Anti-Mucin 17 antibodies, conjugates thereof and uses thereof

Technical Field

The invention relates to an antibody specifically binding to target mucin 17 (MUC17), an antibody conjugate and application thereof, a composition and a detection system containing the antibody molecule.

Background

Mucins (MUCs) are high-molecular glycoproteins produced and secreted by epithelial cells and containing mucus as a main component. To date, over twenty Mucin proteins have been discovered and classified into two groups, membrane-bound Mucin and secreted Mucin, according to the function of Mucin. Secreted Mucins form a physical barrier that acts as a mucus gel and provides protection to the epithelial cells of the respiratory and gastrointestinal tract. Transmembrane mucins form a rod-like structure by O-glycosylated tandem repeated sequence of their extracellular domains, building a protective mucus gel layer.

MUC17 (Mucin-17) is a transmembrane Mucin encoded by MUC17 gene located at position q22 on chromosome 7. MUC17 was discovered and identified in 2002 and consists of three parts, a transmembrane segment, an intracellular segment and an extracellular segment. The amino terminus is followed by a mucin-like structure (tandem repeat), an EGF (epidermal growth factor) -like region, an N-glycosylation region, a second EGF-like region, a hydrophobic transmembrane segment, and a carboxyl terminus within the cytoplasm. MUC17 is involved in intracellular signaling by binding to the cell membrane via a transmembrane region near the carboxy terminus. The extracellular domain determines the specific spatial structure and immunogenicity of MUC. Expression of MUC17 enhances the intestinal mucus barrier and promotes inflammatory healing. In epithelial cells, MUC17 functions to participate in signal transduction, maintain luminal structure, provide cytoprotection, and confer anti-adhesion properties to cancer cells that lose polarity, thereby rendering tumor cells non-polar.

MUC17 is mainly expressed in intestinal tract, and researches show that the expression of MUC17 is gradually and obviously increased in the development process of normal gastric mucosa, intestinal metaplasia mucosa and advanced gastric cancer, and the low expression of the MUC17 is related to poor prognosis of the gastric cancer. Further research shows that the expression of MUC17 is in negative correlation with the differentiation degree of tumors, and suggests that MUC17 can be used as a diagnosis and treatment target of gastric cancer.

As the MUC17 is a membrane-bound mucin with important biological functions, the expression level of MUC17 is related to various inflammations and tumor cell proliferation, a large number of researches suggest that the mucin is over-expressed in different malignant tumors, the close relationship between the mucin and the tumors and the induced immune response provide important

clues for designing mucin-based antitumor drugs, and the unmet medical requirements for diseases or disorder expressing MUC17 still exist.

Disclosure of Invention

The present invention provides novel anti-MUC17 antibodies or antigen-binding fragments thereof that have the advantages of high affinity and high specificity for human MUC17. The anti-MUC17 antibodies provided by the invention may be used as a independent therapy or in combination with other therapies or other anti-cancer agents, for example, in the treatment of cancer/tumors. The MUC17 antibodies can be used in diagnostic methods on tissue samples from an individual, particularly a patient, who may have a MUC17-mediated tumor and/or cancer, or a tumor and/or cancer associated with MUC17 aberrant expression, and/or a tumor and/or cancer identifiable by aberrant expression of MUC17. The invention also provides nucleic acid molecules encoding the antibody molecules, expression vectors, host cells, and methods for making the antibody molecules.

In a first aspect, the present invention provides an antibody or antigen-binding fragment thereof capable of specifically binding MUC17, wherein said antibody or antigen-binding fragment thereof comprises heavy chain complementarity determining regions (HCDRs) and/or light chain complementarity determining regions (LCDRs) selected from the group consisting of:

(1) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:7 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:8 or variants thereof; or,

(2) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:17 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:18 or variants thereof; or,

(3) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:24 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:25 or variants thereof; or,

(4) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:24 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:31 or variants thereof; or,

(5) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:34 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:35 or variants thereof; or,

(6) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:40 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:41 or variants thereof; or,

(7) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:47 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:48 or variants thereof; or,

(8) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:47 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:53 or variants thereof; or,

(9) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:59 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:60 or variants thereof; or,

(10) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:69 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:70 or variants thereof; or,

(11) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:77 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:78 or variants thereof; or,

(12) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:87 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:88 or variants thereof; or,

(13) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:97 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:98 or variants thereof; or,

(14) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:104 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:105 or variants thereof; or,

(15) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:114 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:115 or variants thereof; or,

(16) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:114 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:119 or variants thereof; or,

(17) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:125 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:126 or variants thereof; or,

(18) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:135 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:136 or variants thereof; or,

(19) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:97 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:140 or variants thereof; or,

(20) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:149 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:150 or variants thereof; or,

(21) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:158

or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:159 or variants thereof; or,

(22) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:167 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:168 or variants thereof; or,

(23) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:172 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:173 or variants thereof; or,

(24) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:179 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:180 or variants thereof; or,

(25) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:189 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:190 or variants thereof; or,

(26) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:198 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:199 or variants thereof; or,

(27) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:204 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:205 or variants thereof; or,

(28) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:214 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:215 or variants thereof;

(29) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:259 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:263 or variants thereof;

(30) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:259 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:260 or variants thereof;

(31) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:261 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:260 or variants thereof;

(32) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:259 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:262 or variants thereof;

(33) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:261 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:262 or variants thereof;

wherein the variant of any one of (1) – (33) has at least 80%, at least 85%, at least 90%, at least

91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity compared to the sequence from which it is derived, or the variant has one or more amino acid substitutions, deletions, or additions (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid substitutions, deletions, or additions) compared to the sequence from which it is derived; in some embodiments, the substitution is a conservative substitution.

In some embodiments, the HCDR1, HCDR2 and HCDR3 comprised in the heavy chain variable region (VH), and/or the LCDR1, LCDR2 and LCDR3 comprised in the light chain variable region (VL) are defined by Kabat, AbM, Chothia or IMGT numbering systems.

In some embodiments, the antibody or antigen-binding fragment thereof comprises heavy chain complementarity determining regions (HCDRs) and/or light chain complementarity determining regions (LCDRs) selected from the group consisting of:

(1) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:7; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:8; or,

(2) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:17; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:18; or,

(3) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:24; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:25; or,

(4) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:24; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:31; or,

(5) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:34; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:35; or,

(6) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:40; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:41; or,

(7) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:47; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:48; or,

(8) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:47; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:53; or,

(9) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:59; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:60; or,

(10) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:69; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:70; or,

(11) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:77; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:78; or,

(12) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:87; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:88; or,

(13) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:97; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:98; or,

(14) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID

NO:104; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:105; or,

(15) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:114; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:115; or,

(16) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:114; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:119; or,

(17) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:125; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:126; or,

(18) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:135; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:136; or,

(19) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:97; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:140; or,

(20) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:149; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:150; or,

(21) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:158; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:159; or,

(22) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:167; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:168; or,

(23) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:172; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:173; or,

(24) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:179; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:180; or,

(25) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:189; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:190; or,

(26) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:198; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:199; or,

(27) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:204; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID

NO:205; or,

(28) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:214; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:215;

(29) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:259; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:263;

(30) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:259; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:260;

(31) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:261; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:260;

(32) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:259; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:262;

(33) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in the VH as shown in SEQ ID NO:261; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in the VL as shown in SEQ ID NO:262.

In some embodiments, the HCDR1, HCDR2 and HCDR3 comprised in the heavy chain variable region (VH), and/or the LCDR1, LCDR2 and LCDR3 comprised in the light chain variable region (VL) are defined by Kabat, AbM, Chothia or IMGT numbering systems.

As a specific embodiment, the antibody or antigen-binding fragment thereof that specifically binds to MUC17 provided by the present invention comprise complementary determining regions (CDRs) selected from the following groups:

the following 3 CDRs (HCDR1, HCDR2, HCDR3) of the heavy chain variable regions (VH), and/or the following 3 CDRs (LCDR1, LCDR2, LCDR3) of the light chain variable regions (VL), wherein the HCDR1, HCDR2 and HCDR3 comprised in the heavy chain variable regions (VH) and/or the LCDR1, LCDR2 and LCDR3 comprised in the light chain variable regions (VL) are defined by the Kabat numbering system:

(1) HCDR1 comprising the sequence as shown in SEQ ID NO:1 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:1;

HCDR2 comprising the sequence as shown in SEQ ID NO:2 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:2;

HCDR3 comprising the sequence as shown in SEQ ID NO:3 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:3;

LCDR1 comprising the sequence as shown in SEQ ID NO:4 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:4;

LCDR2 comprising the sequence as shown in SEQ ID NO:5 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) as compared to the sequence of SEQ ID NO:5;

LCDR3 comprising the sequence as shown in SEQ ID NO:6 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) as compared to the sequence of SEQ ID NO:6;

or,

(2) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:13 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:13;

LCDR1 comprising the sequence as shown in SEQ ID NO:14 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:14;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:16 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:16;

or,

(3) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(4) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:28 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:28;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:30 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:30;

or,

(5) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:33 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:33;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(6) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:38 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:38;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:39 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:39;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(7) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:44 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:44;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:46 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:46;

or,

(8) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:44 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:44;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:51 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:51;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:52 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:52;

or,

(9) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:55 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:55;

LCDR1 comprising the sequence as shown in SEQ ID NO:56 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:56;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:58 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:58;

or,

(10) HCDR1 comprising the sequence as shown in SEQ ID NO:63 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:63;

HCDR2 comprising the sequence as shown in SEQ ID NO:64 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:64;

HCDR3 comprising the sequence as shown in SEQ ID NO:65 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:65;

LCDR1 comprising the sequence as shown in SEQ ID NO:66 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:66;

LCDR2 comprising the sequence as shown in SEQ ID NO:67 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:67;

LCDR3 comprising the sequence as shown in SEQ ID NO:68 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:68;

or;

(11) HCDR1 comprising the sequence as shown in SEQ ID NO:1 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:1;

HCDR2 comprising the sequence as shown in SEQ ID NO:73 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:73;

HCDR3 comprising the sequence as shown in SEQ ID NO:74 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:74;

LCDR1 comprising the sequence as shown in SEQ ID NO:75 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:75;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:76 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:76; or;

(12) HCDR1 comprising the sequence as shown in SEQ ID NO:81 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:81;

HCDR2 comprising the sequence as shown in SEQ ID NO:82 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:82;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:84 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:84;

LCDR2 comprising the sequence as shown in SEQ ID NO:85 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:85;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or;

(13) HCDR1 comprising the sequence as shown in SEQ ID NO:91 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:91;

HCDR2 comprising the sequence as shown in SEQ ID NO:92 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:92;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:94 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:94;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or;

(14) HCDR1 comprising the sequence as shown in SEQ ID NO:81 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:81;

HCDR2 comprising the sequence as shown in SEQ ID NO:101 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:101;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:102 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:102;

LCDR2 comprising the sequence as shown in SEQ ID NO:103 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:103;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or;

(15) HCDR1 comprising the sequence as shown in SEQ ID NO:108 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:108;

HCDR2 comprising the sequence as shown in SEQ ID NO:109 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:109;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:113 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:113;

or;

(16) HCDR1 comprising the sequence as shown in SEQ ID NO:108 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions

or additions) compared to the sequence of SEQ ID NO:108;

HCDR2 comprising the sequence as shown in SEQ ID NO:109 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:109;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:118 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:118;

or;

(17) HCDR1 comprising the sequence as shown in SEQ ID NO:121 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:121;

HCDR2 comprising the sequence as shown in SEQ ID NO:122 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:122;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:123 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:123;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:124 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:124;

or;

(18) HCDR1 comprising the sequence as shown in SEQ ID NO:129 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:129;

HCDR2 comprising the sequence as shown in SEQ ID NO:130 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:130;

HCDR3 comprising the sequence as shown in SEQ ID NO:131 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:131;

LCDR1 comprising the sequence as shown in SEQ ID NO:132 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:132;

LCDR2 comprising the sequence as shown in SEQ ID NO:133 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:133;

LCDR3 comprising the sequence as shown in SEQ ID NO:134 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:134;

or;

(19) HCDR1 comprising the sequence as shown in SEQ ID NO:91 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:91;

HCDR2 comprising the sequence as shown in SEQ ID NO:92 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:92;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:139 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:139;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or;

(20) HCDR1 comprising the sequence as shown in SEQ ID NO:143 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:143;

HCDR2 comprising the sequence as shown in SEQ ID NO:144 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:144;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or;

(21) HCDR1 comprising the sequence as shown in SEQ ID NO:81 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:81;

HCDR2 comprising the sequence as shown in SEQ ID NO:153 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:153;

HCDR3 comprising the sequence as shown in SEQ ID NO:154 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:154;

LCDR1 comprising the sequence as shown in SEQ ID NO:155 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:155;

LCDR2 comprising the sequence as shown in SEQ ID NO:156 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:156;

LCDR3 comprising the sequence as shown in SEQ ID NO:157 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:157;

or;

(22) HCDR1 comprising the sequence as shown in SEQ ID NO:162 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:162;

HCDR2 comprising the sequence as shown in SEQ ID NO:163 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:163;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:165 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:165;

LCDR3 comprising the sequence as shown in SEQ ID NO:166 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:166;

or;

(23) HCDR1 comprising the sequence as shown in SEQ ID NO:143 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:143;

HCDR2 comprising the sequence as shown in SEQ ID NO:144 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:144;

HCDR3 comprising the sequence as shown in SEQ ID NO:171 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:171;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or;

(24) HCDR1 comprising the sequence as shown in SEQ ID NO:176 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:176;

HCDR2 comprising the sequence as shown in SEQ ID NO:177 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:177;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:178 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:178;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or;

(25) HCDR1 comprising the sequence as shown in SEQ ID NO:183 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:183;

HCDR2 comprising the sequence as shown in SEQ ID NO:184 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:184;

HCDR3 comprising the sequence as shown in SEQ ID NO:185 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:185;

LCDR1 comprising the sequence as shown in SEQ ID NO:186 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:186;

LCDR2 comprising the sequence as shown in SEQ ID NO:187 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:187;

LCDR3 comprising the sequence as shown in SEQ ID NO:188 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:188;

or;

(26) HCDR1 comprising the sequence as shown in SEQ ID NO:193 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:193;

HCDR2 comprising the sequence as shown in SEQ ID NO:194 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:194;

HCDR3 comprising the sequence as shown in SEQ ID NO:195 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:195;

LCDR1 comprising the sequence as shown in SEQ ID NO:196 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:196;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:197 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:197;

or;

(27) HCDR1 comprising the sequence as shown in SEQ ID NO:202 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:202;

HCDR2 comprising the sequence as shown in SEQ ID NO:144 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:144;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:203 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:203;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or;

(28) HCDR1 comprising the sequence as shown in SEQ ID NO:208 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:208;

HCDR2 comprising the sequence as shown in SEQ ID NO:209 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:209;

HCDR3 comprising the sequence as shown in SEQ ID NO:210 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:210;

LCDR1 comprising the sequence as shown in SEQ ID NO:211 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:211;

LCDR2 comprising the sequence as shown in SEQ ID NO:212 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:212;

LCDR3 comprising the sequence as shown in SEQ ID NO:213 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:213.

