WHAT IS CLAIMED:

1. A mutated Cpf1 polypeptide comprising one or more mutations affecting PAM recognition.
2. The mutated Cpf1 polypeptide according to claim 1, wherein said mutated Cpf1 polypeptide recognizes a PAM sequence which is not recognized by the corresponding wild type Cpf1.
3. A mutated Cpf1 polypeptide having one or more mutation, wherein said mutated Cpf1 protein recognizes a PAM sequence which is not recognized by the corresponding wild type Cpf1.
4. A mutated Cpf1 polypeptide having one or more mutation and recognizing a PAM consisting of less than 4 nucleotides other than N, with the proviso that said mutated Cpf1 is not mutated FnCpf1.
5. A mutated Cpf1 polypeptide recognizing a PAM having a sequence YCN, (T)YCV, AYV, TYV, RYN, or RCN or having a sequence TNYC or TNYS, with the proviso that said PAM is not TTTV, and/or said PAM is not TTTC, and/or said PAM is not TCTS, preferably wherein said PAM has a sequence or comprises a sequence (T)YCV or RYN; AYV or TYV; YCN or RCN.
6. A mutated Cpf1 polypeptide recognizing a PAM having a sequence or comprising a sequence YCN, YCV, AYV, TYV, RYN, RCN, TGYV, NTTN, TTN, TRTN, TYTV, TYCT, TYCN, TRTN, NTTN, TACT, TYCC, TRTC, TATV, NTTV, TTV, TSTG, TVTS, TYYS, TCYS, TBYS, TCYS, TNYS, TYYS, TNTN, TSTG, TTCC, TCCC, TATC, TGTG, TCTG, TYCV, or TCTC.
7. The mutated Cpf1 according to any of claims 1 to 6, wherein said mutated Cpf1 is mutated AsCpf1 or mutated LbCpf1.
8. A mutated Cpf1, preferably the mutated Cpf1 according to according to any of claims 1 to 7, wherein said mutated Cpf1 comprises one or more mutated amino acid residue at position 11, 12, 13, 14, 15, 16, 17, 34, 36, 39, 40, 43, 46, 47, 50, 54, 57, 58, 111, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553,

554, 555, 556, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 642, 643, 644, 645, 646, 647, 648, 649, 651, 652, 653, 654, 655, 656, 676, 679, 680, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 707, 711, 714, 715, 716, 717, 718, 719, 720, 721, 722, 739, 765, 768, 769, 773, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, or 1048; preferably, one or more mutated amino acid residue at position 130, 131, 132, 133, 134, 135, 136, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 570, 571, 572, 573, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 630, 631, 632, 646, 647, 648, 649, 650, 651, 652, 653, 683, 684, 685, 686, 687, 688, 689, or 690; more preferably one or more mutated amino acid residue at position 539, 542, 547, 548, 550, 551, 552, 167, 604, and/or 607 of AsCpf1, or the corresponding position of an AsCpf1 orthologue, homologue, or variant, preferably mutated amino acid residues at positions 542 or 542 and 607, wherein said mutations preferably are 542R and 607R, such as S542R and K607R; or preferably mutated amino acid residues at positions 542 and 548 (and optionally 552), wherein said mutations preferably are 542R and 548V (and optionally 552R), such as S542R and K548V (and optionally N552R); or at position 532, 538, 542, and/or 595 of LbCpf1, or the corresponding position of an AsCpf1 orthologue, homologue, or variant, preferably mutated amino acid residues at positions 532 or 532 and 595, wherein said mutations preferably are 532R and 595R, such as G532R and K595R; or preferably mutated amino acid residues at positions 532 and 538 (and optionally 542), wherein said mutations preferably are 532R and 538V (and optionally 542R), such as G532R and K538V (and optionally Y542R), most preferably wherein said mutations are S542R and K607R, S542R and K548V, or S542R, K548V and N552R of AsCpf1.

9. The mutated Cpf1 polypeptide according to any of claims 1 to 8, further comprising modifications or mutations affecting Cpf1 catalytic activity and/or Cpf1 stability.

10. The mutated Cpf1 polypeptide according to any of claims 1 to 9, which is comprised in a fusion protein with a functional domain.

