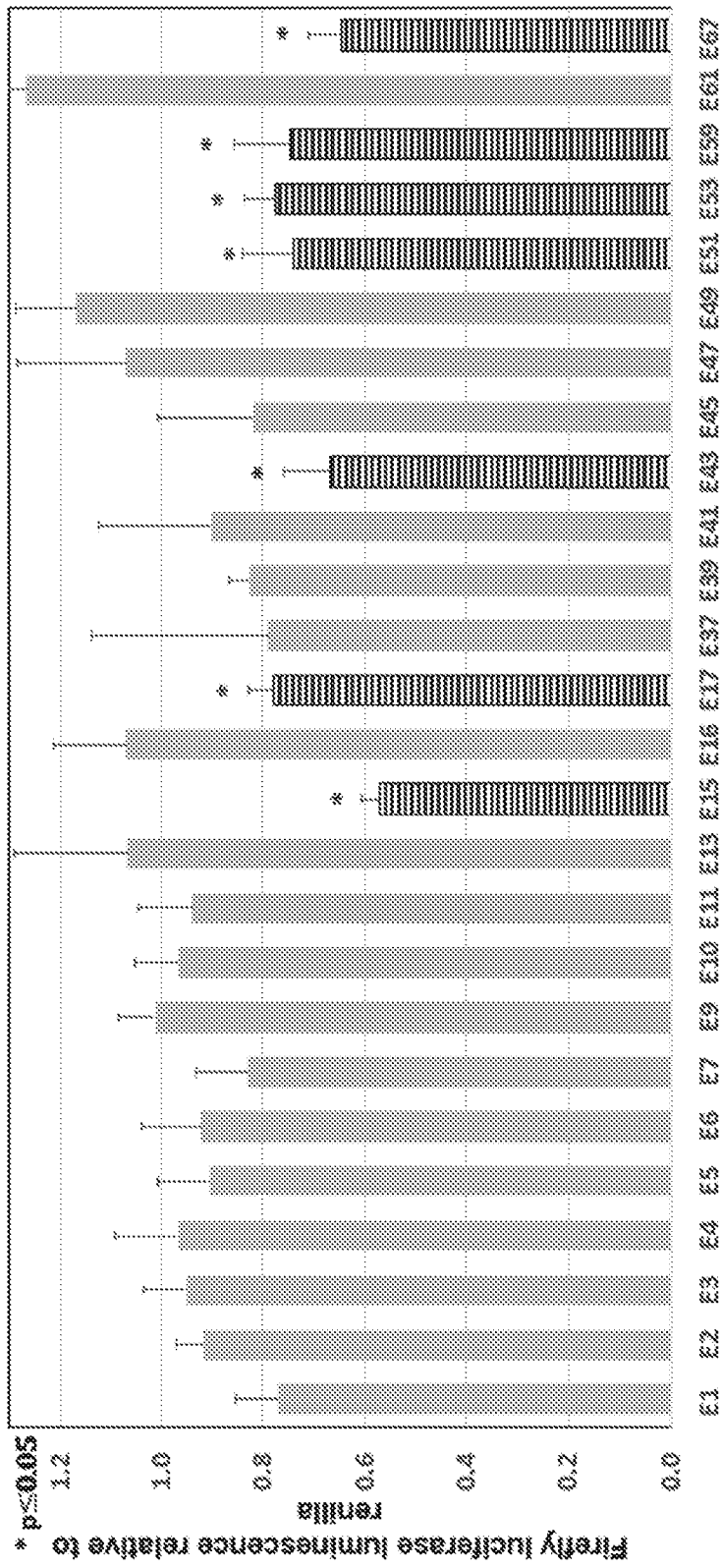
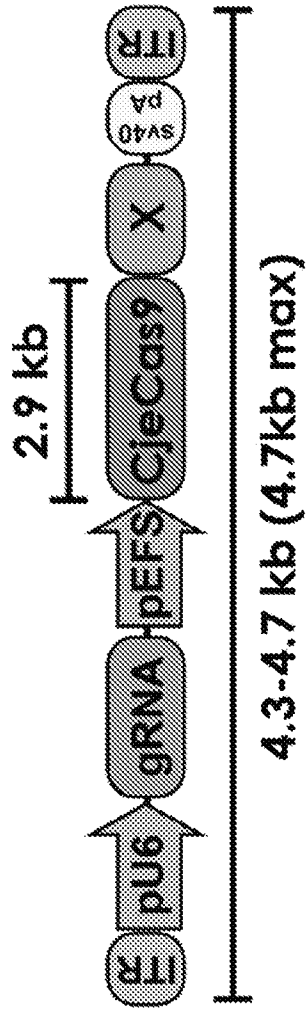