In some embodiments, the substitution recited in any one of (1) - (28) is a conservative substitution.

As a specific embodiment, the antibody or antigen-binding fragment thereof that specifically binds to MUC17 provided by the present invention comprises the following 3 HCDRs (HCDR1, HCDR2, HCDR3) of the heavy chain variable region (VH), and/or the following 3 LCDRs (LCDR1, LCDR2, LCDR3) of the light chain variable region (VL), wherein the HCDR1, HCDR2 and HCDR3 comprised in the heavy chain variable regions (VH) and/or the LCDR1, LCDR2 and LCDR3 comprised in the light chain variable regions (VL) are defined by the AbM numbering system:

(1) HCDR1 comprising the sequence as shown in SEQ ID NO:225 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:225;

HCDR2 comprising the sequence as shown in SEQ ID NO:226 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:226;

HCDR3 comprising the sequence as shown in SEQ ID NO:3 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:3;

LCDR1 comprising the sequence as shown in SEQ ID NO:4 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:4;

LCDR2 comprising the sequence as shown in SEQ ID NO:5 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:5;

LCDR3 comprising the sequence as shown in SEQ ID NO:6 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:6;

or,

(2) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:13 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:13;

LCDR1 comprising the sequence as shown in SEQ ID NO:14 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:14;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:16 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:16;

or,

(3) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(4) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:28 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:28;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:30 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:30;

or,

(5) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:33 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:33;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(6) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:38 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:38;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:39 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:39;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(7) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:229 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:229;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:46 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:46;

or,

(8) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:229 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:229;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:51 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:51;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:52 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:52;

or,

(9) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:55 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:55;

LCDR1 comprising the sequence as shown in SEQ ID NO:56 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:56;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:58 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:58;

or,

(10) HCDR1 comprising the sequence as shown in SEQ ID NO:230 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:230;

HCDR2 comprising the sequence as shown in SEQ ID NO:231 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:231;

HCDR3 comprising the sequence as shown in SEQ ID NO:65 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:65;

LCDR1 comprising the sequence as shown in SEQ ID NO:66 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:66;

LCDR2 comprising the sequence as shown in SEQ ID NO:67 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:67;

LCDR3 comprising the sequence as shown in SEQ ID NO:68 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:68;

or,

(11) HCDR1 comprising the sequence as shown in SEQ ID NO:232 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:232;

HCDR2 comprising the sequence as shown in SEQ ID NO:233 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:233;

HCDR3 comprising the sequence as shown in SEQ ID NO:74 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:74;

LCDR1 comprising the sequence as shown in SEQ ID NO:75 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:75;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:76 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:76;

or,

(12) HCDR1 comprising the sequence as shown in SEQ ID NO:234 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:234;

HCDR2 comprising the sequence as shown in SEQ ID NO:235 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:235;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:84 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:84;

LCDR2 comprising the sequence as shown in SEQ ID NO:85 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:85;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or,

(13) HCDR1 comprising the sequence as shown in SEQ ID NO:236 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:236;

HCDR2 comprising the sequence as shown in SEQ ID NO:237 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:237;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:94 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:94;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or,

(14) HCDR1 comprising the sequence as shown in SEQ ID NO:234 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:234;

HCDR2 comprising the sequence as shown in SEQ ID NO:238 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:238;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:102 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:102;

LCDR2 comprising the sequence as shown in SEQ ID NO:103 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:103;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or,

(15) HCDR1 comprising the sequence as shown in SEQ ID NO:239 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:239;

HCDR2 comprising the sequence as shown in SEQ ID NO:240 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:240;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:113 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:113;

or,

(16) HCDR1 comprising the sequence as shown in SEQ ID NO:239 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:239;

HCDR2 comprising the sequence as shown in SEQ ID NO:240 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:240;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:118 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:118;

or,

(17) HCDR1 comprising the sequence as shown in SEQ ID NO:241 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:241;

HCDR2 comprising the sequence as shown in SEQ ID NO:242 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:242;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:123 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:123;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:124 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:124;

or,

(18) HCDR1 comprising the sequence as shown in SEQ ID NO:243 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:243;

HCDR2 comprising the sequence as shown in SEQ ID NO:244 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:244;

HCDR3 comprising the sequence as shown in SEQ ID NO:131 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:131;

LCDR1 comprising the sequence as shown in SEQ ID NO:132 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:132;

LCDR2 comprising the sequence as shown in SEQ ID NO:133 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:133;

LCDR3 comprising the sequence as shown in SEQ ID NO:134 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or

additions) compared to the sequence of SEQ ID NO:134;

or,

(19) HCDR1 comprising the sequence as shown in SEQ ID NO:236 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:236;

HCDR2 comprising the sequence as shown in SEQ ID NO:237 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:237;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:139 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:139;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or,

(20) HCDR1 comprising the sequence as shown in SEQ ID NO:245 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:245;

HCDR2 comprising the sequence as shown in SEQ ID NO:246 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:246;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(21) HCDR1 comprising the sequence as shown in SEQ ID NO:234 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:234;

HCDR2 comprising the sequence as shown in SEQ ID NO:247 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:247;

HCDR3 comprising the sequence as shown in SEQ ID NO:154 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:154;

LCDR1 comprising the sequence as shown in SEQ ID NO:155 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:155;

LCDR2 comprising the sequence as shown in SEQ ID NO:156 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:156;

LCDR3 comprising the sequence as shown in SEQ ID NO:157 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:157;

or,

(22) HCDR1 comprising the sequence as shown in SEQ ID NO:248 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:248;

HCDR2 comprising the sequence as shown in SEQ ID NO:249 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:249;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:165 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:165;

LCDR3 comprising the sequence as shown in SEQ ID NO:166 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:166;

or,

(23) HCDR1 comprising the sequence as shown in SEQ ID NO:245 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:245;

HCDR2 comprising the sequence as shown in SEQ ID NO:246 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:246;

HCDR3 comprising the sequence as shown in SEQ ID NO:171 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:171;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(24) HCDR1 comprising the sequence as shown in SEQ ID NO:250 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:250;

HCDR2 comprising the sequence as shown in SEQ ID NO:251 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:251;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:178 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:178;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(25) HCDR1 comprising the sequence as shown in SEQ ID NO:252 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions

or additions) compared to the sequence of SEQ ID NO:252;

HCDR2 comprising the sequence as shown in SEQ ID NO:253 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:253;

HCDR3 comprising the sequence as shown in SEQ ID NO:185 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:185;

LCDR1 comprising the sequence as shown in SEQ ID NO:186 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:186;

LCDR2 comprising the sequence as shown in SEQ ID NO:187 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:187;

LCDR3 comprising the sequence as shown in SEQ ID NO:188 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:188;

or,

(26) HCDR1 comprising the sequence as shown in SEQ ID NO:254 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:254;

HCDR2 comprising the sequence as shown in SEQ ID NO:255 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:255;

HCDR3 comprising the sequence as shown in SEQ ID NO:195 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:195;

LCDR1 comprising the sequence as shown in SEQ ID NO:196 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:196;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:197 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:197;

or,

(27) HCDR1 comprising the sequence as shown in SEQ ID NO:256 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:256;

HCDR2 comprising the sequence as shown in SEQ ID NO:246 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:246;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:203 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:203;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(28) HCDR1 comprising the sequence as shown in SEQ ID NO:257 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:257;

HCDR2 comprising the sequence as shown in SEQ ID NO:258 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:258;

HCDR3 comprising the sequence as shown in SEQ ID NO:210 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:210;

LCDR1 comprising the sequence as shown in SEQ ID NO:211 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:211;

LCDR2 comprising the sequence as shown in SEQ ID NO:212 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:212;

LCDR3 comprising the sequence as shown in SEQ ID NO:213 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:213.

In some embodiments, the substitution recited in any one of (1) - (28) is a conservative substitution.

In some embodiments, the present invention provides anti-MUC17 antibodies and antigen-binding fragments thereof that specifically bind MUC17, comprising a heavy chain variable

region (VH), wherein:

(1) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:7, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:7, or consists of SEQ ID NO:7;

(2) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:17, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:17, or consists of SEQ ID NO:17;

(3) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:24, or consists of SEQ ID NO:24;

(4) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:34, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:34, or consists of SEQ ID NO:34;

(5) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:40, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:40, or consists of SEQ ID NO:40;

(6) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:47, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:47, or consists of SEQ ID NO:47;

(7) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:59, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:59, or consists of SEQ ID NO:59;

(8) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:69, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:69, or consists of SEQ ID NO:69;

(9) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:77, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:77, or consists of SEQ ID NO:77;

(10) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:87, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:87, or consists of SEQ ID NO:87;

(11) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:97, or consists of SEQ ID NO:97;

(12) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:104, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:104, or consists of SEQ ID NO:104;

(13) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:114, or consists of SEQ ID NO:114;

(14) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:125, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:125, or consists of SEQ ID NO:125;

(15) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:135, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:135, or consists of SEQ ID NO:135;

(16) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:149, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:149, or consists of SEQ ID NO:149;

(17) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:158, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:158, or consists of SEQ ID NO:158;

(18) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:167, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:167, or consists of SEQ ID NO:167;

(19) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:172, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:172, or consists of SEQ ID NO:172;

(20) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:179, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:179, or consists of SEQ ID NO:179;

(21) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:189, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:189, or consists of SEQ ID NO:189;

(22) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:198, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:198, or consists of SEQ ID NO:198;

(23) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:204, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:204, or consists of SEQ ID NO:204;

(24) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:214, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:214, or consists of SEQ ID NO:214;

(25) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259;

(26) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; or

(27) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID

NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264.

In some embodiments, the present invention provides anti-MUC17 antibodies and antigen-binding fragments thereof that specifically bind MUC17, comprising a light chain variable region (VL), wherein:

(1) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:8, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:8, or consists of SEQ ID NO:8;

(2) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:18, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:18, or consists of SEQ ID NO:18;

(3) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:25, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:25, or consists of SEQ ID NO:25;

(4) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:31, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:31, or consists of SEQ ID NO:31;

(5) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:35, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:35, or consists of SEQ ID NO:35;

(6) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:41, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:41, or consists of SEQ ID NO:41;

(7) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:48, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:48, or consists of SEQ ID NO:48;

(8) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:53, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:53, or consists of SEQ ID NO:53;

(9) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:60, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:60, or consists of SEQ ID NO:60;

(10) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:70, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:70, or consists of SEQ ID NO:70;

(11) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:78, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:78, or consists of SEQ ID NO:78;

(12) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:88, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:88, or consists of SEQ ID NO:88;

(13) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:98, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:98, or consists of SEQ ID NO:98;

(14) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:105, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:105, or consists of SEQ ID NO:105;

(15) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:115, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:115, or consists of SEQ ID NO:115;

(16) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:119, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:119, or consists of SEQ ID NO:119;

(17) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:126, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:126, or consists of SEQ ID NO:126;

(18) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:136, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:136, or consists of SEQ ID NO:136;

(19) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:140, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:140, or consists of SEQ ID NO:140;

(20) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:150, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:150, or consists of SEQ ID NO:150;

(21) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:159, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:159, or consists of SEQ ID NO:159;

(22) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:168, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:168, or consists of SEQ ID NO:168;

(23) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:173, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:173, or consists of SEQ ID NO:173;

(24) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:180, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:180, or consists of SEQ ID NO:180;

(25) the light chain variable region comprises the amino acid sequence as shown in SEQ ID

NO:190, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:190, or consists of SEQ ID NO:190;

(26) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:199, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:199, or consists of SEQ ID NO:199;

(27) The light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:205, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:205, or consists of SEQ ID NO:205;

(28) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:215, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:215, or consists of SEQ ID NO: 215;

(29) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(30) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(31) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262;

(32) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(33) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266; or

(34) The light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO: 267.

In another embodiment, the invention provides anti-MUC17 antibodies and antigen-binding fragments thereof that specifically bind MUC17, comprising a heavy chain variable region (VH) and a light chain variable region (VL), wherein:

(1) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:7, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:7, or consists of SEQ ID NO:7; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:8, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:8, or consists of SEQ ID NO:8;

(2) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:17, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%

or 99% identity to the amino acid sequence of SEQ ID NO:17, or consists of SEQ ID NO:17; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:18, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:18, or consists of SEQ ID NO:18;

(3) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:24, or consists of SEQ ID NO:24; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:25, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:25, or consists of SEQ ID NO:25;

(4) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:24, or consists of SEQ ID NO:24; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:31, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:31, or consists of SEQ ID NO:31;

(5) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:34, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:34, or consists of SEQ ID NO:34; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:35, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:35, or consists of SEQ ID NO:35;

(6) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:40, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:40, or consists of SEQ ID NO:40; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:41, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:41, or consists of SEQ ID NO:41;

(7) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:47, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:47, or consists of SEQ ID NO:47; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:48, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:48, or consists of SEQ ID NO:48;

(8) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:47, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:47, or consists of SEQ ID NO:47; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:53, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:53, or consists of SEQ ID NO:53;

(9) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID

NO:59, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:59, or consists of SEQ ID NO:59; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:60, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:60, or consists of SEQ ID NO:60;

(10) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:69, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:69, or consists of SEQ ID NO:69; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:70, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:70, or consists of SEQ ID NO:70;

(11) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:77, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:77, or consists of SEQ ID NO:77; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:78, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:78, or consists of SEQ ID NO:78;

(12) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:87, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:87, or consists of SEQ ID NO:87; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:88, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:88, or consists of SEQ ID NO:88;

(13) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:97, or consists of SEQ ID NO:97; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:98, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:98, or consists of SEQ ID NO:98;

(14) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:104, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:104, or consists of SEQ ID NO:104; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:105, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:105, or consists of SEQ ID NO:105;

(15) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:114, or consists of SEQ ID NO:114; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:115, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:115, or consists of SEQ ID NO:115;

(16) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:114, or consists of SEQ ID NO:114; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:119, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:119, or consists of SEQ ID NO:119;

(17) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:125, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:125, or consists of SEQ ID NO:125; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:126, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:126, or consists of SEQ ID NO:126;

(18) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:135, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:135, or consists of SEQ ID NO:135; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:136, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:136, or consists of SEQ ID NO:136;

(19) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:97, or consists of SEQ ID NO:97; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:140, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:140, or consists of SEQ ID NO:140;

(20) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:149, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:149, or consists of SEQ ID NO:149; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:150, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:150, or consists of SEQ ID NO:150;

(21) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:158, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:158, or consists of SEQ ID NO:158; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:159, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:159, or consists of SEQ ID NO:159;

(22) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:167, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:167, or consists of SEQ ID NO: 167; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:168, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%

identity to the amino acid sequence of SEQ ID NO:168, or consists of SEQ ID NO:168;

(23) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:172, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:172, or consists of SEQ ID NO:172; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:173, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:173, or consists of SEQ ID NO:173;

(24) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:179, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:179, or consists of SEQ ID NO:179; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:180, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:180, or consists of SEQ ID NO:180;

(25) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:189, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:189, or consists of SEQ ID NO:189; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:190, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:190, or consists of SEQ ID NO:190;

(26) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:198, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:198, or consists of SEQ ID NO:198; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:199, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:199, or consists of SEQ ID NO:199;

(27) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:204, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:204, or consists of SEQ ID NO:204; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:205, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:205, or consists of SEQ ID NO:205;

(28) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:214, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:214, or consists of SEQ ID NO:214; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:215, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:215, or consists of SEQ ID NO: 215;

(29) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO: 259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an

amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(30) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO: 259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(31) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(32) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO: 259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262;

(33) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262;

(34) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(35) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(36) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the

light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(37) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO: 259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(38) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(39) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(40) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266;

(41) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO: 259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266;

(42) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266;

(43) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%

or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO: 267;

(44) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO: 259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO: 267;

(45) the heavy chain variable region comprises an amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO: 267;

(46) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262.