11. The mutated Cpf1 polypeptide according to claim 10, wherein said functional domain comprises a, activator domain, a repressor domain, a recombinase, a transposase, a histone remodeler, a DNA methyltransferase, a cryptochrome, a light inducible/controllable domain, or a chemically inducible/controllable domain.
12. The mutated Cpf1 polypeptide according to any of claims 1 to 11 which is not capable of inducing a DNA double strand break.
13. The mutated Cpf1 polypeptide according to any of claims 1 to 12 which is a nickase.
14. The mutated Cpf1 polypeptide according to any of claims 1 to 13 which is a catalytically inactive Cpf1 polypeptide.
15. The mutated Cpf1 polypeptide according to any of claims 1 to 14 which is not capable of inducing a DNA single strand break.
16. A polynucleotide encoding the mutated Cpf1 polypeptide according to any of claims 1 to 15.
17. The polynucleotide according to claim 16, which is codon optimized for expression in a cell of interest.
18. The polynucleotide according to claim 16 or 17, wherein said polynucleotide further comprises one or more sequence encoding one or more NLS.
19. A vector comprising the polynucleotide according to any of claims 16 to 18.
20. The vector according to claim 19, which is an expression vector.
21. The vector according to claim 19 or 20, which is an inducible, conditional, or constitutive expression vector.
22. A vector system comprising one or more vector, said one or more vector comprising a polynucleotide according to any of claims 16 to 18 and on the same or a different vector one or more polynucleotide encoding a gRNA.
23. The vector system according to claim 22, wherein said one or more vector is an expression vector.
24. A complex comprising a mutated Cpf1 polypeptide according to any of claims 1 to 15 and a gRNA.
25. The vector system or complex according to any of claims 22 to 24, wherein said guide comprises a guide sequence and a direct repeat sequence.

26. The vector system of complex according to any of claims 22 to 25, wherein said gRNA comprises a polynucleotide sequence comprising a 3' guide sequence and a 5' direct repeat sequence.
27. The vector system or complex according to any of claims 22 to 26, wherein said guide sequence is capable of hybridizing to a target DNA sequence.
28. The vector system or complex according to any of claims 22 to 27, wherein said guide sequence is modified to alter functionality, specificity, and/or stability.
29. The vector system or complex according to any of claims 22 to 28, wherein said mutated Cpf1 is capable of binding said gRNA.
30. The vector system or complex according to any of claims 22 to 29, wherein said mutated Cpf1 is capable of forming a complex with said gRNA, and wherein said complex is capable of modifying or targeting a target DNA locus upon binding to said target DNA locus.
31. The vector system or complex according to any of claims 22 to 30, wherein said mutated Cpf1 is capable of forming a complex with said gRNA and effecting sequence specific binding of said complex to a target DNA locus.
32. A delivery system comprising the polypeptide, polynucleotide, vector, vector system, or complex according to any of claims 1 to 31.
33. The delivery system according to claim 32, wherein said delivery system is a liposomal, particle, exosomal, microvesicle, gene-gun, or viral delivery system.
34. A host cell comprising the mutated Cpf1 polypeptide, polynucleotide, vector, vector system, complex or delivery system according to any of claims 1 to 33.
35. A host cell expressing or capable of expressing the mutated Cpf1 polypeptide according to any of claims 1 to 15.
36. The host cell according to any of claims 34 to 35, which is a prokaryotic or eukaryotic host cell.
37. The host cell according to any of claims 34 to 36, which is an isolated host cell.
38. A composition comprising the mutated Cpf1 polypeptide, polynucleotide, vector, vector system, complex, delivery system, or host cell according to any of claims 1 to 37.
39. A kit comprising the mutated Cpf1 polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any claims 1 to 38.

40. A transgenic organism comprising the mutated Cpf1 polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any of claims 1 to 38.

41. A transgenic organism expressing or capable of expressing the mutated Cpf1 polypeptide according to any of claims 1 to 15.

42. A method of modifying or targeting a target DNA locus, the method comprising delivering to said locus a polypeptide, polynucleotide, vector, vector system, delivery system, or complex according to any of claims 1 to 33.

43. A method of modifying or targeting a target DNA locus, the method comprising delivering to said locus a composition according to claim 38.