FIGURE 6

Endonuclease Name Key

E1	RNaseI	E53	EXOg
E2	RNase4	E55	ZC3H13D
E3	RNase6	E57	ERM2
E4	NOB1	E59	ENDOG
E5	EndoV	E61	PELO
E6	FEN1	E63	YBEY
E7	SLFN14	E65	ENDOD1
E8	LACTB2	E67	CPSF4L
E9	RNase7	E69	MCG_2802731
E10	RNase8	E71	MCG_2802731
E11	RNase2	E73	ERCC1
E12	ANG	E75	RAC1
E13	HRSP12	E77	APEX2
E14	RNase6Pl	E79	APEX2_1-350
E15	RNaseL	E81	RAA1_25-156
E16	RNaseT2	E83	RAB1
E17	ZC3H12A	E85	RNaseK
E37	RIDA	E87	DNA2_FL
E39	RNase11	E89	RNaseI{K41R}
E41	PDL6	E91	RNaseI{K41R, D121E}
E43	NTHL1	E93	RNaseI{K41R, D121E, H119W}
E45	KIP40391	E95	RNaseI{H119R}
E47	APEX1	E97	RNaseI{R39D, M67D, N88A, G89D, R91D, H119W}
E49	AgO2	E99	RNaseI{R39D, M67D, N88A, G89D, R91D, H119W, K41R, D121E}
E51	ZC3H12A	E100	RNaseI{R39D, M67D, N88A, G89D, R91D, H119W, K41R, D121E}
		E101	RNaseI{R39D, M67D, N88A, G89D, R91D}