In a specific embodiment, the invention provides anti-MUC17 antibodies and antigen-binding fragments thereof that specifically bind MUC17, comprising a heavy chain variable region (VH) and a light chain variable region (VL), wherein:

(1) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:7 or consists of SEQ ID NO:7; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:8 or consists of SEQ ID NO:8;

(2) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:17 or consists of SEQ ID NO:17; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:18 or consists of SEQ ID NO:18;

(3) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24 or consists of SEQ ID NO:24; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:25 or consists of SEQ ID NO:25;

(4) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24 or consists of SEQ ID NO:24; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:31 or consists of SEQ ID NO:31;

(5) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:34 or consists of SEQ ID NO:34; the light chain variable region comprises the amino acid

sequence as shown in SEQ ID NO:35 or consists of SEQ ID NO:35;

(6) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:40 or consists of SEQ ID NO:40; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:41 or consists of SEQ ID NO:41;

(7) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:47 or consists of SEQ ID NO:47; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:48 or consists of SEQ ID NO:48;

(8) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:47 or consists of SEQ ID NO:47; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:53 or consists of SEQ ID NO:53;

(9) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:59 or consists of SEQ ID NO:59; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:60 or consists of SEQ ID NO:60;

(10) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:69 or consists of SEQ ID NO:69; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:70 or consists of SEQ ID NO:70;

(11) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:77 or consists of SEQ ID NO:77; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:78 or consists of SEQ ID NO:78;

(12) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:87 or consists of SEQ ID NO:87; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:88 or consists of SEQ ID NO:88;

(13) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97 or consists of SEQ ID NO:97; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:98 or consists of SEQ ID NO:98;

(14) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:104 or consists of SEQ ID NO:104; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:105 or consists of SEQ ID NO:105;

(15) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114 or consists of SEQ ID NO:114; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:115 or consists of SEQ ID NO:115;

(16) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114 or consists of SEQ ID NO:114; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:119 or consists of SEQ ID NO:119;

(17) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:125 or consists of SEQ ID NO:125; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:126 or consists of SEQ ID NO:126;

(18) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:135 or consists of SEQ ID NO:135; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:136 or consists of SEQ ID NO:136;

(19) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97 or consists of SEQ ID NO:97; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:140 or consists of SEQ ID NO:140;

(20) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:149 or consists of SEQ ID NO:149; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:150 or consists of SEQ ID NO:150;

(21) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:158 or consists of SEQ ID NO:158; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:159 or consists of SEQ ID NO:159;

(22) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:167 or consists of SEQ ID NO:167; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:168 or consists of SEQ ID NO:168;

(23) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:172 or consists of SEQ ID NO:172; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:173 or consists of SEQ ID NO:173;

(24) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:179 or consists of SEQ ID NO:179; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:180 or consists of SEQ ID NO:180;

(25) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:189 or consists of SEQ ID NO:189; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:190 or consists of SEQ ID NO:190;

(26) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:198 or consists of SEQ ID NO:198; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:199 or consists of SEQ ID NO:199;

(27) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:204 or consists of SEQ ID NO:204; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:205 or consists of SEQ ID NO:205;

(28) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:214 or consists of SEQ ID NO:214; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:215 or consists of SEQ ID NO:215;

(29) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259 or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263 or consists of SEQ ID NO:263;

(30) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259 or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260 or consists of SEQ ID NO:260;

(31) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261 or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260 or consists of SEQ ID NO:260;

(32) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID

NO:259 or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262 or consists of SEQ ID NO:262;

(33) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261 or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262 or consists of SEQ ID NO:262;

(34) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264 or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263 or consists of SEQ ID NO:263;

(35) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261 or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263 or consists of SEQ ID NO:263;

(36) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264 or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265 or consists of SEQ ID NO:265;

(37) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259 or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265 or consists of SEQ ID NO:265;

(38) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261 or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265 or consists of SEQ ID NO:265;

(39) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264 or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260 or consists of SEQ ID NO:260;

(40) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264 or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266 or consists of SEQ ID NO:266;

(41) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259 or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266 or consists of SEQ ID NO:266;

(42) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261 or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266 or consists of SEQ ID NO:266;

(43) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264 or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267 or consists of SEQ ID NO:267;

(44) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259 or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267 or consists of SEQ ID NO:267;

(45) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261 or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid

sequence as shown in SEQ ID NO:267 or consists of SEQ ID NO:267;

(46) The heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264 or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262 or consists of SEQ ID NO:262.

In some embodiments, the above-described antibody or antigen-binding fragment thereof further comprises a heavy constant region or variant thereof and a light chain constant region or variant thereof from a human antibody germline consensus sequence, wherein the variant has one or more amino acid substitutions, deletions, or additions (e.g., substitutions, deletions, or additions of up to 20, up to 15, up to 10, or up to 5 amino acids; e.g., substitutions, deletions, or additions of 1, 2, 3, 4, or 5 amino acids) as compared to the wild-type sequence from which it was derived. In some embodiments, the heavy chain constant region is an IgG heavy chain constant region, e.g., an IgG1, IgG2, IgG3, or IgG4 heavy chain constant region; the light chain constant region is selected from a kappa or lambda light chain constant region. In another embodiment, the heavy chain constant region comprises the sequence as shown in SEQ ID NO:223, or consists of the sequence. In one embodiment, the light chain constant region comprises the sequence as shown in SEQ ID NO:224, or consists of the sequence.

It will be appreciated that sequence variants of these constant region domains may also be used, for example containing one or more amino acid modifications, wherein amino acid positions are identified according to the EU index system of Kabat et al. (1991).

As a specific embodiment, the heavy chain variable region (VH) and/or the light chain variable region (VL) are defined by the Kabat numbering system.

As a specific embodiment, the heavy chain variable region (VH) and/or the light chain variable region (VL) are defined by the AbM numbering system.

In one embodiment, the invention provides anti-MUC17 antibodies and antigen-binding fragments thereof that specifically bind MUC17, comprising a heavy chain and a light chain, wherein:

(1) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:9, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:9, or consists of SEQ ID NO:9; the light chain comprises an amino acid sequence as shown in SEQ ID NO:10, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:10, or consists of SEQ ID NO:10;

(2) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:19, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:19, or consists of SEQ ID NO:19; the light chain comprises the amino acid sequence as shown in SEQ ID NO:20, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:20, or consists of SEQ ID NO:20;

(3) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:26, or an amino

acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:26, or consists of SEQ ID NO:26; the light chain comprises the amino acid sequence as shown in SEQ ID NO:27, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:27, or consists of SEQ ID NO:27;

(4) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:26, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:26, or consists of SEQ ID NO:26; the light chain comprises the amino acid sequence as shown in SEQ ID NO:32, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:32, or consists of SEQ ID NO:32;

(5) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:36, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:36, or consists of SEQ ID NO:36; the light chain comprises the amino acid sequence as shown in SEQ ID NO:37, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:37, or consists of SEQ ID NO:37;

(6) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:42, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:42, or consists of SEQ ID NO:42; the light chain comprises the amino acid sequence as shown in SEQ ID NO:43, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:43, or consists of SEQ ID NO:43;

(7) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:49, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:49, or consists of SEQ ID NO:49; the light chain comprises the amino acid sequence as shown in SEQ ID NO:50, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:50, or consists of SEQ ID NO:50;

(8) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:49, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:49, or consists of SEQ ID NO:49; the light chain comprises the amino acid sequence as shown in SEQ ID NO:54, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:54, or consists of SEQ ID NO:54;

(9) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:61, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:61, or consists of SEQ ID NO:61; the light chain comprises the amino acid sequence as shown in SEQ ID NO:62, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:62, or consists of SEQ ID NO:62;

(10) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:71, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:71, or consists of SEQ ID NO:71; the light chain comprises the amino acid sequence as shown in SEQ ID NO:72, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:72, or consists of SEQ ID NO:72;

(11) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:79, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:79, or consists of SEQ ID NO:79; the light chain comprises the amino acid sequence as shown in SEQ ID NO:80, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:80, or consists of SEQ ID NO:80;

(12) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:89, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:89, or consists of SEQ ID NO:89; the light chain comprises the amino acid sequence as shown in SEQ ID NO:90, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:90, or consists of SEQ ID NO:90;

(13) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:99, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:99, or consists of SEQ ID NO:99; the light chain comprises the amino acid sequence as shown in SEQ ID NO:100, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:100, or consists of SEQ ID NO:100;

(14) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:106, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:106, or consists of SEQ ID NO:106; the light chain comprises the amino acid sequence as shown in SEQ ID NO:107, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:107, or consists of SEQ ID NO:107;

(15) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:116, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:116, or consists of SEQ ID NO:116; the light chain comprises the amino acid sequence as shown in SEQ ID NO:117, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:117, or consists of SEQ ID NO:117;

(16) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:116, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:116, or consists of SEQ ID NO:116; the light chain comprises the amino acid sequence as shown in SEQ ID NO:120, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of

SEQ ID NO:120, or consists of SEQ ID NO:120;

(17) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:127, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:127, or consists of SEQ ID NO:127; the light chain comprises the amino acid sequence as shown in SEQ ID NO:128, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:128, or consists of SEQ ID NO:128;

(18) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:137, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:137, or consists of SEQ ID NO:137; the light chain comprises the amino acid sequence as shown in SEQ ID NO:138, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:138, or consists of SEQ ID NO:138;

(19) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:141, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:141, or consists of SEQ ID NO:141; the light chain comprises the amino acid sequence as shown in SEQ ID NO:142, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:142, or consists of SEQ ID NO:142;

(20) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:151, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:151, or consists of SEQ ID NO:151; the light chain comprises the amino acid sequence as shown in SEQ ID NO:152, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:152, or consists of SEQ ID NO:152;

(21) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:160, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:160, or consists of SEQ ID NO:160; the light chain comprises the amino acid sequence as shown in SEQ ID NO:161, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:161, or consists of SEQ ID NO:161;

(22) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:169, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:169, or consists of SEQ ID NO:169; the light chain comprises the amino acid sequence as shown in SEQ ID NO:170, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:170, or consists of SEQ ID NO:170;

(23) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:174, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:174, or consists of SEQ ID NO:174; the light chain comprises the amino acid sequence as shown in SEQ ID NO:175, or an amino acid sequence having at

least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:175, or consists of SEQ ID NO:175;

(24) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:181, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:181, or consists of SEQ ID NO:181; the light chain comprises the amino acid sequence as shown in SEQ ID NO:182, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:182, or consists of SEQ ID NO:182;

(25) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:191, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:191, or consists of SEQ ID NO:191; the light chain comprises the amino acid sequence as shown in SEQ ID NO:192, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:192, or consists of SEQ ID NO:192;

(26) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:200, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:200, or consists of SEQ ID NO:200; the light chain comprises the amino acid sequence as shown in SEQ ID NO:201, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:201, or consists of SEQ ID NO:201;

(27) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:206, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:206, or consists of SEQ ID NO:206; the light chain comprises the amino acid sequence as shown in SEQ ID NO:207, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:207, or consists of SEQ ID NO:207;

(28) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:216, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:216, or consists of SEQ ID NO:216; the light chain comprises the amino acid sequence as shown in SEQ ID NO:217, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to the amino acid sequence of SEQ ID NO:217, or consists of SEQ ID NO:217.

In an embodiment of any one of the preceding antibodies, the antibody is a monoclonal antibody.

In an embodiment of any one of the preceding antibodies, the antibody is a full length antibody.

In some embodiments, the antibody or antigen binding fragment of the invention is a murine antibody, a chimeric antibody, a humanized antibody, or a fully human antibody.

In some embodiments, the anti-MUC17 antibodies of the invention are whole antibodies, e.g., IgG1, IgG2, IgG3, IgG4 antibodies.

In another embodiment, the anti-MUC17 antibodies of the invention encompass only antigen

binding portions thereof, such as: Fab, Fab'-SH, Fv, scFv or $(Fab')_2$ fragments.

In another aspect, the invention provides an isolated polynucleotide molecule encoding any of the MUC17 antibodies or antigen-binding fragments thereof described herein.

In another aspect, the invention provides an expression vector comprising a nucleotide molecule of the invention. In one embodiment, the vector is a eukaryotic expression vector.

In another aspect, the invention provides a host cell comprising an expression vector or nucleotide molecule described in the present invention. In some embodiments, the host cell is prokaryotic, such as E. coli. In other embodiments, the host cell is eukaryotic, such as a 293 cell, CHO cell, yeast cell, or plant cell.

Further, the present invention provides a pharmaceutical composition comprising the anti-MUC17 antibody or antigen-binding fragment thereof described in the present invention, or the polynucleotide molecule described in the present invention, or the expression vector described in the present invention, or the host cell described in the present invention, and a pharmaceutically acceptable carrier or excipient.

The invention provides a method of preparing an anti-MUC17 antibody or antigen-binding fragment thereof described herein, the method comprising expressing the antibody or antigen-binding fragment thereof in a host cell described herein under conditions suitable for expression of the antibody or antigen-binding fragment thereof, and recovering the expressed antibody or antigen-binding fragment thereof from the host cell or a culture medium containing the host cell.