44. A method of modifying or targeting a target DNA locus, the method comprising delivering to said locus a mutated Cpf1 polypeptide according to any of claims 1 to 15, or a polynucleotide encoding said mutated Cpf1, and a gRNA, or a polynucleotide encoding said gRNA, wherein said mutated Cpf1 polypeptide forms a complex with said gRNA and wherein said target DNA locus is modified or targeted upon binding of said complex to said target DNA locus.

45. The method according to any of claims 42 to 44, wherein said modifying or targeting a target locus comprises inducing a DNA strand break.

46. The method according to any of claims 42 to 45, wherein said modifying or targeting a target locus comprises inducing a DNA double strand break.

47. The method according to any of claims 42 to 46, wherein said modifying or targeting a target locus comprises altering gene expression of one or more genes.

48. The method according to any of claims 42 to 47, wherein said modifying or targeting a target locus comprises epigenetic modification of said target DNA locus.

49. The method of any one of claims 42 to 48, which is a method of modifying a cell, a cell line, or an organism by manipulation of one or more target sequences at genomic loci of interest.

50. A cell from the method of claim 49, or progeny thereof, wherein the cell comprises a modification not present in a cell not subjected to the method.

51. The cell of claim 50, of progeny thereof, wherein the cell not subjected to the method comprises an abnormality and the cell from the method has the abnormality addressed or corrected.

52. A cell product from the cell or progeny thereof of claim 50, wherein the product is modified in nature or quantity with respect to a cell product from a cell not subjected to the method.

53. The cell product of claim 52, wherein the cell not subjected to the method comprises an abnormality and the cell product reflects the abnormality having been addressed or corrected by the method.

54. A method of identifying a mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition, comprising the steps of

(a) providing a host cell

- comprising or expressing a candidate mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition,
- comprising or expressing a gRNA,
- comprising a polynucleotide comprising a particular PAM sequence linked to a DNA target sequence, wherein said polynucleotide further comprises a selection marker, wherein said DNA target sequence is capable of hybridizing with said gRNA,

(b) identifying a mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition based on the activity of said selection marker.

55. The method according to claim 54, comprising the steps of

(a1) providing a host cell comprising or expressing a candidate mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition and a gRNA;

(b1) introducing in said host cell a polynucleotide comprising a particular PAM sequence linked to a DNA target sequence with which said gRNA is capable of hybridizing, wherein said polynucleotide further comprises a selection marker; or

(a2) providing a host cell comprising a polynucleotide comprising a particular PAM sequence linked to a DNA target sequence, wherein said polynucleotide further comprises a selection marker;

(b2) introducing in said host cell a candidate mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition, or a polynucleotide expressing such, and a gRNA

capable of hybridizing with said DNA target sequence, or a polynucleotide expressing such;

(c) identifying a mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition based on the activity of said selection marker.

56. The method according to claim 54 or 55, wherein said particular PAM sequence is not recognized by the corresponding wild type Cpf1.

57. The method according to any of claims 54 or 56, wherein said host cell is a prokaryotic or eukaryotic host cell.

58. The method according to any of claims 54 to 57, wherein said selection marker is a positive or negative selection marker.

59. The method according to any of claims 54 to 58, wherein said selection marker is an antibiotic resistance gene.

60. The method according to any of claims 54 to 59, wherein said mutated Cpf1 polypeptide is catalytically active.

61. The method according to any of claims 54 to 58, wherein said host cell in step (a), (a1) or (a2) is a host cell library.

62. The method according to claim 61, wherein said host cell library comprises a library of candidate mutated Cpf1 polypeptides having one or more mutation affecting PAM recognition.

63. The method according to claim 61, wherein said host cell library comprises a PAM library of polynucleotides.

64. The method according to any of claims 54 to 63, wherein said polynucleotide in step (a) or (b1) is a PAM library of polynucleotides.

65. The method according to any of claims 54 to 63, wherein said candidate mutated Cpf1 polypeptide having one or more mutation affecting PAM recognition in step (a) or (b2) is a Cpf1 mutant library.

66. A mutated Cpf1 polypeptide identified by the method according to any of claims 54 to 65.

67. A polynucleotide encoding the mutated polypeptide according to claim 66.

68. Use of the polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any of claims 1 to 38, 66, or 67 for modifying or targeting a DNA target locus, preferably in vitro or ex vivo.