FIGURE 7A



Endonuclease-
C. jejuni Cas9

FIGURE 7B

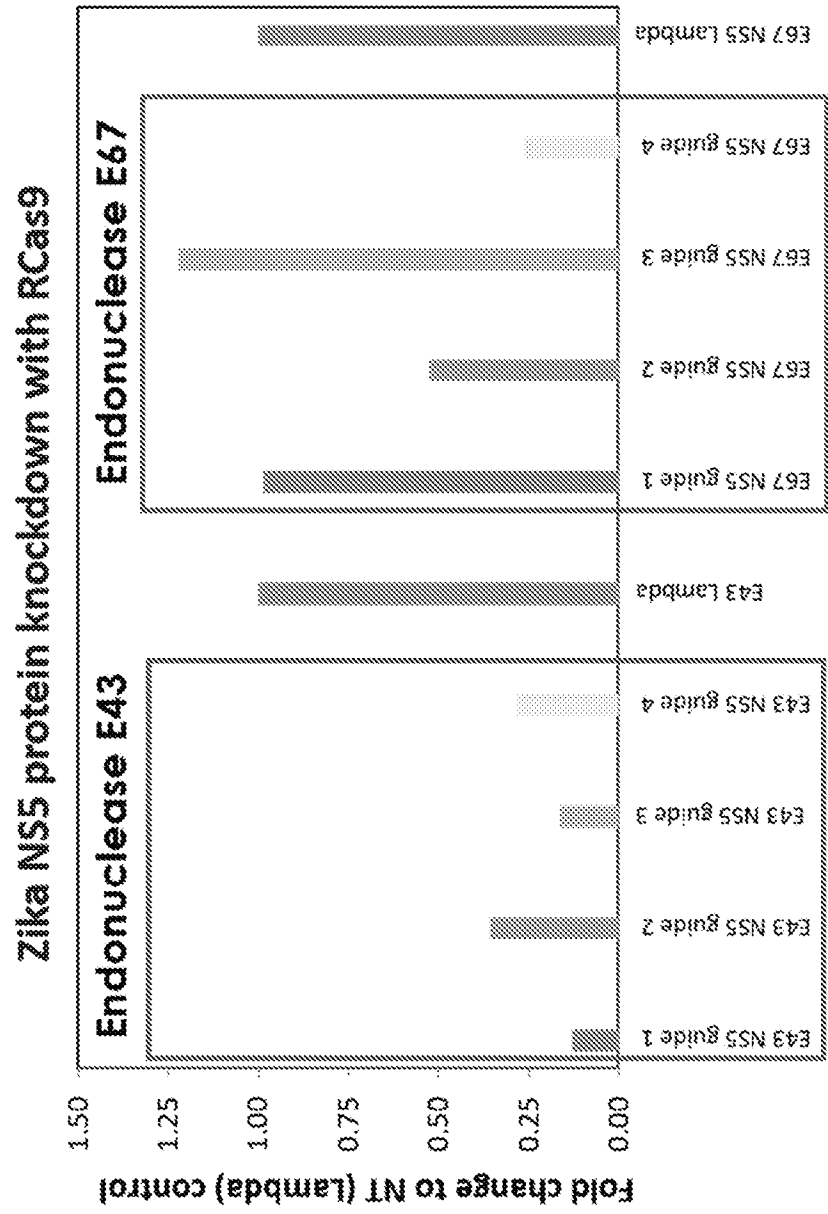


