WHAT IS CLAIMED IS:

1. A Cas12 protein, wherein

the Cas12 protein comprises an amino acid sequence having at least 70% sequence identity to the amino acid sequence shown in SEQ ID NO: 696.

2. The Cas12 protein of claim 1, wherein the Cas12 protein forms a complex with a guide polynucleotide, the guide polynucleotide comprises a guide sequence that is reverse complementary to a target nucleic acid; and the guide polynucleotide comprises a scaffold sequence interacting with the Cas12 protein.

3. The Cas12 protein of claim 1, wherein the Cas12 protein has one or more mutations of the amino acid sequence shown in SEQ ID NO: 696.

4. The Cas12 protein of claim 1, wherein the Cas12 protein has at least one mutation at one or more amino acid residues corresponding to positions 1,2,3,4,5,6,7,8,9,10,12,13,14,15,16,19,21,22,23,24,25,26,27,28,29,30,32,33,34,35,36,37,38,39,40,41,42,43,44,46,47,48,49,50,51,53,54,55,56,57,58,59,60,61,62,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,88,89,90,91,92,93,94,95,96,97,98,99,101,102,103,104,105,106,108,109,110,111,112,114,115,116,117,118,119,120,121,123,124,125,126,127,128,129,130,131,132,133,13

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938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,9
56,957,958,959,960,961,963,964,965,966,967,968,969,970,971,972,973,974,97

5,976,977,979,980,981,982,983,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1021,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1035,1036,1037,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,1049,1050,1052,1053,1055,1056,1057,1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093,1094,1095,1096,1097,1098,1100,1101,1102,1103,1104,1105,1107,1108,1109,1110,1111,1112,1113,1115,1116,1117,1120,1122,1123,1124,1125,1128,1129,1130,1131,1132,1133,1134, or 1135 of the amino acid sequence shown in SEQ ID NO: 696.

5. The Cas12 protein of claim 1, wherein the Cas12 protein has at least one mutation at one or more amino acid residues corresponding to positions selected from I33, G184, S185, Q186, G194, N195, G196, G197, N245, G256, L260, Y278, S285, Y316, H350, D352, A355, A356, C385, P386, H387, G390, K391, N392, D429, Q461, Q462, Q469, E485, S491, K521, P525, L611, K629, K631, N633, D841, N898, K987, A988, G989, Q990, T991, D1010, E1013, A1136, K1138, or T1139 of the amino acid sequence shown in SEQ ID NO: 696.

6. The Cas12 protein of claim 1, wherein the Cas12 protein has mutations at

amino acid residues corresponding to a combination of positions of SEQ ID NO: 696, wherein the combination of positions is selected from the group consisting of: 186+352+1+426+846+858+860, 186+352+1+426+846+860, 186+352+1+5+426+858+860, 186+352+1+3+426+858+860, 186+352+3+426+860, 186+352+1+333+426+858+860, 186+352+1+426+485+858+860, 186+352+1+5+426+860, 186+352+3+426+858+860, 186+352+5+426+858+860, 186+352+333+426+858+860, 186+352+333+426+860, 186+352+426+846+860, 186+352+5+426+860, 186+352+1+3+426+860, 5+426+860, 186+352+426+846+858+860, 186+352+1+426+485+860, 426+858+860, 7+426+858, 186+352+426+860, 186+352+426+485+858+860, 186+352+426+485+860, 426+846+858+860, 7+426+846, 186+352+860, 184+186+352+376+1132, 5+333+426, 5+426+858, 186+352+1+333+426+860, 184+186+352+3+107+426, 186+352+5+426, 333+376+426, 186+352+5, 2+5+846+858, 186+352+3+426, 5+846+858, 186+352+426+846, 186+352+7, 186+352+3+376+426, 186+352+376+426+860+865, 186+352+376+426, 3+846+860, 846+858+988, 3+426+858, 3+846+858+860, 3+858+860, 186+352+858, 184+186+352+860, 333+426, 184+186+352+3+376, 3+426+860, 846+860+988, 3+860, 184+186+352+3+639, 186+352+333+426, 846+858+860, 186+352+426, 333+426+846, 333+426+485, 5+846+860, 3+846+988, 184+186+352+376, 3+333+426, 186+352+426+485, 333+426+858,