The anti-MUC17 antibodies or antigen-binding fragments thereof or pharmaceutical compositions described in the present invention can also be administered in combination with one or more other therapies, e.g., therapeutic modalities and/or other therapeutic agents, for uses described herein, e.g., for the prevention and/or treatment of related diseases or disorders mentioned herein.

The invention also provides a pharmaceutical combination comprising an antibody or antigen-binding fragment thereof or a pharmaceutical composition as described herein, and one or more additional therapeutic agents.

The present invention provides a method for preventing or treating a MUC17-mediated disease in a subject in need thereof, comprising administering to the subject a prophylactically or therapeutically effective amount of an antibody or antigen-binding fragment thereof of the invention, a polynucleotide molecule described herein, an expression vector described herein, a host cell described herein, a pharmaceutical composition described herein, or a pharmaceutical combination described herein, wherein the disease or disorder is a MUC17-associated tumor and/or cancer, wherein the tumor and/or cancer is gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junction cancer, gastric cardiac cancer, gastric body cancer, gastric antrum cancer, liver cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, renal cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer, and rectal cancer.

The invention provides use of an antibody or antigen-binding fragment thereof as described herein, a polynucleotide molecule as described herein, an expression vector as described herein, a host cell as described herein, a pharmaceutical composition as described herein, or a pharmaceutical combination as described herein in the manufacture of a medicament for treating and/or preventing a disease or disorder mediated by MUC17. In one embodiment, the disease or disorder is a tumor and/or cancer associated with MUC17. In one embodiment, the disease or disorder is selected from the group consisting of gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junction cancer, gastric cardia cancer, gastric body cancer, gastric antrum cancer, liver cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, renal cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer, and rectal cancer.

In one embodiment, the present invention provides an antibody or antigen-binding fragment thereof as described herein, a polynucleotide molecule as described herein, an expression vector as described herein, a host cell as described herein, a pharmaceutical composition as described herein, or a pharmaceutical combination as described herein for use as a medicament.

In one embodiment, the present invention provides an antibody or antigen-binding fragment thereof as described herein, a polynucleotide molecule as described herein, an expression vector as described herein, a host cell as described herein, a pharmaceutical composition as described herein, or a pharmaceutical combination as described herein for use in treatment.

In one embodiment, the present invention provides an antibody or antigen-binding fragment thereof as described herein, a polynucleotide molecule as described herein, an expression vector as described herein, a host cell as described herein, a pharmaceutical composition as described herein, or a pharmaceutical combination as described herein for use in treating MUC17-associated tumors and/or cancers. In one embodiment, the MUC17-associated tumor and/or cancer is selected from the group consisting of gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junction cancer, gastric cardia cancer, gastric body cancer, gastric antrum cancer, liver cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, renal cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer and rectal cancer.

The invention also provides a kit comprising the anti-MUC17 antibody or antigen-binding fragment thereof of the invention, the polynucleotide molecule described in the invention, the expression vector described in the invention, the host cell described in the invention, the pharmaceutical composition described in the invention or the pharmaceutical combination described in the invention, and instructions for use. The kit may also comprise a suitable container. In certain embodiments, the kit further comprises a device for administering the drug. The kit generally includes a label indicating the intended use and/or method of use of the kit contents. The term "label" includes any written or recorded material provided on or with the kit or otherwise provided with the kit.

The invention provides a method of detecting the presence of MUC17 in a sample using an

antibody or antigen-binding fragment thereof of the invention or a detection composition comprising the antibody or antigen-binding fragment thereof.

The invention provides a method for detecting MUC17, wherein a sample to be detected is contacted with the antibody or the antigen-binding fragment thereof described in the invention under the condition that a complex can be formed between the antibody or the antigen-binding fragment thereof and MUC17.

In some embodiments, the antibodies or antigen binding fragments thereof described in the invention are linked to a detectable label.

In some embodiments, the detectable label is selected from the group consisting of an enzyme (e.g., horseradish peroxidase or alkaline phosphatase), a chemiluminescent reagent (e.g., acridinium ester compounds, luminol and its derivatives, or ruthenium derivatives), a fluorescent dye (e.g., fluorescein or fluorescent protein), a radionuclide or biotin.

In some embodiments, the method of detecting MUC17 further comprises: after the sample to be tested is contacted with the antibody or antigen-binding fragment of the present invention, another reagent (e.g., a second antibody) is used to specifically recognize the antibody or antigen-binding fragment thereof of the present invention. In some embodiments, the additional agent (e.g., a second antibody) further comprises a detectable label, such as an enzyme (e.g., horseradish peroxidase or alkaline phosphatase), a chemiluminescent agent (e.g., acridinium ester compounds, luminol and its derivatives, or ruthenium derivatives), a fluorescent dye (e.g., fluorescein or fluorescent protein), a radionuclide or biotin.

The invention provides a kit comprising the antibody or antigen-binding fragment thereof, an expression vector, a host cell, a polynucleotide fragment, or a pharmaceutical composition.

The invention provides a detection system comprising an antibody or antigen-binding fragment thereof according to the invention. The invention also provides the use of the detection system in a diagnostic method.

In some embodiments, in the detection system, the antibody or antigen-binding fragment thereof of the present invention is free or binds to an antigen (e.g., an antigen present in a sample to be tested) to form a complex. Thus, in some embodiments, the detection system further comprises a complex of an antibody or antigen-binding fragment thereof of the present invention bound to an antigen.

In some embodiments, the antibodies or antigen binding fragments thereof described in the invention are linked to a detectable label.

In some embodiments, the detectable label is selected from the group consisting of an enzyme (e.g., horseradish peroxidase or alkaline phosphatase), a chemiluminescent reagent (e.g., acridinium ester compounds, luminol and its derivatives, or ruthenium derivatives), a fluorescent dye (e.g., fluorescein or fluorescent protein), a radionuclide or biotin.

In some embodiments, the detection system further comprises an additional agent (e.g., a second antibody) that specifically recognizes the antibody or antigen-binding fragment thereof of the

invention. In some embodiments, the additional agent (e.g., a second antibody) further comprises a detectable label, such as an enzyme (e.g., horseradish peroxidase or alkaline phosphatase), a chemiluminescent agent (e.g., acridinium ester compounds, luminol and its derivatives, or ruthenium derivatives), a fluorescent dye (e.g., fluorescein or fluorescent protein), a radionuclide or biotin.

The invention provides a method of detecting tumor growth comprising using an antibody or antigen-binding fragment thereof of the invention to determine the amount of MUC17 expression in a sample from a patient suspected of having cancer and optionally a negative control sample and further optionally a positive control sample.

The method for detecting the tumor growth comprises: determining the amount of MUC17 expression in a sample from a patient suspected of having cancer and a negative control sample, further comprising comparing the amount of MUC17 expression between the samples, optionally wherein the amount of expression in the negative control and/or the positive control can be derived from stored data in at least one negative control sample and/or at least one positive control sample obtained in a method of detecting tumor growth, the method comprising determining the amount of MUC17 expression, further optionally wherein the amount of expression in the negative control sample and/or the positive control sample can be derived from stored data comprising the average amount of expression of more than one negative control sample and/or more than one positive control sample obtained in a method of detecting tumor growth, the method comprising determining the amount of MUC17 expression.

The sample and the control in the detecting method of the invention can be a positive expression cell, a solid tissue sample or a liquid tissue sample.

The present invention provides a method for detecting and/or quantifying MUC17 in a sample, comprising (a) using an antibody according to any one of preceding embodiments or produced according to any one of preceding embodiments, or using the detection system described above, for determining the amount of MUC17 expression in a sample; and; (b) comparing the expression level of MUC17 determined in step (a) to: (i) a predefined value for the amount of MUC17 expression, (ii) the amount of MUC17 expression determined in a control sample, or (iii) the amount of MUC17 expression determined in a sample obtained from the same source or subject at a previous time point.

The antibody or antigen binding fragment thereof targeting human MUC17 provided by the invention has the following advantages:

(1) binding target cells expressing human MUC17 with high affinity in the range of 10-100nM, more preferably 0-10nM; having cross binding activity with monkey antigen;

(2) capable of entering cells through endocytosis to kill target cells; in some embodiments, the antibodies of the invention have high endocytic efficiency;

(3) treating, preventing, ameliorating a disorder (e.g., cancer) associated with MUC17 in a subject, or treating, preventing, ameliorating one or more symptoms of the disease;

(4) reducing or inhibiting tumor growth or progression in a subject;

(5) induces MUC17-associated tumor regression (e.g., long-term regression);

(6) exert cytotoxic activity in MUC17-associated cells;

In another aspect of the present invention, the present invention provides an anti-MUC17 antibody-drug conjugate of formula (I), an isomer thereof, a pharmaceutical acceptable salt thereof, or a mixture thereof:

Ab-(L-D)m [Formula (I)]

wherein,

L is a linker unit;

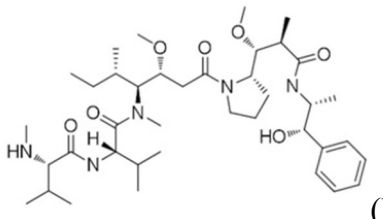
D is a cytotoxic small molecule drug;

m is an average number of L-D units conjugated to Ab, and m is selected from 1 to 10, preferably 2 to 8;

Ab is an anti-MUC17 antibody or an antigen-binding fragment thereof, preferably the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

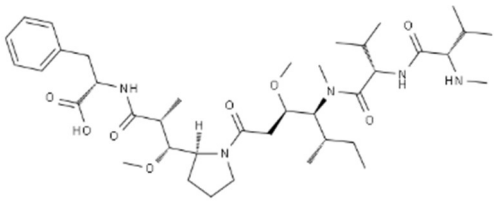
In some embodiments, the small molecule drug D of the present invention is a monomethyl auristatins, camptothecins or mertansine alkaloids.

In some embodiments, the monomethyl auristatins may be monomethyl auristatin E (MMAE)



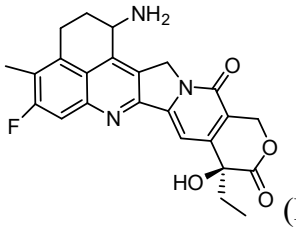
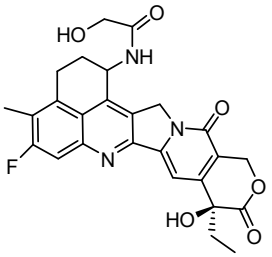
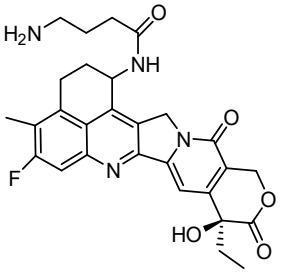
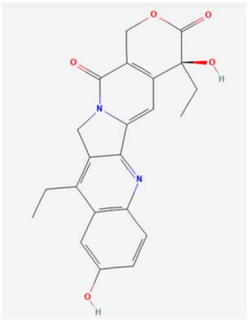
(MMAE)

or monomethyl auristatin F (MMAF)



(MMAF).

In some embodiments, the mertansine alkaloids may be DM1, DM3 or DM4.

In some embodiments, the camptothecins may be  (Exatecan),  (Dxd(1)),  (Dxd(2) or  (SN-38).

In some embodiments, the antibody-drug conjugate of the present invention comprises multiple D components, said multiple D components may be a combination of different therapeutic active substances or pharmaceutical active ingredients, or a combination of same therapeutic active substances or pharmaceutical active ingredients.

In some embodiments, the antibody-drug conjugate of the present invention has a drug/antibody ratio (DAR) of 1-15, for example a DAR of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

In some embodiments, the DAR is an average DAR.

In some embodiments, the average DAR is 1 to 15, for example 1 to 10.

As a specific embodiment, the average DAR of the antibody-drug conjugate of the present invention is preferably 2 to 10, for example 2 to 8.

As a specific embodiment, when D is a camptothecins, the average DAR of the antibody-drug conjugate of the present invention is preferably 4 to 8.

In some embodiments, a cytotoxin is covalently linked to an anti-MUC17 antibody or an antigen-binding fragment thereof via a linker in a non-site-specific or site-specific manner.

The “linker”, “linker unit” and “connnector” used in the present invention can be used interchangeably.

The “drug-containing linker” as used in the present invention refers to a compound obtained from direct or indirect covalent bonding of a drug, for example the cytotoxic small molecule drug as described in D, with a linker.

In some embodiments, said L is a combination of one or more L’.

In some embodiments, said L’ is selected from carbonyl, amino, amido, aminoacyl, -$(PEG)_n$-, -$(CH_2)_n$-, -$(CH_2)_n$- comprising a hetreoatom, -(C≡C)-, -(CH=CH)-, -O-, -S-, maleimido (mc), maleimide propionyl (MP), methylsulfonyl pyrimidinyl, valine-citrulline (val-cit), valine-alanine (val-ala), N-succinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate (SMCC),

alanine-phenylalanine (ala-phe), phenylalanine-lysine (phe-lys), p-aminobenzyloxycarbonyl (PAB), dimethyl ethanediamine (DMED), N-succinimidyl 4-(2-pyridinylthio)pentanoate (SPP), N-succinimidyl 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (SMCC), N-succinimidyl (4-iodo-acetyl)aminobenzoate (SIAB), N-succinimidyl 4-(2-pyridinyldithio)butanoate (SPDB), N-succinimidyl 3-(pyridin-2-yldithio)-propionate (SPDP), glycine-glycine-phenylalanine-glycine (GGFG), acetyl-lysine-valine-citrulline-p-aminobenzyloxycarbonyl (AcLys-vc-PABC).

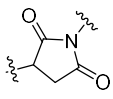
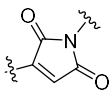
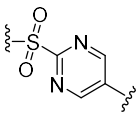
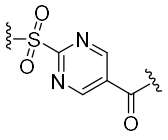
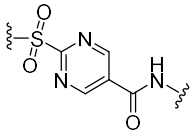
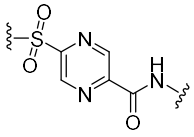
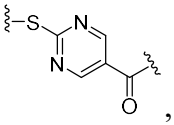
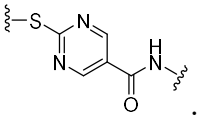
In some embodiments, n is independently selected from an integer of 1 to 20.

As a specific embodiment, when L' is selected from $(PEG)_n$, n is independently preferably 2, 4, 6 or 8.

As a specific embodiment, when L' is selected from $(CH_2)_n$, n is independently preferably an integer of 1 to 16.

As a specific embodiment, when L' is selected from $(CH_2)_n$ comprising a heteroatom, n is independently preferably an integer of 1 to 16; the heteroatoms is selected from N, O or S, the number of heteroatoms is independently preferably an integer of 1 to 8.

In some embodiments, said L may be J-L_1-L_2-X-L_3.