FIGURE 8A

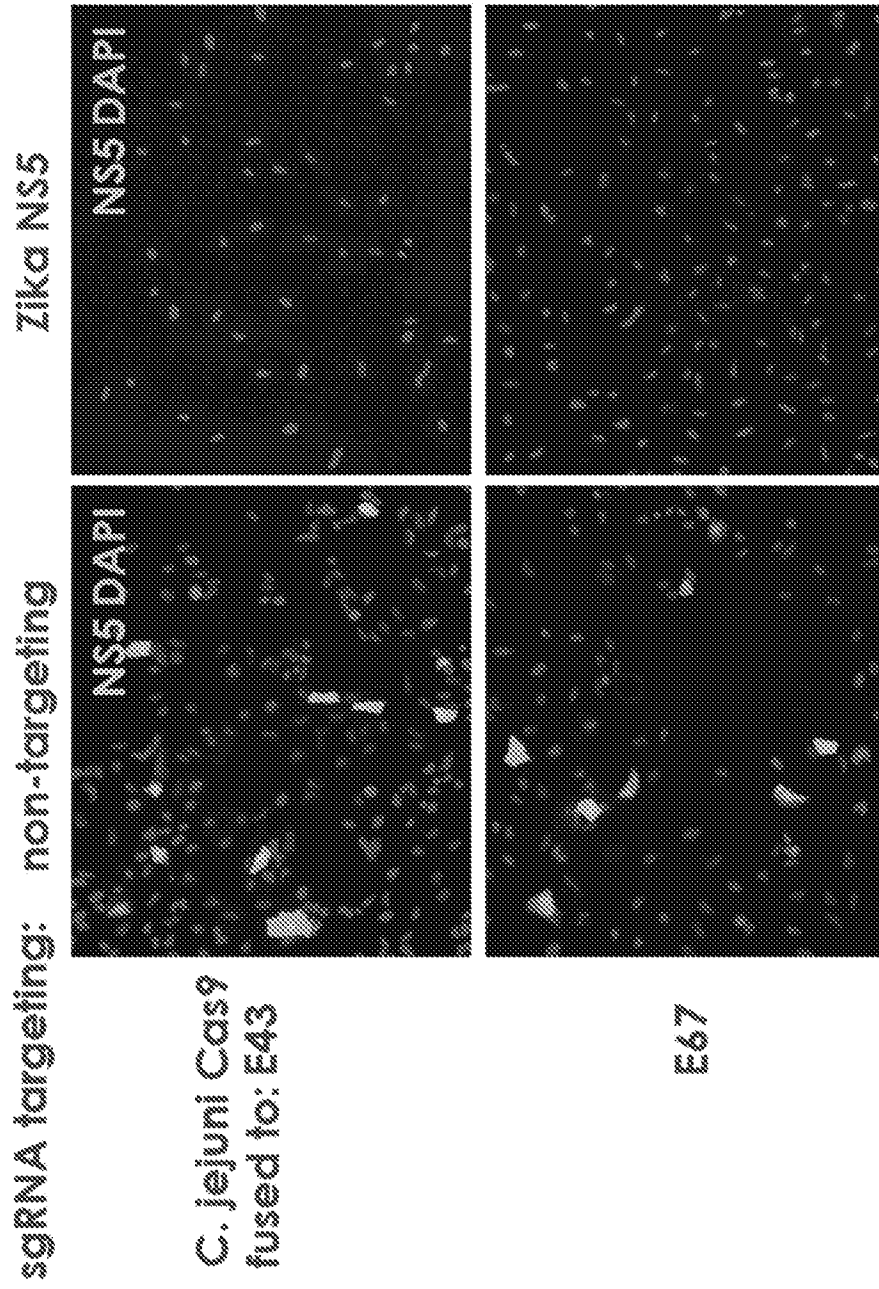


FIGURE 8B

