CLAIMS

1. A CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 472, 473 and 465.

2. The CRISPR-associated protein according to claim 1, wherein the variant of Cas12a is SEQ ID NO.: 472.

3. The CRISPR-associated protein according to claim 1, wherein the variant of Cas12a is SEQ ID NO.: 473.

4. The CRISPR-associated protein according to claim 1, wherein the variant of Cas12a is SEQ ID NO.: 465.

5. A CRISPR ribonucleoprotein complex, comprising:
a guide RNA; and
a CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 472, 473 and 465.

6. The CRISPR ribonucleoprotein complex of claim 5, wherein the variant of Cas12a is SEQ ID NO.: 472.

7. The CRISPR ribonucleoprotein complex of claim 5, wherein the variant of Cas12a is SEQ ID NO.: 473.

8. The CRISPR ribonucleoprotein complex of claim 5, wherein the variant of Cas12a is SEQ ID NO.: 465.

9. An *in vitro* method of increasing efficiency of gene editing at TTT**N** PAM sites in a cell with a CRISPR ribonucleoprotein complex, comprising:
contacting a cell with the CRISPR ribonucleoprotein complex according to any one of claims 5-8.

10. The method according to claim 9, wherein the TTT**N** PAM sites consists of one selected form the group of TTTA, TTTT and TTTC PAM sites.

11. A kit comprising a guide RNA and a CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 472, 473 and 465.

12. The kit according to claim 11, wherein the variant of Cas12a is SEQ ID NO.: 472.

13. The kit according to claim 11, wherein the variant of Cas12a is SEQ ID NO.: 473.

14. The kit according to claim 11, wherein the variant of Cas12a is SEQ ID NO.: 465.

15. A CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 59-245, provided that the variant Cas12a provides an improvement in CRISPR/Cas12a-associated nuclease activity at non-canonical TTTT PAM sites.

16. The CRISPR-associated protein according to claims 15, wherein the variant of Cas12a further comprises mutations of SEQ ID NO.: 465.

17. A CRISPR ribonucleoprotein complex, comprising:

a guide RNA; and

a CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 59-245, provided that the variant Cas12a provides an improvement in CRISPR/Cas12a-associated nuclease activity at non-canonical TTTT PAM sites.

18. The CRISPR ribonucleoprotein complex of claim 17, wherein the variant of Cas12a further comprises mutations of SEQ ID NO.: 465.

19. An *in vitro* method of increasing efficiency of gene editing at non-canonical TTTT PAM sites in a cell with a CRISPR ribonucleoprotein complex, comprising:

contacting a cell with the CRISPR ribonucleoprotein complex according to claim 17 or 18.

20. A kit comprising a guide RNA and a CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 59-245, provided that the variant Cas12a provides an improvement in CRISPR/Cas12a-associated nuclease activity at non-canonical TTTT PAM sites.

21. The kit according to claims 20, wherein the variant of Cas12a further comprises mutations of SEQ ID NO.: 465.

22. A nucleic acid encoding a CRISPR-associated protein comprising a polypeptide comprising a variant of Cas12a, wherein the variant of Cas12a is selected from the group consisting of SEQ ID NOs.: 59-245, provided that the variant Cas12a provides an improvement in CRISPR/Cas12a-associated nuclease activity at non-canonical TTTT PAM sites.

23. The nucleic acid of claim 22, wherein the variant of Cas12a further comprises mutations of SEQ ID NO.: 465.

24. The nucleic acid of claim 22 or 23, wherein the nucleic acid is operably linked to suitable transcription elements to express the nucleic acid.

25. The nucleic acid of any one of claims 22-24, wherein the nucleic acid is DNA or RNA.

26. A polynucleotide encoding a Cas12a polypeptide, comprising one member selected from the group consisting of SEQ ID NOs: 5-17.

27. A Cas12a polypeptide, comprising one member selected from the group consisting of SEQ ID NOs.: 18-30.

28. A CAS endonuclease system comprising an expression cassette comprising a polynucleotide encoding a Cas12a polypeptide, comprising one member selected from the group consisting of SEQ ID NOs: 5-17.

29. A CAS endonuclease system comprising an amino acid sequence comprising a Cas12a polypeptide, comprising one member selected from the group consisting of SEQ ID NOs.: 18-30.

30. An *in vitro* method of performing genome editing in a eukaryotic cell, comprising:

introducing an CAS endonuclease system into the eukaryotic cell, said CAS endonuclease system comprising an expression cassette comprising a polynucleotide encoding a Cas12a polypeptide selected from the group consisting of SEQ ID NOs.: 5-17.

31. An *in vitro* method of performing genome editing in a eukaryotic cell, comprising:

introducing an CAS endonuclease system into the eukaryotic cell, said CAS endonuclease system comprising a Cas12a polypeptide selected from the group consisting of SEQ ID NOs.: 18-30.

32. A CRISPR-associated protein comprising a fusion polypeptide comprising a Cas12a open reading frame, a nuclear localization signal, optionally an amino acid linker and optionally an affinity tag, wherein the Cas12a open reading frame is selected from the group consisting of SEQ ID NOs.: 59-245.

33. A CRISPR-associated protein comprising a fusion polypeptide comprising a Cas12a open reading frame, a nuclear localization signal, optionally an amino acid linker and optionally an affinity tag, wherein the Cas12a open reading frame is selected from the group consisting of SEQ ID Nos.: 59-245 and wherein the nuclear localization signal is selected from SEQ ID NOs.: 475, 477, 479, 481 and 483.

34. A CRISPR-associated protein comprising a fusion polypeptide comprising a Cas12a open reading frame, a nuclear localization signal, optionally an amino acid linker and optionally an affinity tag, wherein the CRISPR-associated protein is selected from SEQ ID NOs.: 488-491.

35. A CRISPR-associated protein comprising a fusion polypeptide comprising a Cas12a open reading frame, a nuclear localization signal, optionally an amino acid linker and optionally an affinity tag, wherein the CRISPR-associated protein is selected from SEQ ID NOs.: 492 and 493.

36. An *in vitro* method of performing genome editing in a eukaryotic cell, comprising:

introducing an CAS endonuclease system into the eukaryotic cell, said CAS endonuclease system comprising a CRISPR-associated protein of any one of claims 32-35.