69. Use of the polypeptide, polynucleotide, vector, vector system, complex, delivery system, or host cell according to any of claims 1 to 38, 66, or 67 for genome editing, preferably in vitro or ex vivo.

70. The polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any of claims 1 to 38, 66, or 67 for use in modifying or targeting a DNA target locus.

71. The polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any of claims 1 to 38, 66, or 67 for use in genome editing.

72. The polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any of claims 1 to 38, 66, or 67 for use in therapy.

73. Use of the polypeptide, polynucleotide, vector, vector system, complex, delivery system, host cell, or composition according to any of claims 1 to 38, 66, or 67 for the manufacture of a medicament.

74. An engineered, non-naturally occurring Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)-CRISPR associated (Cas) (CRISPR-Cas) system comprising

c) one or more Type V CRISPR-Cas polynucleotide sequences comprising a guide RNA which comprises a guide sequence linked to a direct repeat sequence, wherein the guide sequence is capable of hybridizing with a target sequence, or one or more nucleotide sequences encoding the one or more Type V CRISPR-Cas polynucleotide sequences, and

d) a Cpf1 effector protein, or one or more nucleotide sequences encoding the Cpf1 effector protein;

wherein the one or more guide sequences hybridize to said target sequence, said target sequence is 3' of a Protospacer Adjacent Motif (PAM), and said guide forms a complex with the Cpf1 effector protein; wherein the Cpf1 effector comprises the mutated Cpf1 polypeptide of any one of claims 1 to 15.

75. An engineered, non-naturally occurring Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)-CRISPR associated (Cas) (CRISPR-Cas) vector system comprising one or more vectors encoding the non-naturally occurring Clustered Regularly Interspersed Short Palindromic Repeat (CRISPR)-CRISPR associated (Cas) (CRISPR-Cas) system of claim 1, comprising

c) a first regulatory element operably linked to one or more nucleotide sequences encoding one or more Type V CRISPR-Cas polynucleotide sequences comprising a guide which comprises a guide sequence linked to a direct repeat sequence, wherein the guide sequence is capable of hybridizing with a target sequence,

d) a second regulatory element operably linked to a nucleotide sequence encoding a Cpf1 effector protein;

wherein components (a) and (b) are located on the same or different vectors of the system,

wherein when transcribed, the one or more guide sequences hybridize to said target sequence, said target sequence is 3' of a Protospacer Adjacent Motif (PAM), and said guide forms a complex with the Cpf1 effector protein; wherein the Cpf1 effector comprises the mutated Cpf1 polypeptide of any one of claims 1 to 15.

76. A method of producing a plant, having a modified trait of interest encoded by a gene of interest, said method comprising contacting a plant cell with a system according to claim 74 or 75 or subjecting the plant cell to a method according to claim 44, thereby either modifying or introducing said gene of interest, and regenerating a plant from said plant cell.

77. A method of identifying a trait of interest in a plant, said trait of interest encoded by a gene of interest, said method comprising contacting a plant cell with a system according to claim 74 or 75 or subjecting the plant cell to a method according to claim 44, thereby identifying said gene of interest.

78. The method of claim 77, further comprising introducing the identified gene of interest into a plant cell or plant cell line or plant germplasm and generating a plant therefrom, whereby the plant contains the gene of interest.

79. The method of claim 78wherein the plant exhibits the trait of interest.

80. A particle comprising a system according to claim 74 or 75.

81. The particle of claim 80, wherein the particle contains the Cpf1 effector protein complexed with the guide.

82. The system or method of claim 74, 75 or 44, wherein the complex, guide or protein is conjugated to at least one sugar moiety, optionally N-acetyl galactosamine (GalNAc), in particular triantennary GalNAc.

83. The system or method of claim 74, 75 or 44, wherein the concentration of Mg^{2+} is about 1mM to about 15 mM.

84. The system or method of claim 74, 75 or 44, wherein the Cpf1 effector protein is fused to a cytidine deaminase.

85. The system or method of claim 84, wherein the cytidine deaminase is fused to the carboxy terminus of the Cpf1 effector protein.

86. The system or method of claim 84or 85, wherein the Cpf1 effector protein or the cytidine deaminase is further fused to a uracil DNA glycosylase inhibitor.