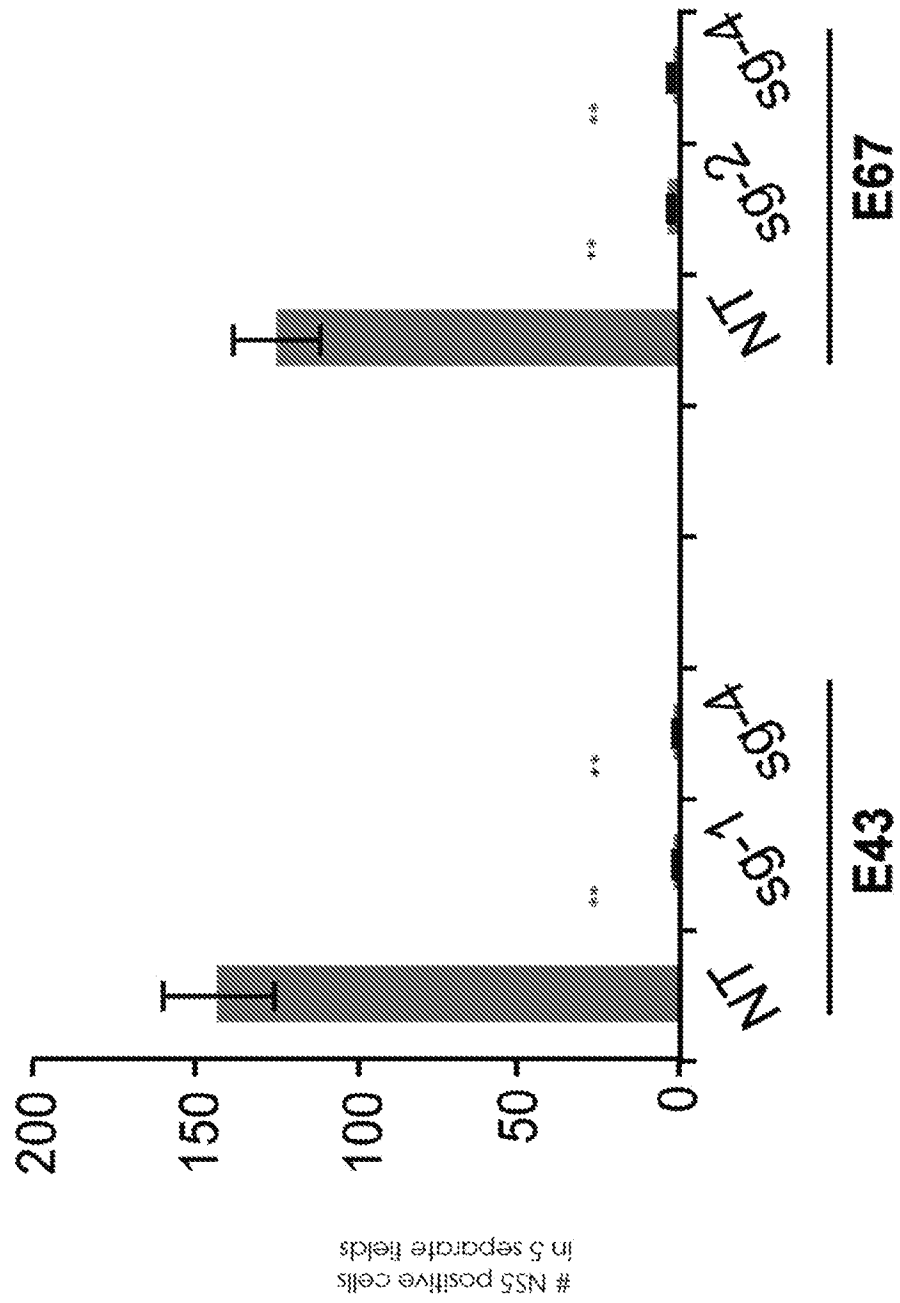
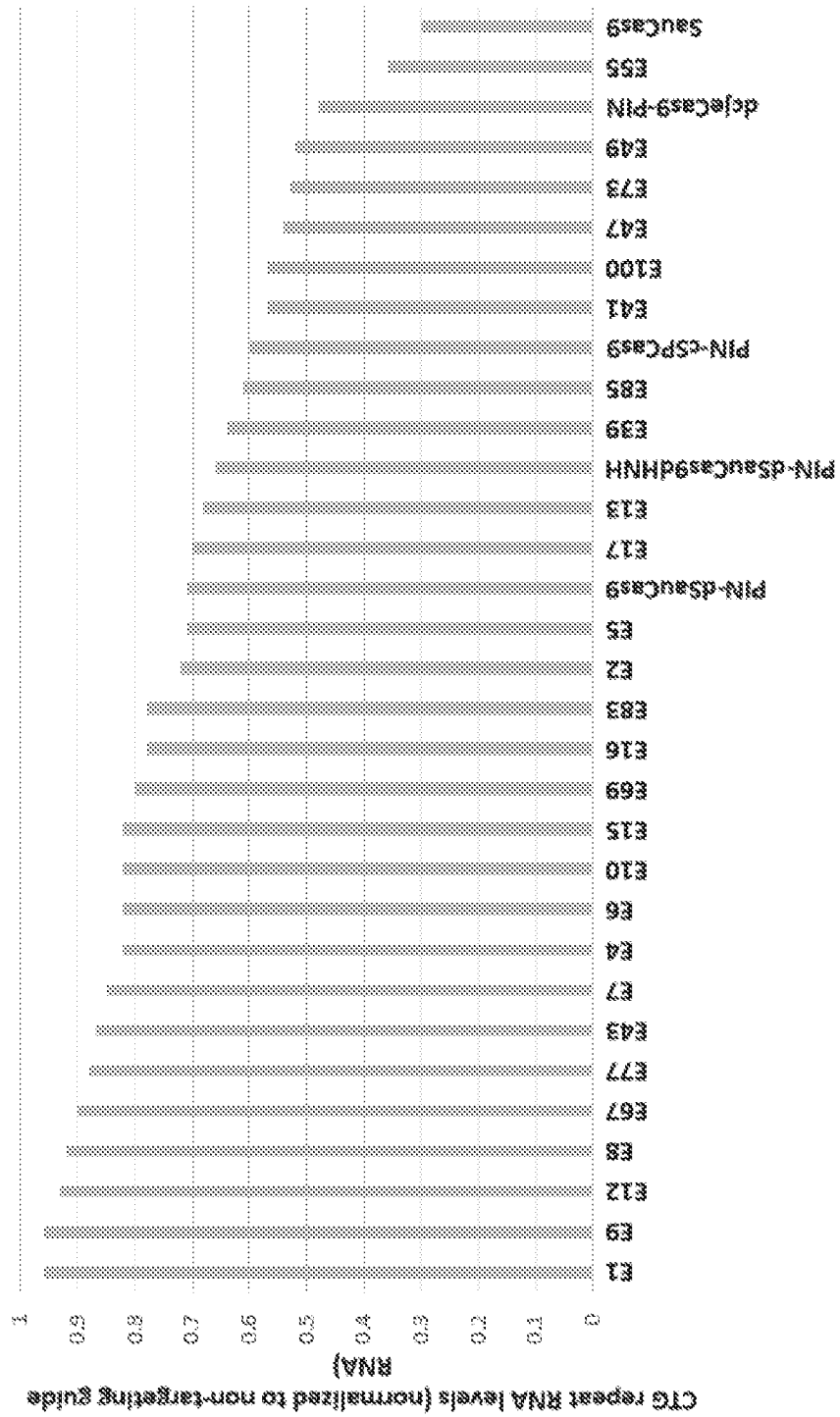