In some embodiments, said J is selected from , , , , , , , .

In some embodiments, L_1 is selected from a single bond, -$(PEG)_n$- or -$(CH_2)_n$-, said -$(CH_2)_n$- optionally comprises 1 to 6 heteroatoms selected from N, O, S; wherein n is independently selected from an integer of 1 to 20. Preferably, L_1 is selected from -$(PEG)_n$-, wherein n is independently 2, 4, 6 or 8.

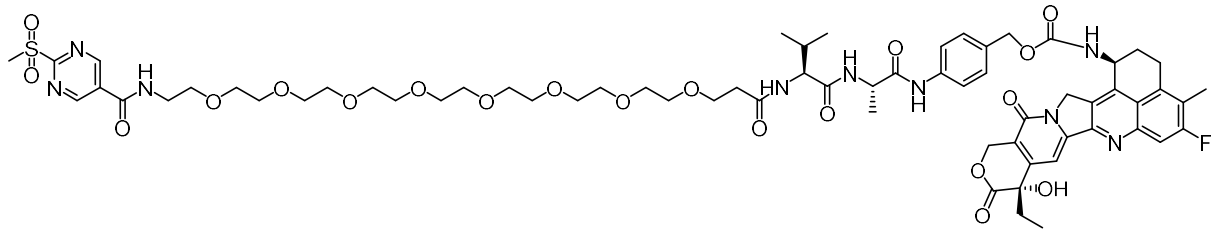
In some embodiments, L_2 is selected from a combination of one or more of a single bond, -O-, -S-, -CH_2-, -NH-, -C(O)-; wherein said -CH_2- and -NH- may be optionally substituted 1 to 3 times by $C_{1\sim6}$ alkyl or halogen.

In some embodiments, X is selected from a single bond or a combination of 1~4 X', said X' is independently selected from amino acid, for example glycine, alanine, phenylalanine, valine, lysine and citrulline. In some embodiments, X is selected from a single bond or valine-citrulline (val-cit), valine-alanine (val-ala), alanine-phenylalanine (ala-phe), phenylalanine-lysine (phe-lys), glycine-glycine-phenylalanine-glycine (GGFG).

In some embodiments, L_3 is selected from a combination of one or more of a single bond, -O-, -S-, -CH_2-, -NH-, -C(O)-, -phenyl-, -cyclopropyl-, -cyclobutyl-, -cyclohexyl-; wherein said -CH_2-, -NH-, -phenyl-, -cyclopropyl-, -cyclobutyl-, -cyclohexyl- may be optionally substituted 1 to 3 times

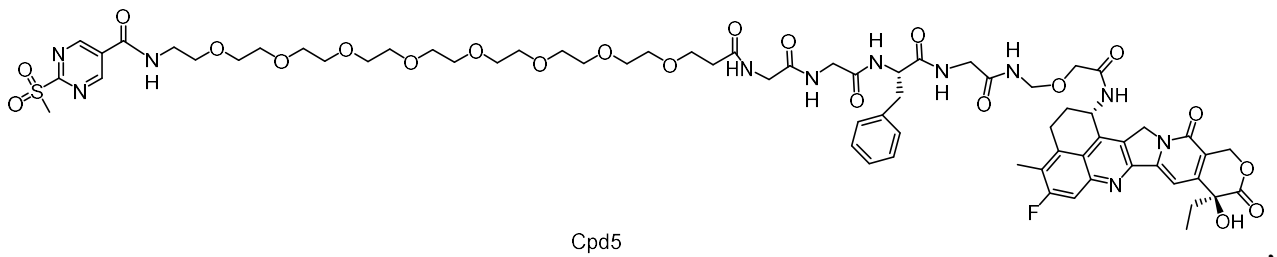
by $C_{1\sim6}$ alkyl, halogen, cyano or hydroxy.

Further, the present invention provides three linker unit-cytotoxic small molecule drugs of formula (L-D), as shown in Formula Cpd3, Formula Cpd5 and Formula Cpd6:



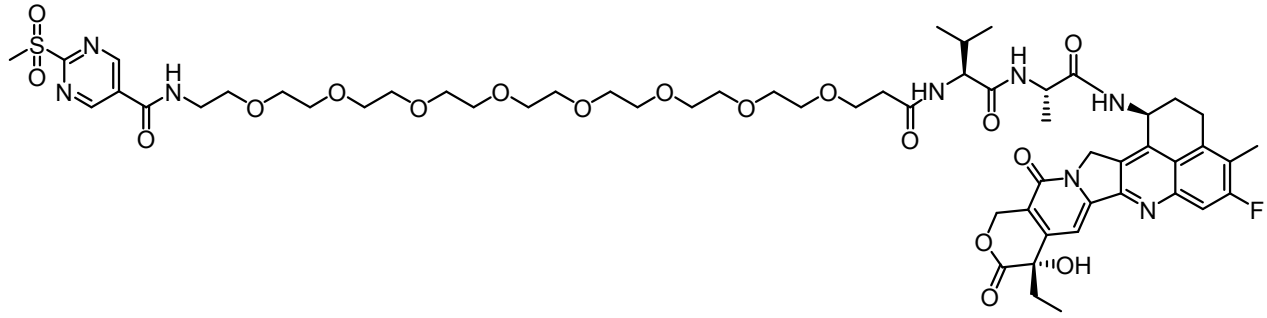
Cpd3

,



Cpd5

,

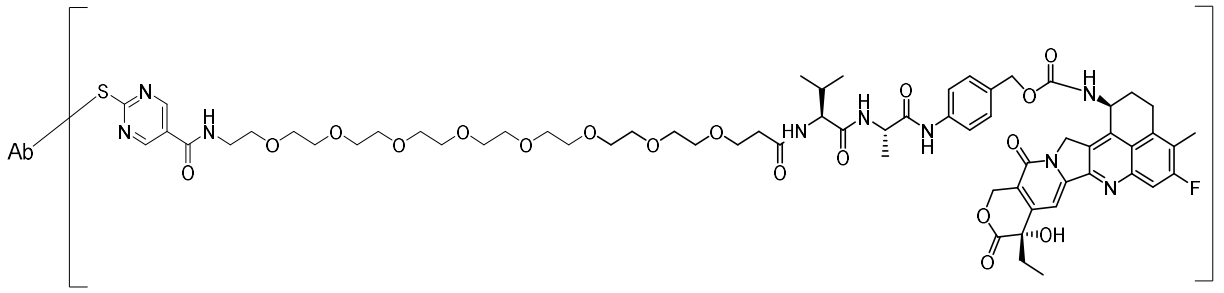


Cpd6

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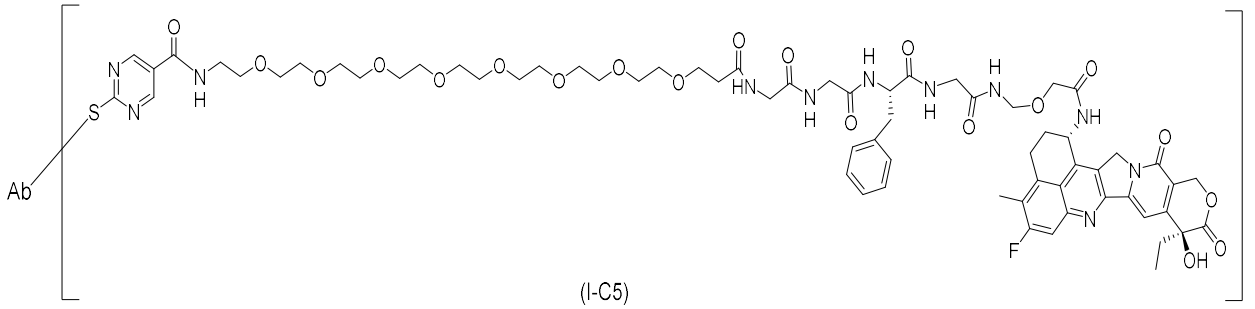
In some embodiments, the linker unit-cytotoxic small molecule drugs (linker-payload) as shown in Formula Cpd3, Formula Cpd5 and Formula Cpd6 provided in the present invention are suitable for conjugating with an antibody, for example an anti-MUC17 antibody or an antigen-binding fragment thereof, a Her2 antibody or an antigen-binding fragment thereof, and have high conjugating efficiency and mild reaction conditions. For example, as proved by the following examples, Cpd3, as a hydrophilic linker-payload may be used for preparing an ADC with a high DAR value (DAR of about 8) with excellent purity.

In some embodiments, the present invention provides an anti-MUC17 antibody-drug conjugate, an isomer thereof, a pharmaceutical acceptable salt thereof, or a mixture thereof, wherein the structure of the anti-MUC17 antibody-drug conjugate is as shown in Formula (I-C3), Formula (I-C5) and Formula (I-C6):



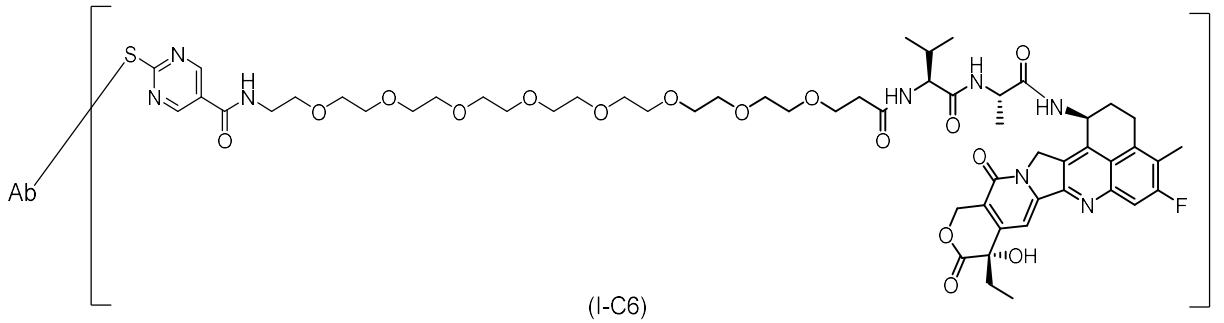
(I-C3)

,



(I-C5)

,



(I-C6)

;

wherein,

m is an average conjugation number, and m is independently selected from 1 to 10, for example 2 to 8, especially 4 to 8;

Ab is the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

In some embodiments, the Ab of the present invention comprises three heavy chain complementarity determining regions (HCDR), HCDR1, HCDR2 and HCDR3, which are heavy chain complementarity determining regions (HCDR) of the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

In some embodiments, Ab of the present invention comprises three light chain complementarity determining regions (LCDR), LCDR1, LCDR2 and LCDR3, which are light chain complementarity determining regions (LCDR) of the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

In some embodiments, Ab of the present invention comprises three heavy chain complementarity determining regions (HCDR) and three light chain complementarity determining

regions (LCDR), which are heavy chain complementarity determining regions (HCDR) and light chain complementarity determining regions (LCDR) of the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

In some embodiments, Ab comprises a heavy chain variable region (VH), which is the heavy chain variable region (VH) of the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

In some embodiments, the heavy chain variable region comprises three heavy chain complementarity determining regions (HCDR).

In some embodiments, Ab comprises a light chain variable region (VL), which is the light chain variable region (VL) of the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

In some embodiments, the light chain variable region comprises three heavy chain complementarity determining regions (LCDR).

In some embodiments, the heavy chain variable region (VH) and light chain variable regions (VL) of Ab are the heavy chain variable region (VH) and light chain variable region (VL) of the aforementioned anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention.

The present invention provides an antibody-drug conjugate targeting human MUC17, an isomer thereof, a pharmaceutical acceptable salt thereof, or a mixture thereof, the antibody-drug conjugate has the following advantages:

(1) binding to target cells expressing human MUC17 and having high affinity therefor, the affinity ranges from 10-100 nM, and preferably 0-10 nM; has cross-binding activity with monkey antigens;

(2) capable of entering cells through endocytosis to kill target cells; in some embodiments, the ADC of the present invention has high endocytosis efficiency;

(3) treating, preventing, and improving conditions associated with MUC17 (e.g., cancer) in a subject or treating, preventing, and improving one or more symptoms of the conditions;

(4) reducing or inhibiting the growth or progression of tumor (tumor associated with MUC17) in a subject;

(5) inducing the regression of MUC17-related tumor (e.g., long-term regression);

(6) exerting cytotoxic activity in MUC17-related cells;

(7) having bystander killing effect.

In another aspect, the present invention provides a use of the antibody-drug conjugate for (1) preparing a diagnostic reagent; and/or, (2) preparing a medicament for treating and/or preventing a disease or condition associated with MUC17.

In another aspect, the present invention provides a use of an active ingredient for (a) preparing a medicament for preventing and/or treating a disease or condition associated with MUC17; (b) a method for preventing and/or treating a disease mediated by MUC17; (c) preparing a detection reagent, detection plate or kit, wherein said active ingredient is selected from: the heavy chain variable region (VH) of the anti-MUC17 antibody or the antigen-binding fragment thereof of the present invention; and/or, the light chain variable region (VL) of the anti-MUC17 antibody or the antigen-binding fragment thereof as described herein; and/or, the heavy chain of the anti-MUC17 antibody or the antigen-binding fragment thereof as described herein; and/or, the light chain of the anti-MUC17 antibody or the antigen-binding fragment thereof as described herein; and/or, the antibody-drug conjugate targeting human MUC17, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof as described herein.

The present invention further provides a pharmaceutical composition comprising the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof as described herein, as well as a pharamaceutical acceptable carrier or excipient.

The present invention provides a pharmaceutical combination comprising the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, or the pharmaceutical composition as described herein, as well as one or more additional therapeutic agents.

The present invention provides a kit comprising the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, or the pharmaceutical composition as described herein.

The present invention provides a use of the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, or the pharmaceutical composition, or the pharmaceutical combination, or the kit as described herein in preparing a medicament for treating and/or preventing a disease or condition mediated by MUC17.

The present invention provides the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, or the pharmaceutical composition, or the pharmaceutical combination, or the kit as described herein, for use as a medicament.

The present invention provides the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, or the pharmaceutical composition, or the pharmaceutical combination, or the kit as described herein, for use in treatment.

The present invention provides the anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, or the pharmaceutical composition, or the pharmaceutical combination, or the kit as described herein, for treating tumor and/or cancer associated with MUC17.

In an embodiment, the tumor and/or cancer associated with MUC17 is selected from gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junctional carcinoma, gastric cardiac carcinoma, gastric body cancer, gastric antrum cancer, liver

cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, kidney cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer, and rectal cancer.

The present invention provides a method for treating and/or preventing a disease or condition mediated by MUC17, comprising administering the antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof or the pharmaceutical composition as described herein to a subject in need thereof.