87. The system or method of any of claims 84-86, wherein the Cpf1 effector protein comprises a catalytically inactive Nuc domain.

88. The system or method of any of claims 84-87, wherein the Cpf1 effector protein comprises a catalytically inactive RuvC domain.

89. The system or method of any of claims 84-88, wherein the guide forms a complex with the Cpf1 effector protein and directs the complex to bind a target DNA, and wherein the cytidine deaminase converts a C to a U in the non-targeted strand of the target DNA.

90. The system of claim 74, comprising a plurality of guides each comprising a different guide sequence, wherein the plurality of guide sequences are capable of hybridizing with a plurality of different target sequences.

91. The system of claim 75, wherein the one or more vectors encodes a plurality of guide RNAs each comprising a different guide sequence, wherein the plurality of guide sequences are capable of hybridizing with a plurality of different target sequences.

92. The method of claim 44, comprising deliverying to each of a plurality of different target loci of interest a different nucleic acid component.

93. The system or method of claim 74, 75 or 44, wherein the Cpf1 effector protein is a dead Cpf1 comprising a catalytically inactive RuvC domain.

94. The system or method of claim 93, wherein the Cpf1 effector protein is fused to a heterologous functional domain having methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, or nucleic acid binding activity.

95. The system or method of claim 93, wherein the Cpf1 effector protein is fused to a transcriptional activation domain or a transcriptional repression domain.

CLAIMS

1. A mutated Cpf1 polypeptide comprising a mutated amino acid residue corresponding to amino acid position S542 of AsCpf1, in which the mutated Cpf1 polypeptide is not naturally-occurring and recognizes a PAM sequence which is not recognized by the corresponding wild-type Cpf1.

2. A mutated Cpf1 polypeptide according to Claim 1, in which the mutated amino acid residue corresponding to amino acid position S542 of AsCpf1 is R.

3. A mutated Cpf1 polypeptide according to Claim 1 or 2, in which the mutated Cpf1 polypeptide further comprises one or more mutated amino acid residues corresponding to amino acid positions K548, M604, K607, or T167 of AsCpf1.

4. A mutated Cpf1 polypeptide according to Claim 3, in which the mutated amino acid residue corresponding to amino acid position K548 of AsCpf1 is R or V.

5. A mutated Cpf1 polypeptide according to Claim 3, in which the mutated amino acid residue corresponding to amino acid position K607 of AsCpf1 is R.

6. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide further comprises one or more mutated amino acid residues corresponding to amino acid positions N547, K550, N551, or N552 of AsCpf1.

7. A mutated Cpf1 polypeptide according to Claim 6, in which the mutated amino acid residue corresponding to amino acid position N552 of AsCpf1 is R.

8. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide is a mutated AsCpf1.

9. A mutated Cpf1 polypeptide according to Claim 8, in which the mutated AsCpf1 comprises an S542R mutation.

10. A mutated Cpf1 polypeptide according to Claim 8 or 9, in which the mutated AsCpf1 comprises a K548R or a K548V mutation.

11. A mutated Cpf1 polypeptide according to Claim 8, 9 or 10, in which the mutated AsCpf1 comprises one of the following combinations of mutations: S542R and K548R; S542R and K548V; S542R and K607R; S542R and K607A; K548R and N552R; K548V and

N552R; K548V and N552G; S542R, K548V and N552R; S542R, K550Y and K607R; S542R, K607R and N547K; S542R, K607R and K548V; S542R, K607R and N551R; S542R, K607R and N552S; S542R, K548V and N552G; S542R, K548R, K550Y and K607R; S542R, K548V, N551R and N552R; S542R, K607R, N547K and K550Y; S542R, K607R, N547K and N551R; S542R, K607R, N547K and N552S; S542R, K607R ,K550Y and N551R; S542R, K607R, K550Y and N552S; S542R, K607R, N551R and N552S; S542R, K548V, N551R and N552G; or S542R, K607R, N547K, K550Y, N551R and N552S.

12. A mutated Cpf1 polypeptide according to any of Claims 8 to 11, in which the mutated AsCpf1 comprises one of the following combinations of mutations: S542R and K548R; S542R and K548V; S542R and K607R; or S542R, K548V and N552R.