333+426+1132, 428+485, 186+352+333+376+426, 858+860, 186+352+376+426+485+860, 184+186+352+426, 186+352+639, 5+858+988, 3+858+988, 5+858, 3+858, 184+186+352+846, 184+186+352+639, 858+988, 184+186+352+426+1132, 186+352+1132, 184+186+352+5, 184+186+352+858, 858+860+1132, 3+5, 426+649, 186+352+426+485+860, 186+352+333, 184+186+352, 186+376, 846+860, 858+988+1132, 846+858, 333+376, 376+426, 184+186+352+3, 3+846+1132, 5+846+1132, 186+352+426+1132, 376+426+485+660, 426, 5+846, 846+860+1132, 333+376+485, 184+186+352+639+1132, 352+426, 333+485, 184+186+352+333, 846+858+1132, 333+426+860, 186+352+988, 5+860, 846+988, 186+352, 3+846, 846+1132, 184+186+352+1132, 186+485, 988+1132, 184+186+352+485, 376+485, 5+1132, 3+7, 186+352+485, 184+186+352+7, 184+186+352+333+336, 3+1132, 426+858+988, 186+352+376, 186+352+3, and 186+352+333+336+376+426.

7. A nuclease-inactive variant of the Cas12 protein of claim 1; wherein an inactivating mutation of the nuclease-inactivated mutant is selected from one or more of D651A, E891A, and D1082A at positions corresponding to the amino acid sequence shown in SEQ ID NO: 696.

8. A fusion protein or conjugate, comprising:

(1) a Cas12 protein comprising an amino acid sequence having at least 70% sequence identity to the amino acid sequence shown in SEQ ID NO: 696; and

(2) a homologous or heterologous functional domain.

9. The fusion protein or conjugate of claim 8, wherein the homologous or heterologous functional domain is selected from one or more of the following: a subcellular positioning signal, a DNA binding domain, a protease domain, a transcriptional activation domain, a transcriptional repression domain, a nuclease domain, a deaminase domain, a uracil DNA glycosylase domain (UDG), a uracil DNA glycosylase inhibitor domain (UGI), a DNA methyltransferase, a DNA demethylase, a histone methyltransferase, a histone demethylase, a transcriptional release factor, a histone acetylase domain, a histone deacetylase domain, a DNA ligase, an affinity tag, a reporter tag, an affinity domain, and a reporter domain.

10. The fusion protein or conjugate of claim 9, wherein the subcellular positioning signal is selected from the group consisting of a nuclear localization signal, a nuclear export signal, a mitochondrial localization signal, and a chloroplast localization signal.

11. An isolated nucleic acid, wherein the isolated nucleic acid encodes the

fusion protein or conjugate of claim 8.

12. A CRISPR-Cas12 system, comprising:

a. a fusion protein comprising a Cas12 protein, wherein the Cas12 protein comprises an amino acid sequence having at least 70% sequence identity to the amino acid sequence shown in SEQ ID NO: 696, or an isolated nucleic acid encoding the fusion protein; and

b. a guide polynucleotide, or a polynucleotide sequence encoding the guide polynucleotide;

wherein the fusion protein or conjugate forms a complex with the guide polynucleotide; and the guide polynucleotide comprises a guide sequence engineered to guide a sequence-specific binding of the complex to a target nucleic acid.

13. The CRISPR-Cas12 system of claim 12, wherein the target nucleic acids are the genes listed in Table 27; or

the guide polynucleotide comprises a scaffold sequence that interacts with the Cas12 protein, and the scaffold sequence comprises a sequence having at least 80% sequence identity to the sequence shown in SEQ ID NO: 704.

14. A vector system, comprising one or more recombinant vectors, wherein

at least one recombinant vector of the one or more recombinant vectors comprises the fusion protein or conjugate of claim 12 and a polynucleotide sequence encoding the guide polynucleotide.

15. A cell, comprising the CRISPR-Cas12 system of claim 12.

16. The cell of claim 15, wherein the cell is a human cell.

17. A kit, comprising the Cas12 protein of claim 1.

18. The Cas12 protein of claim 1 for use in detecting, binding, or cleaving a target nucleic acid, comprising: contacting the target nucleic acid with the Cas12 protein.

19. The CRISPR-Cas12 system of claim 12 for use in diagnosing, treating, or preventing a disease or disorder associated with a target nucleic acid.

20. The CRISPR-Cas12 system for use of claim 19, wherein the target nucleic acid is selected from genes as listed in Table 27, and the disease or disorder is the disease or disorder as listed in Table 27.