In some embodiments, the disease or condition associated with MUC17 and/or mediated by MUC17 is cancer and/or tumor.

In some embodiments, the tumor and/or cancer associated with MUC17 is selected from gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junctional carcinoma, gastric cardiac carcinoma, gastric body cancer, gastric antrum cancer, liver cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, kidney cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer, and rectal cancer.

Further, the present invention provides a preparation method for the aforementioned antibody-drug conjugate targeting MUC17, the isomer thereof, the pharmaceutical acceptable salt thereof or the mixture thereof, which comprises: conjugating the antibody to the linke-payload compound under conditions sufficient to form an antibody-drug conjugate.

It should be understood that, within the scope of the present invention, each above-mentioned technical features of the present invention and each technical features specified below (such as Examples) can be combined with each other to constitute a novel or preferred technical solution. To save space, it will not be specified in detail herein.

Definition

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are within the technical scope of the art.

In order that the present invention may be more readily understood, certain technical and scientific terms are specifically defined as follows. Unless otherwise defined herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. For definitions and terminology in this field, the skilled person can refer in particular to Current protocol Molecular Biology (Ausubel). Abbreviations for amino acid residues are standard 3-letter and/or 1-letter codes used in the art to refer to one of the 20 commonly used L-amino acids. As used herein, including the claims, the singular forms "a", "an", and "the" include plural referents unless the context clearly dictates otherwise.

The term "about" when used in conjunction with a numerical value is intended to encompass the numerical value within a range having a lower limit that is 5% less than the stated numerical value and an upper limit that is 5% greater than the stated numerical value.

The term "and/or" should be understood to mean any one of the options or a combination of any two or more of the options.

The term "MUC17" refers to any recombinant or naturally occurring form of mucin 17(MUC17), variants or homologs thereof that maintain, e.g., at least 50%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or 100% of the activity of MUC17. The variant or homologue has at least 90%, 95%, 96%, 97%, 98%, 99% or 100% amino acid sequence identity to the naturally occurring FGFR2 protein in the complete sequence or in partial sequence (e.g., 50, 100, 150, or 200 contiguous amino acid portions).

The term "antibody" is used herein in the broadest sense and encompasses a variety of antibody constructs, including, but not limited to, monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments, so long as they exhibit the desired antigen-binding activity. A complete antibody will typically comprise at least two full length heavy chains and two full length light chains, but in some cases may comprise fewer chains, for example an antibody naturally occurring in a camel may comprise only heavy chains.

The term "antigen-binding molecule" is used in the broadest sense and refers to a molecule that specifically binds an antigen. Exemplary antigen binding molecules include, but are not limited to, antibodies or antibody mimetics. By "antibody mimetic" is meant an organic compound or binding domain that is capable of specific binding to an antigen, but is not structurally related to an antibody, and illustratively, antibody mimetics include, but are not limited to, affibody, affitin, affilin, designed ankyrin repeat protein (DARPin), nucleic acid aptamers, or Kunitz type domain peptides.

The term "anti-MUC17 antibody" refers to an antibody molecule that specifically binds MUC17, which is capable of inhibiting MUC17 activity. The anti-MUC17 antibody is capable of inhibiting MUC17 activity relative to the absence of MUC17 antibody, e.g., by at least partially or completely blocking stimulation by MUC17, reducing, preventing or delaying activation of MUC17, or inactivating, desensitizing or downregulating the signaling, activity or amount of MUC17. In some embodiments, the antibody may inhibit MUC17 activity by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or more compared to a control.

The term "MUC17-associated cancer and/or tumor", “MUC17- mediated cancer and/or tumor” or “a cancer and/or tumor associated with MUC17 aberrant expression” are used interchangeably, and refers to various tumors formed due to abnormal cell proliferation, invasion, metastasis and other malignant behaviors resulted by abnormal expression, mutation or dysfunction of MUC17 gene or protein, which is commonly found in gastrointestinal tract, pancreas, liver, gallbladder and other parts.

The term "antibody fragment" refers to a molecule distinct from an intact antibody, which comprises a portion of an intact antibody and is capable of binding to the antigen to which the intact antibody binds. Examples of antibody fragments include, but are not limited to, Fv, Fab, Fab', Fab'-SH, F(ab')2; a diabody; a linear antibody; single chain antibodies (e.g., scFv); a single domain antibody; a bivalent or bispecific antibody or fragment thereof; camelid antibodies (heavy chain antibodies); and

multispecific antibodies (e.g., bispecific antibodies) formed from antibody fragments.

The term "valency" denotes the presence of a defined number of binding sites in an antibody/antigen binding molecule. Thus, the terms "monovalent", "divalent", "tetravalent", and "hexavalent" denote the presence of one binding site, two binding sites, four binding sites, and six binding sites, respectively, in an antibody/antigen binding molecule.

The terms "antigen-binding fragment" and "antibody fragment" are used interchangeably herein and do not have the full structure of an intact antibody, and only encompass partial or variants thereof of an intact antibody that have the ability to bind antigen. "antigen-binding fragments" or "antibody fragments" herein include, but are not limited to, Fab, Fab', Fab'-SH, F (ab') 2 , Fd, Fv, scFv, diabodies, and single domain antibodies.

The term "Chimeric antibody" refers to an antibody in which a portion of the light chain or/and heavy chain is derived from one antibody (which may be derived from a particular species or belong to a particular antibody class or subclass) and another portion of the light chain or/and heavy chain is derived from another antibody (which may be derived from the same or different species or belong to the same or different antibody class or subclass), but which nevertheless retains binding activity to an antigen of interest. For example, the term "chimeric antibody" can include an antibody (e.g., a human-mouse chimeric antibody) in which the heavy and light chain variable regions of the antibody are from a first antibody (e.g., a mouse antibody) and the heavy and light chain constant regions of the antibody are from a second antibody (e.g., a human antibody).

The term "humanized antibody" refers to a non-human antibody that has been genetically engineered to have its amino acid sequence modified to increase homology to the sequence of a human antibody. Generally, all or part of the CDR regions of a humanized antibody are derived from a non-human antibody (donor antibody), and all or part of the non-CDR regions (e.g., variable region FRs and/or constant regions) are derived from a human immunoglobulin (acceptor antibody). Humanized antibodies typically retain or partially retain the desired properties of the donor antibody, including, but not limited to, antigen specificity, affinity, reactivity, the ability to increase the activity of immune cells, the ability to enhance an immune response, and the like.

The term "fully human antibody" refers to an antibody having variable regions in which both the FR and CDR are derived from human germline immunoglobulin sequences. Furthermore, if the antibody comprises a constant region, the constant region is also derived from a human germline immunoglobulin sequence. Fully human antibodies herein may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis in vitro or by somatic mutation in vivo). However, herein "fully human antibody" does not include antibodies in which CDR sequences derived from the germline of another mammalian species (e.g., a mouse) have been grafted onto human framework sequences.

The term "variable region" or "variable domain" refers to the domain of an antibody heavy or light chain that is involved in binding of the antibody to an antigen. The variable domains of the heavy and light chains of natural antibodies typically have similar structures, wherein each domain comprising four conserved Framework Regions (FRs) and three Complementarity Determining

Regions (CDRs) (see, e.g., Kindt et al., Kuby Immunology, 6th ed., W.H.Freeman and Co. page 91, (2007)). A single VH or VL domain is sufficient to confer antigen binding specificity.

The term "complementarity determining region" or "CDR" is a region of an antibody variable domain that is highly variable in sequence and forms structurally defined loops ("hypervariable loops") and/or contains antigen-contacting residues ("antigen-contacting points"). The CDRs are primarily responsible for binding to an antigenic epitope. The CDRs in the variable domain are commonly referred to as CDR1, CDR2 and CDR3, numbered sequentially from the N-terminus. The precise amino acid sequence boundaries of the CDRs within a given variable region amino acid sequence can be determined using any one or combination of a number of well-known antibody CDR assignment systems, including, for example: Chothia (Chothia et al., (1989) Nature 342: 877-883, Al-Lazikani et al., “Standard conformations for the canonical structures of immunoglobulins”, Journal of Molecular Biology, 273, 927-948(1997)), based on the three-dimensional structure of the antibody and the topology of the CDR loops, Kabat (Kabat et al., Sequences of Proteins of Immunological Interest, 4th Ed, U.S. Department of Health and Human Services, National instruments of Health (1987)), based on antibody sequence variability, AbM (University of Bath), Contact (University College London), the international ImMunoGeneTics database (IMGT) (http://imgt.cines.fr/), and the North CDR definition based on affinity propagation clustering using a large number of crystal structures.

It should be noted that the boundaries of the CDRs of the variable regions of the same antibody obtained based on different assignment systems may differ. That is, the CDR sequences of the same antibody variable region defined under different assignment systems are different. Thus, in reference to defining an antibody with a particular CDR sequence as defined herein, the scope of the antibody also encompasses antibodies whose variable region sequences comprise the particular CDR sequence, but whose claimed CDR boundaries differ from the particular CDR boundaries as defined herein due to the application of different schemes (e.g., different assignment systems or combinations).

Unless otherwise indicated, in the present invention, the term "CDR" or "CDR sequence" encompasses CDR sequences determined in any of the ways described above.

CDRs may also be determined based on having the same Kabat or AbM numbering position as a reference CDR sequence (e.g., any of the CDRs exemplified herein). In some embodiments, the CDRs of an antibody of the invention are positioned according to the Kabat or AbM numbering scheme.

Unless otherwise indicated, in the present invention, when referring to residue positions in antibody variable regions and CDRs (including heavy chain variable region residues), it refers to the numbered positions according to the Kabat or AbM numbering system.

As used herein, the term "comprising" or "comprises" is intended to mean that the stated element, integer or step is included, but not to the exclusion of any other element, integer or step. When the term "comprising" or " comprises " is used herein, unless otherwise indicated, it also encompasses the case where it consists of the stated elements, integers or steps. For example, when referring to an antibody variable region "comprising" a particular sequence, it is also intended to encompass antibody variable regions consisting of that particular sequence.

The term "Fc region" is used to define the C-terminal region of an immunoglobulin heavy chain

comprising at least a portion of a constant region. The term includes native sequence Fc regions and variant Fc regions. In some embodiments, the human IgG heavy chain Fc region extends from Cys226 or Pro230 to the carboxy-terminus of the heavy chain. However, the C-terminal lysine (Lys447) of the Fc region may or may not be present (numbering in this paragraph is according to the EU numbering system, also known as the EU index, e.g. Rabat et al., Sequences of Proteins of Immunological Interest,5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991).

The term "conserved amino acids" generally refers to amino acids that belong to the same class or have similar characteristics (e.g., charge, side chain size, hydrophobicity, hydrophilicity, backbone conformation, and rigidity).

The term "affinity" or "binding affinity" refers to the intrinsic binding affinity that reflects the interaction between members of a binding pair. The affinity of a molecule X for its partner Y can be generally represented by the equilibrium dissociation constant (KD), which is the ratio of the dissociation and association rate constants (kdis and kon, respectively). Affinity can be measured by common methods known in the art. One particular method for measuring affinity is the ForteBio kinetic binding assay herein.

The term " not binding" to a protein or cell means that it does not bind to the protein or cell, or does not bind to it with high affinity, that is, the KD for binding to the protein or cell is 1.0×10^{-6}M or higher, more preferably 1.0×10^{-5}M or higher, more preferably 1.0×10^{-4}M or higher, 1.0×10^{-3}M or higher, more preferably 1.0×10^{-2}M or higher.

The term "high affinity" for IgG antibodies means a KD for the antigen of 1.0×10^{-6}M or less, preferably 5.0×10^{-8}M or less, more preferably 1.0×10^{-8}M or less, 5.0×10^{-9}M or less, more preferably 1.0×10^{-9}M or less. For other antibody subtypes, "high affinity" binding may vary. For example, "high affinity" binding of an IgM subtype means a KD of 10^{-6}M or less, preferably 10^{-7}M or less, more preferably 10^{-8}M or less.

As used herein, the term "binding" or "specific binding" means that the binding is selective for the antigen and can be distinguished from unwanted or non-specific interactions. The ability of an antigen binding site to bind to a particular antigen can be determined by enzyme-linked immunosorbent assay (ELISA) or conventional binding assays known in the art such as by Radioimmunoassay (RIA) or biofilm thin layer interferometry or MSD assay or Surface Plasmon Resonance (SPR).

The term "median effective concentration (EC_{50})" refers to the concentration of a drug, antibody or toxin that induces a response that is 50% between baseline and maximum after a specified exposure time.

The term "therapeutic agent" encompasses any substance effective in preventing or treating tumors, such as cancer, including chemotherapeutic agents, cytokines, angiogenesis inhibitors, cytotoxic agents, other antibodies, small molecule drugs, or immunomodulatory agents (e.g., immunosuppressive agents).

The term "expression vector" refers to a nucleic acid molecule capable of amplifying another nucleic acid to which it is linked. The term includes vectors which are self-replicating nucleic acid

structures as well as vectors which integrate into the genome of a host cell into which the vector has been introduced. Certain vectors are capable of directing the expression of nucleic acids to which they are operably linked. Such vectors are referred to herein as "expression vectors".

The term "host cell" refers to a cell into which an exogenous nucleic acid has been introduced, including progeny of such a cell. Host cells include "transformants" and "transformed cells," which include primary transformed cells and progeny derived therefrom, regardless of the number of passages. Progeny may not be identical in nucleic acid content to the parent cell, but may contain mutations. Included herein are mutant progeny that have the same function or biological activity as screened or selected in the originally transformed cell.

The term "antibody drug conjugate" or "ADC" refers to an antibody or antibody fragment covalently conjugated to a therapeutically active substance or active pharmaceutical ingredient such that the therapeutically active substance or active pharmaceutical ingredient is targeted to the binding target of the antibody to exhibit its pharmacological function. The therapeutically active substance or active pharmaceutical ingredient may be a cytotoxin capable of killing a cell, preferably a cancer cell, targeted by the ADC. Covalent attachment of the therapeutically active substance, active pharmaceutical ingredient or cytotoxin can be performed in a non-site-specific manner using a linker, or in a site-specific manner.

The term "site-specific conjugation " refers to a means of attachment that specifically links a therapeutically active substance or active pharmaceutical ingredient to a specific site of an antibody. In some embodiments, the conjugation is accomplished via a linker.

The term "cytotoxic agent" is used interchangeably with "cytotoxin" and in the present invention refers to a substance that inhibits or disrupts cellular function and/or causes cell death or destruction.