13. A mutated Cpf1 polypeptide according to any of Claims 1 to 7, in which the mutated Cpf1 polypeptide is a mutated LbCpf1.

14. A mutated Cpf1 polypeptide according to Claim 13, in which the mutated LbCpf1 comprises a G532R mutation.

15. A mutated Cpf1 polypeptide according to Claim 13 or 14, in which the mutated LbCpf1 comprises a K538R or a K538V mutation.

16. A mutated Cpf1 polypeptide according to Claim 13, 14 or 15, in which the mutated LbCpf1 comprises one of the following combinations of mutations: G532R and K595R; G532R and K538V; or G532R, K538V and Y542R.

17. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide further comprises a mutated amino acid residue corresponding to amino acid position E174 of AsCpf1.

18. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide further comprises a mutated amino acid residue corresponding to amino acid position M537 of AsCpf1.

19. A mutated Cpf1 polypeptide according to Claim 18, in which the mutated amino acid residue corresponds to amino acid position M537 of AsCpf1 is R.

20. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide further comprises a mutated amino acid residue in a catalytic domain.

21. A mutated Cpf1 polypeptide according to Claim 20, in which the mutated Cpf1 polypeptide is a nickase.

22. A mutated Cpf1 polypeptide according to Claim 20, in which the mutated Cpf1 polypeptide is a catalytically inactive Cpf1.

23. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide is fused to a heterologous functional domain.

24. A mutated Cpf1 polypeptide according to Claim 23, in which the heterologous functional domain has one or more of the following activities: methylase activity, demethylase activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, RNA cleavage activity, DNA cleavage activity, or nucleic acid binding activity.

25. A mutated Cpf1 polypeptide according to Claim 23, in which the mutated Cpf1 polypeptide is fused to a transcriptional activation domain or a transcriptional repression domain.

26. A mutated Cpf1 polypeptide according to Claim 23, in which the mutated Cpf1 polypeptide is fused to a deaminase domain.

27. A mutated Cpf1 polypeptide according to Claim 26, in which the mutated Cpf1 polypeptide is fused to a cytidine deaminase, in which the cytidine deaminase converts a C to a U in the non-targeted strand of the target DNA.

28. A mutated Cpf1 polypeptide according to Claim 27, in which the cytidine deaminase is fused to the carboxy terminus of the mutated Cpf1 polypeptide.

29. A mutated Cpf1 polypeptide according to Claim 27 or 28, in which the mutated Cpf1 polypeptide or the cytidine deaminase is further fused to a uracil DNA glycosylase inhibitor

30. A mutated Cpf1 polypeptide according to any preceding claim, in which the mutated Cpf1 polypeptide is fused to one or more nuclear localization signals (NLSs).

31. A polynucleotide encoding a mutated Cpf1 polypeptide according to any preceding claim.

32. A polynucleotide according to Claim 31, in which the polynucleotide is codon optimized for expression in a eukaryotic cell.

33. A polynucleotide according to Claim 31 or 32, in which the polynucleotide is an mRNA.

34. An expression vector comprising a polynucleotide according to Claim 31, 32 or 33.

35. A CRISPR-Cas system comprising (a) a mutated Cpf1 polypeptide according to any of Claims 1 to 30 or a polynucleotide encoding the mutated Cpf1 polypeptide and (b) a gRNA capable of forming a CRISPR-Cpf1 complex with the mutated Cpf1 polypeptide.

36. A CRISPR-Cas system according to Claim 35, in which the gRNA comprises a 3' guide sequence linked to a 5' direct repeat sequence.

37. A delivery system comprising a mutated Cpf1 polypeptide according to any of Claims 1 to 30 or a polynucleotide encoding the mutated Cpf1 polypeptide.

38. A delivery system according to Claim 37, in which the delivery system comprises a liposomal, particle, exosomal, microvesicle, gene-gun, or viral delivery system.

39. An isolated eukaryotic host cell comprising a mutated Cpf1 polypeptide according to any of Claims 1 to 30 or a polynucleotide encoding the mutated Cpf1 polypeptide.

40. A method of modifying or targeting a target DNA locus in a eukaryotic cell or cell line *in vitro* or *ex vivo*, the method comprising delivering the CRISPR-Cas system according to Claim 35 or 36 into the eukaryotic cell.