FIGURE 9



<p>A. CLASSIFICATION OF SUBJECT MATTER IPC(8) - C12N 9/22; C12N 15/113 (2019.01) CPC - C07K 2319/85; C12N 9/22; C12N 15/113; C12N 2310/20 (2019.08)</p> <p>According to International Patent Classification (IPC) or to both national classification and IPC</p>																				
<p>B. FIELDS SEARCHED</p> <p>Minimum documentation searched (classification system followed by classification symbols) See Search History document</p> <p>Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched USPC - 435/199; 435/69.7 (keyword delimited)</p> <p>Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) See Search History document</p>																				
<p>C. DOCUMENTS CONSIDERED TO BE RELEVANT</p> <table border="1"> <thead> <tr> <th>Category*</th> <th>Citation of document, with indication, where appropriate, of the relevant passages</th> <th>Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>X -- Y</td> <td>US 2017/0145394 A1 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 25 May 2017 (25.05.2017) entire document</td> <td>1-12, 14-17, 19, 20 ----- 13, 18</td> </tr> <tr> <td>Y</td> <td>US 2017/0088845 A1 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA et al) 30 March 2017 (30.03.2017) entire document</td> <td>13</td> </tr> <tr> <td>Y</td> <td>US 2013/0178513 A1 (ISIS PHARMACEUTICALS, INC. et al) 11 July 2013 (11.07.2013) entire document</td> <td>18</td> </tr> <tr> <td>A</td> <td>US 2017/0314002 A1 (BIO-RAD LABORATORIES, INC.) 02 November 2017 (02.11.2017) entire document</td> <td>1-20</td> </tr> <tr> <td>A</td> <td>WO 2015/089486 A2 (THE BROAD INSTITUTE INC. et al) 18 June 2015 (18.06.2015) entire document</td> <td>1-20</td> </tr> </tbody> </table>			Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	X -- Y	US 2017/0145394 A1 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 25 May 2017 (25.05.2017) entire document	1-12, 14-17, 19, 20 ----- 13, 18	Y	US 2017/0088845 A1 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA et al) 30 March 2017 (30.03.2017) entire document	13	Y	US 2013/0178513 A1 (ISIS PHARMACEUTICALS, INC. et al) 11 July 2013 (11.07.2013) entire document	18	A	US 2017/0314002 A1 (BIO-RAD LABORATORIES, INC.) 02 November 2017 (02.11.2017) entire document	1-20	A	WO 2015/089486 A2 (THE BROAD INSTITUTE INC. et al) 18 June 2015 (18.06.2015) entire document	1-20
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<p><input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.</p>																				
<p>* Special categories of cited documents:</p> <table border="0"> <tr> <td style="vertical-align: top;"> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </td> <td style="vertical-align: top;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p> </td> </tr> </table>			<p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p>	<p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p>																
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<p>Date of the actual completion of the international search</p> <p>04 September 2019</p>		<p>Date of mailing of the international search report</p> <p style="font-size: 1.5em; text-align: center;">16 OCT 2019</p>																		
<p>Name and mailing address of the ISA/US</p> <p>Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300</p>		<p>Authorized officer</p> <p style="text-align: center;">Blaine R. Copenheaver</p> <p>PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774</p>																		