The terms " linker ", " linker unit" are used interchangeably herein and refer to a chemical moiety that covalently links an antibody to a therapeutically active substance or active pharmaceutical ingredient in an ADC. In some embodiments, the linker may comprise amino acid residues that link the antigen to the payload. The amino acid residues may form dipeptide, tripeptide, tetrapeptide, pentapeptide, hexapeptide, heptapeptide, octapeptide, nonapeptide, decapeptide, undecapeptide or dodecapeptide units. Amino acid residues include those that occur naturally as well as non-naturally occurring amino acid analogs, such as citrulline or a beta-amino acid, such as beta-alanine, or an omega-amino acid such as 4-amino-butyric acid.

Depending on the nature classification, linkers suitable for use in the present invention may be cathepsin degradable linkers, such as valine-citrulline (val-cit) linkers, cBu-Cit linkers and CX linkers; a non-cleavable linker such as a SMCC linker or an MD linker; acid sensitive linkers, linkers of silicone structure, disulfide-carbamate linkers, MC-GGFG linkers, TRX linkers, galactoside containing linkers, pyrophosphate linkers, near-infrared-sensitive linkers, UV-sensitive linkers such as PC4AP.

The linker of the invention may also be a combination of one or more linkers, e.g., a cathepsin degradable linker may be combined with other types of linkers to form a new linker. Thus, the term "linker" as used herein encompasses a single type of linker, or a combination of different types of

linkers, as long as it is capable of conjugation the antibody of the invention to a drug.

The term "loading" or "drug loading" or "payload" refers to the average number of payloads per antibody within an ADC molecule (herein "payload" is used interchangeably with "therapeutically active substance or active pharmaceutical ingredient"). The drug load may range from 1 to 20 therapeutically active substances or active pharmaceutical ingredients per antibody. The term "drug/antibody ratio" or "DAR" refers to the ratio of therapeutically active substance or active pharmaceutical ingredient (D) conjugated to an antibody to the antibody. The ADCs described herein typically have a DAR of 1-20, and in certain embodiments 1-8, 2-8, 2-6, 2-5, 2-18, 4-16, 5-12, 6-10, 3-8, 4-6, 6-10, and 2-4. Representative DAR values are 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15, typically expressed as a combination of the letters D and a number, where the number represents the value of the DAR, e.g. D2 represents the drug/antibody ratio for a DAR value of 2. In some embodiments, the DAR is an average DAR, i.e., the total ratio of the small molecule drug moiety (D) coupled to the Ab moiety described herein to the Ab moiety in the product as characterized by a detection method (e.g., by conventional methods such as UV/visible spectroscopy, mass spectrometry, ELISA assay, and HPLC). The DAR may be limited by the number of attachment sites on the antibody. For example, in the case where the attachment site is a cysteine thiol, the antibody may have only one or a few cysteine thiol groups or may have only one or a few sufficiently reactive thiol groups (through which the linker unit can be attached).

The term "treating" refers to slowing, interrupting, arresting, relieving, stopping, reducing, or reversing the progression or severity of an existing symptom, disorder, condition, or disease. Desirable therapeutic effects include, but are not limited to, preventing the occurrence or recurrence of disease, alleviating symptoms, reducing any direct or indirect pathological consequences of the disease, preventing metastasis, reducing the rate of disease progression, improving or palliating the disease state, and alleviating or improving prognosis. In some embodiments, the antibodies of the invention are used to delay disease development or to slow the progression of disease.

The term "preventing" includes the inhibition of the onset or development of a disease or disorder or symptoms of a particular disease or disorder. In some embodiments, subjects with a family history of cancer are candidates for a prophylactic regimen. Generally, in the context of cancer, the term "preventing" refers to the administration of a drug prior to the onset of signs or symptoms of cancer, particularly in a subject at risk for cancer.

The term "effective amount" refers to an amount or dose of an antibody or conjugate or composition of the invention that produces the desired effect in a patient in need of treatment or prevention following administration to the patient in a single or multiple dose. An effective amount can be readily determined by the attending physician, as one skilled in the art, by considering a number of factors including: a species such as a mammal; body weight, age, and general health; the specific diseases involved; the degree or severity of the disease; the response of the individual patient; the specific antibody administered; a mode of administration; bioavailability characteristics of the administered formulation; a selected dosing regimen; and the use of any concomitant therapies.

The term "therapeutically effective amount" refers to an amount that is effective to achieve the desired therapeutic outcome at the desired dosage and for the desired period of time. A therapeutically

effective amount of an antibody or antibody fragment, or conjugate or composition thereof, may vary according to factors such as the disease state, the age, sex, and weight of the individual, and the ability of the antibody or antibody portion to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or deleterious effects of the antibody or antibody fragment or conjugate or composition thereof are less than the therapeutically beneficial effects. A "therapeutically effective amount" preferably inhibits a measurable parameter (e.g., tumor growth rate, tumor volume, etc.) by at least about 20%, more preferably by at least about 40%, even more preferably by at least about 50%, 60%, or 70%, and still more preferably by at least about 80% or 90%, relative to an untreated subject. The ability of a compound to inhibit a measurable parameter (e.g., cancer) can be evaluated in an animal model system predictive of efficacy in human tumors.

The term "prophylactically effective amount" refers to an amount effective to achieve the desired preventive result at the required dosage and for the required period of time. Typically, since a prophylactic dose is used in a subject prior to or at an earlier stage of disease, the prophylactically effective amount will be less than the therapeutically effective amount.

The term "pharmaceutical composition" refers to a composition that is present in a form that allows for the biological activity of the active ingredients contained therein to be effective, and that contains no additional ingredients that have unacceptable toxicity to the subject to which the composition is administered.

The term "in combination" refers to administration of one or more additional therapeutic agents including simultaneous (co-) administration and sequential administration in any order.

The term "pharmaceutically acceptable salt" refers to a salt of the drug conjugate of the present application. Such salts may be safe and/or effective when used in mammals and may have the required biological activity. The antibody drug conjugate of the present application may form a salt with an acid.

The term "pharmaceutically acceptable carrier" refers to an ingredient of a pharmaceutical formulation or composition other than an active ingredient that is not toxic to a subject.

The term "subject" includes any human or non-human animal. The term "non-human animal" includes all vertebrates, e.g., mammals and non-mammals, such as non-human primates, sheep, dogs, cats, horses, cattle, chickens, amphibians, reptiles, and the like.

Drawings

FIG. 1: Elisa detection of binding of the recombinant antibodies M1~M19 to huMucin17-His protein as described in Example 6.1.

FIG. 2 Elisa detection of binding of recombinant antibodies M20~M27 to huMucin17-His protein as described in Example 6.1.

FIG. 3: Cross-species (monkey) activity binding assay of candidate antibodies as described in example 7.

FIG. 4: Effect of candidate antibody drug conjugates as described in Example 12 on tumor

volume in animal models.

FIG. 5: Results of the antibody endocytosis assay as described in Example 9.

FIG. 6: Results of FACS binding activity of the humanized antibody as described in Example 13.

FIG. 7: Killing of the antibody drug conjugate M21-17-Cpd3 in tumor cells.

FIG. 8: Experimental results for the bystander killing effect of antibody drug conjugate M21-17-Cpd3.

FIG. 9: Results of antibody drug conjugates M21-17-Cpd3 on the inhibition of GSU tumor volume.

FIG. 10: Results of antibody drug conjugates M21-17-Cpd3 on the inhibition of NUGC4 tumor volume.

FIG. 11: Results of antibody drug conjugates M21-17-Cpd3 on the inhibition of SW480 tumor volume.

FIG. 12: SEC spectrum of antibody drug conjugate Trastuzumab-Cpd3.

FIG. 13: HIC spectrum of antibody drug conjugate Trastuzumab-Cpd3.

FIG. 14: RP spectrum of antibody drug conjugate Trastuzumab-Cpd3.

Detailed Description

The following examples further illustrate the present invention, however, it is to be understood that the examples are described by way of illustration and not limitation, and that various modifications may be made by those skilled in the art. The examples, in which specific conditions are not specified, were carried out according to conventional conditions or conditions recommended by the manufacturer. The reagents and instruments used without indicating the manufacturer are all conventional products which are commercially available.

In some embodiments, the invention provides a method of preparing an anti-MUC17 antibody, wherein the method comprises culturing a host cell comprising a nucleic acid encoding the anti-MUC17 antibody or an expression vector comprising the nucleic acid under conditions suitable for expression of the nucleic acid encoding the anti-MUC17 antibody, and optionally isolating the anti-MUC17 antibody. In a certain embodiment, the method further comprises recovering the anti-MUC17 antibody from the host cell (or host cell culture medium).

To recombinantly produce the anti-MUC17 antibodies of the invention, the nucleic acid encoding the anti-MUC17 antibodies of the invention is first isolated and inserted into a vector for further cloning and/or expression in a host cell. Such nucleic acids are readily isolated and sequenced using conventional procedures, e.g., by using oligonucleotide probes that are capable of binding specifically to nucleic acids encoding the anti-MUC17 antibodies of the invention.

The anti-MUC17 antibodies of the invention prepared as described herein can be purified by known prior art techniques such as high performance liquid chromatography, ion exchange chromatography, gel electrophoresis, affinity chromatography, size exclusion chromatography, and the like. The actual conditions used to purify a particular protein also depend on net charge, hydrophobicity, hydrophilicity, etc., and these will be apparent to those skilled in the art. The purity of the anti-MUC17 antibodies of the invention can be determined by any of a variety of well-known analytical methods, including size exclusion chromatography, gel electrophoresis, high performance liquid chromatography, and the like.

The prior art describes various methods for conjugation cytotoxic or other therapeutic agents to antibodies. For example, conjugation can occur in an antibody through the amino group of the lysine side chain and the amino group at the N-terminus of the antibody, aspartic acid, glutamic acid, and the carboxyl group at the C-terminus or activated cysteine thiol group.

The sequence of the DNA molecule of the antibody or fragment thereof of the present invention can be obtained by conventional techniques, such as by PCR amplification or genomic library screening. Alternatively, the coding sequences for the light and heavy chains may be fused together to form a single chain antibody.

Once the sequence of interest has been obtained, it can be obtained in large quantities by recombinant methods. This is usually done by cloning into a vector, transferring into cells, and isolating the sequence of interest from the propagated host cells by conventional methods.

In addition, synthetic methods can be used to synthesize the sequences of interest, especially when the sequence fragments are short in length. Generally, long fragments are obtained by first synthesizing a plurality of small fragments and then connecting them.

The practice of the present invention will employ, unless explicitly indicated to the contrary, conventional methods of chemistry, biochemistry, organic chemistry, molecular biology, microbiology, recombinant DNA techniques, genetics, immunology and cell biology, which are within the skill of the art.

The structures of the compounds disclosed herein can be confirmed by conventional methods well known to those skilled in the art. If the disclosure involves the absolute configuration of the compounds, the absolute configuration can be confirmed by conventional technical means in the art.

Compounds were named according to conventional naming principles in the art or using ChemDraw® software, and commercially available compounds were given the supplier catalog name. When the name of a compound is inconsistent with its structure, the structure of the compound shall prevail.

Example 1: Preparation and identification of raw material

1.1 Preparation and identification of Mucin17 control antibody

Preparation of Mucin17 control antibody: the application refers to the sequence disclosed in patent WO/2021/188851 to prepare anti-Mucin 17 antibody Tab1 as a positive control antibody.

Gene synthesis was performed by GenScript Biotechnology to construct an expression plasmid. The specific heavy chain and light chain sequences of Tab-1 are respectively shown in SEQ ID NO:218 and SEQ ID NO:219. Expi293F (Gibco) cells were transiently transfected, and after 6 days of culture, the supernatant was collected and purified using a Protein A affinity column (Cytiva).

Mucin17 control antibody identification: the activity of the prepared positive control antibody Tab-1 was measured using the commercially available Mucin17-His antigen protein (Acro Biosysterm, MU7-H52H3) as follows: Mucin17-His (0.5 μg/mL, 100 μL/well) was coated on a 96-well ELISA plate at 4 ℃ overnight for 16 hours; the plate was washed once and blocked with 1% BSA prepared in PBS for 1 hour; the plate was washed 3 times and control antibody Tab-1 diluted in gradients with PBS was added and incubated at room temperature for 1 hour; the plate was washed and a PBS-diluted secondary antibody Anti-Human IgG (H&L) (GOAT) Antibody Peroxidase Conjugated (Rockland, 609-103-123) was added for incubation at 37 ℃ for 1 hour. The plate was washed 3 times, TMB was added at room temperature (25 ℃) for 5-20 min, and data was read at OD450 with a microplate reader (Thermo Fisher (Shanghai) Instrument Co., Ltd., MultiskanFC) after termination of color development. The results showed that the expressed control antibody Tab-1 bound to Mucin17-His protein in a concentration gradient-dependent manner, with an EC_{50} of 3.545ng/ml, indicating that the control antibody had normal anti-Mucin17 activity.

Table 1: OD450 readings for Elisa binding detection of control antibody

Coating antigen 0.5μg/mL	Muc17-His
Primary antibody concentration (ng/mL)	Tab 1
1000.000	2.074
333.333	2.024
111.111	2.227
37.037	2.038
12.346	1.730
4.115	1.186
1.372	0.560
0.457	0.253
0.152	0.121
0.051	0.072
0.017	0.057
0.000	0.050
EC50 (ng/ml)	3.545

Wherein the sequences of the heavy chain and the light chain of Tab1 are shown as SEQ ID NO:218 and SEQ ID NO:219.

1.2 Preparation of Mucin17 Immune antigen

The Mucin 17 extracellular region (NP_001035194.1) was ligated to a mouse Fc fragment (SEQ

ID NO:220), plasmid construction was entrusted to HOEKBIO. Expi293F cells were transiently transfected and cultured for 6 days. The supernatant was collected, purified using Protein A affinity column. The eluate was collected and dialyzed at 2-8 ℃ for 16 hours to replace the eluate, and the antibody in the dialysis bag was collected and stored.

Antigen identification: Mucin17-Mouse FC (0.5 μg/mL, 100 μL /well) protein was coated on a 96-well ELISA plate, and the detection was performed using Tab 1 antibody, the specific method was performed as described in Example 1.1. The results show that expressed Mucin17-Mouse FC could be bound by Tab-1 in a concentration gradient-dependent manner, with an EC_{50} of 5.299 ng/ml.

Coating antigen 0.5μg/mL	Mucin17-Mouse FC
Primary antibody concentration (ng/mL)	Tab 1
1000.000	2.500
333.333	2.550
111.111	2.623
37.037	2.435
12.346	1.877
4.115	1.153
1.372	0.535
0.457	0.219
0.152	0.122
0.051	0.081
0.017	0.067
0.000	0.057
EC50 (ng/ml)	5.299

Example 2: Construction and identification of cell lines overexpressing human Mucin17 and monkey Mucin17

Construction of CHO-K1 (ECACC) cell line overexpressing human Mucin17 and monkey Mucin17 (hereinafter abbreviated as huMucin17-CHO K1; cynoMucin17-CHO K1): the coding nucleic acid sequences of the extracellular region fragments SEQ ID NO:221, 222 of human Mucin17 protein (NP_001035194.1) and monkey Mucin17 protein (XM_045389603.1) were constructed into a proprietary lentiviral vector (ProBio). Then, the lentiviral plasmid was transfected into HEK293T cells (Clontech, 632180) for virus packaging, and after 4 days of culture, the cell culture supernatant was collected. CHO-K1 cells were transfected with harvested lentiviral supernatants and Puromycin was used as the screening pressure. After 3 days of screening, the cell

pool was screened for antigen expression using flow cytometry. After obtaining the positive cell pool, the single cell clone selection is carried out on the positive cell pool by utilizing a limiting dilution method or a flow sorting method. After the single clone was selected, the cells were cultured for 1 week for identification of the antigen expression of the cell line.

FACS assay for antigen expression of cell line: the cells of the above cell line in the logarithmic growth phase were digested and plated in a 96-well plate, washed with FACS buffer (99% DPBS +1% FBS), added with primary antibody Tab 1 (10 ng/ml), and incubated at 4 ℃ for 60 min; after washing, the prepared fluorescent secondary antibody PE Goat anti-mouse IgG antibody (BioLegend, Cat. NO: 410708) was added and incubated at 4°C for 20 min; finally, detection was performed by flow cytometry (BD FACS Celesta). The detection results showed that huMucin17-CHO K1 and cynoMucin17-CHO K1 cell strains with high surface expression of human Mucin17 and monkey Mucin17 were obtained.

PE fluorescent signal (MFI)		
huMucin17-CHO K1	CHO-K1	fold change
14737	75.8	194.42
cynoMucin17-CHO K1	CHO-K1	fold change
48344	87.5	552.20

Example 3: animal immunization and hybridoma cell screening

3.1 immunization protocol

Use immunogens the Mucin17-His or Mucin17-Mouse Fc protein antigen obtained in Example 2; Mucin17 expressing plasmid-DNA antigen; Mucin17 overexpressing CHO-K1 cells, alone or in alternation, to immunize mice of different species (Balb/c, SJL, A/J). Mice were immunized by subcutaneous/intraperitoneal or gene gun injection once every two weeks for a total of 3-5 immunizations, depending on the type of selected antigen. One week after the last immunization, the blood of the mice is taken for the detection of the immunity titer, and finally, the antigens are used for boosting immunization once more.

3.2 Detection of serum antibody titers in mice after immunization

The antigen was diluted to 0.5μg/mL using coating liquid, uniformly mixed, and added to a designed ELISA plate, 100 μL/well, and placed in a refrigerator overnight for 16 h at 4 ℃. Discarding the coating solution, washing the plate once, and patting the plate to dry. Blocking solution (1% BSA in PBS solution) was added into wells 150μL each, and placed in a 37 ℃ incubator (Shanghai Yiheng Science Co., Ltd.) for 1 hour. Discarding the blocking solution and the mice serum were serially diluted then added to the well plate at 100 μL/well and incubated for 1 h at 37 ℃. Discarding the liquid and the plate was washed for 3 times and patted to dry. 100 μL of diluted enzyme-labeled secondary antibody was added to each well and incubated for 0.5 hour at

37 ℃. Discarding the liquid and the plate was washed for 3 times and patted to dry. 100 μL of developing solution was added to each well, and reacting for 15 minutes at 25 ℃. The reaction was stopped by adding 50 μL of 1M HCl each well, and the data was read at OD450nm using microplate reader (Thermo Fisher Scientific (Shanghai) Instrument Co., Ltd., Multiskan FC). Mice with an antibody titer greater than 512000 were selected for hybridoma fusion.

3.3 hybridoma cell fusion

A suspension of myeloma cells (SP2/0, cell bank of Chinese Academy of Sciences) was prepared, and the total amount of SP2/0 cells was counted using a hemocytometer. Spleen cell suspensions were prepared and counted using a hemocytometer to calculate the total cell mass. Myeloma cells and Spleen cells were mixed at a ratio of 1:2 for cell electrofusion. After cell fusion, HAT (Sigma) medium was used to mix the fused cells to form a cell suspension, and the cells were plated into a 96-well cell plate using a multi-channel pipette. The 96-well cell culture plate is placed in a 5.5% carbon dioxide incubator and cultured at a constant temperature of 37 ℃. After hybridoma cell culture, the supernatant was taken for parent clone screening, and the cell culture supernatant was screened for antigen binding ability at the protein and cell levels. For specific screening methods, see Examples 1 and 2.

3.4 hybridoma subclone selection

After the first round of parent clone screening, the screened parent clone cell strain is retained. Using a pipette to gently blow the cells in the wells to be subcloned and mix them. Taking out 20μl of the cell suspension and adding it to 20μl of trypan blue solution and mix it. Taking out 20μl and counting it with a hemacytometer. The cells were plated in a 96-well cell culture plate with 1×HT feeder cell replacement medium using the limiting dilution method. Marking the 96-well plate and place it in a CO_2 incubator. The 96-well plate after subcloning is placed in a 37°C, 5.5% carbon dioxide incubator for culture. After 7 days of culture, taking the supernatant for monoclonal screening. For specific screening methods, see Examples 1 and 2.

Through subclone screening, 28 antibodies were selected and sequenced, and the sequences of the antibodies are shown in TABLE 2 below. The CDR sequences were determined using Kabat scheme and AbM scheme to define the CDRs.

TABLE 2. Amino acid sequences of CDR regions of the 28 antibodies

Clone	CDR	SEQ ID	Sequence (Kabat coding)	SEQ ID	Sequence（AbM coding）
M1	HCDR1	SEQ ID NO:1	SYWMN	SEQ ID NO:225	GYAFSSYWMN
	HCDR2	SEQ ID NO:2	QIYPGDGDARYNG KFNG	SEQ ID NO:226	QIYPGDGDAR

	HCDR3	SEQ ID NO:3	SMGLGLDY	SEQ ID NO:3	SMGLGLDY
	LCDR1	SEQ ID NO:4	RSSQSLVHSNGNTYLH	SEQ ID NO:4	RSSQSLVHSNGNTYLH
	LCDR2	SEQ ID NO:5	KVSNRFS	SEQ ID NO:5	KVSNRFS
	LCDR3	SEQ ID NO:6	SQTTHVPPYT	SEQ ID NO:6	SQTTHVPPYT
M2	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:12	HIYWDDDKRYNPSLKS	SEQ ID NO:228	HIYWDDDKR
	HCDR3	SEQ ID NO:13	RAPYFDSPFAY	SEQ ID NO:13	RAPYFDSPFAY
	LCDR1	SEQ ID NO:14	KSSQSVLYSSNQKNYLA	SEQ ID NO:14	KSSQSVLYSSNQKNYLA
	LCDR2	SEQ ID NO:15	WASTRES	SEQ ID NO:15	WASTRES
	LCDR3	SEQ ID NO:16	HQYLSSLT	SEQ ID NO:16	HQYLSSLT
M3	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:12	HIYWDDDKRYNPSLKS	SEQ ID NO:228	HIYWDDDKR
	HCDR3	SEQ ID NO:21	TIPTVVFDY	SEQ ID NO:21	TIPTVVFDY
	LCDR1	SEQ ID NO:22	KSSQSLLYSSNQKNYLA	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2	SEQ ID NO:15	WASTRES	SEQ ID NO:15	WASTRES
	LCDR3	SEQ ID NO:23	QQYYSYRT	SEQ ID NO:23	QQYYSYRT
M4	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:12	HIYWDDDKRYNPSLKS	SEQ ID NO:228	HIYWDDDKR
	HCDR3	SEQ ID NO:21	TIPTVVFDY	SEQ ID NO:21	TIPTVVFDY
	LCDR1	SEQ ID NO:28	HASQVISSNIG	SEQ ID NO:28	HASQVISSNIG
	LCDR2	SEQ ID NO:29	HGTNLED	SEQ ID NO:29	HGTNLED
	LCDR3	SEQ ID NO:30	VRYAQFPWT	SEQ ID NO:30	VRYAQFPWT
M5	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:12	HIYWDDDKRYNPSLKS	SEQ ID NO:228	HIYWDDDKR
	HCDR3	SEQ ID NO:33	TTTTVVFDY	SEQ ID NO:33	TTTTVVFDY
	LCDR1	SEQ ID NO:22	KSSQSLLYSSNQKNYLA	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2	SEQ ID NO:15	WASTRES	SEQ ID NO:15	WASTRES
	LCDR3	SEQ ID NO:23	QQYYSYRT	SEQ ID NO:23	QQYYSYRT
M6	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:12	HIYWDDDKRYNPSLKS	SEQ ID NO:228	HIYWDDDKR
	HCDR3	SEQ ID NO:38	NYAGYFDY	SEQ ID NO:38	NYAGYFDY
	LCDR1	SEQ ID NO:22	KSSQSLLYSSNQKNYLA	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2	SEQ ID NO:39	WASTRDS	SEQ ID NO:39	WASTRDS
	LCDR3	SEQ ID NO:23	QQYYSYRT	SEQ ID NO:23	QQYYSYRT
M7	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS

	HCDR2	SEQ ID NO:44	HIYWDDDKHYNPSLKS	SEQ ID NO:229	HIYWDDDKH
	HCDR3	SEQ ID NO:45	TITTVVFDY	SEQ ID NO:45	TITTVVFDY
	LCDR1	SEQ ID NO:22	KSSQSLLYSSNQKNYLA	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2	SEQ ID NO:15	WASTRES	SEQ ID NO:15	WASTRES
	LCDR3	SEQ ID NO:46	LQYYSYRT	SEQ ID NO:46	LQYYSYRT
M8	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:44	HIYWDDDKHYNPSLKS	SEQ ID NO:229	HIYWDDDKH
	HCDR3	SEQ ID NO:45	TITTVVFDY	SEQ ID NO:45	TITTVVFDY
	LCDR1	SEQ ID NO:51	HASQDIRSNIG	SEQ ID NO:51	HASQDIRSNIG
	LCDR2	SEQ ID NO:29	HGTNLED	SEQ ID NO:29	HGTNLED
	LCDR3	SEQ ID NO:52	VQYAQFSWT	SEQ ID NO:52	VQYAQFSWT
M9	HCDR1	SEQ ID NO:11	TSGMGVS	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2	SEQ ID NO:12	HIYWDDDKRYNPSLKS	SEQ ID NO:228	HIYWDDDKR
	HCDR3	SEQ ID NO:55	MRIITTAFDY	SEQ ID NO:55	MRIITTAFDY
	LCDR1	SEQ ID NO:56	KASQDVSPAVA	SEQ ID NO:56	KASQDVSPAVA
	LCDR2	SEQ ID NO:57	SASYRYT	SEQ ID NO:57	SASYRYT
	LCDR3	SEQ ID NO:58	QQHYSTPFT	SEQ ID NO:58	QQHYSTPFT
M10	HCDR1	SEQ ID NO:63	TYGVH	SEQ ID NO:230	GFSLTTYGVH
	HCDR2	SEQ ID NO:64	VIWRGGSTDYNAAFMT	SEQ ID NO:231	VIWRGGSTD
	HCDR3	SEQ ID NO:65	AGTTEPPFAY	SEQ ID NO:65	AGTTEPPFAY
	LCDR1	SEQ ID NO:66	KSSQSLLYSRNQKNYLA	SEQ ID NO:66	KSSQSLLYSRNQKNYLA
	LCDR2	SEQ ID NO:67	WASTGES	SEQ ID NO:67	WASTGES
	LCDR3	SEQ ID NO:68	QQYYSYPYT	SEQ ID NO:68	QQYYSYPYT
M11	HCDR1	SEQ ID NO:1	SYWMN	SEQ ID NO:232	GYEFSSYWMN
	HCDR2	SEQ ID NO:73	QIYPG**DG**DTNY**N** **G**KFKG	SEQ ID NO:233	QIYPGDGDTN
	HCDR3	SEQ ID NO:74	SMSYSDY	SEQ ID NO:74	SMSYSDY
	LCDR1	SEQ ID NO:75	KSSQSLLYTTNQKNYLA	SEQ ID NO:75	KSSQSLLYTTNQKNYLA
	LCDR2	SEQ ID NO:15	WASTRES	SEQ ID NO:15	WASTRES
	LCDR3	SEQ ID NO:76	QQYSSYPRT	SEQ ID NO:76	QQYSSYPRT
M12	HCDR1	SEQ ID NO:81	SDYAWN	SEQ ID NO:234	GYSITSDYAWN
	HCDR2	SEQ ID NO:82	FISYSGGTIYNPSLKS	SEQ ID NO:235	FISYSGGTI
	HCDR3	SEQ ID NO:83	NNGYGFDY	SEQ ID NO:83	NNGYGFDY
	LCDR1	SEQ ID NO:84	SVSSSISYIH	SEQ ID NO:84	SVSSSISYIH

	LCDR2	SEQ ID NO:85	DTSKLTS	SEQ ID NO:85	DTSKLTS
	LCDR3	SEQ ID NO:86	QQWSTYPLT	SEQ ID NO:86	QQWSTYPLT
M13	HCDR1	SEQ ID NO:91	SYNMH	SEQ ID NO:236	GYTFSSYNMH
	HCDR2	SEQ ID NO:92	SIYPGNGDTSYNQKFKG	SEQ ID NO:237	SIYPGNGDTS
	HCDR3	SEQ ID NO:93	GDGYDRLDY	SEQ ID NO:93	GDGYDRLDY
	LCDR1	SEQ ID NO:94	RASQNVGTNVV	SEQ ID NO:94	RASQNVGTNVV
	LCDR2	SEQ ID NO:95	SASYRFS	SEQ ID NO:95	SASYRFS
	LCDR3	SEQ ID NO:96	QQYKSYPHT	SEQ ID NO:96	QQYKSYPHT
M14	HCDR1	SEQ ID NO:81	SDYAWN	SEQ ID NO:234	GYSITSDYAWN
	HCDR2	SEQ ID NO:101	YISYSGYTTYNPSLKS	SEQ ID NO:238	YISYSGYTT
	HCDR3	SEQ ID NO:83	NNGYGFDY	SEQ ID NO:83	NNGYGFDY
	LCDR1	SEQ ID NO:102	SASSSVSYMH	SEQ ID NO:102	SASSSVSYMH
	LCDR2	SEQ ID NO:103	DTSKLAS	SEQ ID NO:103	DTSKLAS
	LCDR3	SEQ ID NO:86	QQWSTYPLT	SEQ ID NO:86	QQWSTYPLT
M15	HCDR1	SEQ ID NO:108	SYAMS	SEQ ID NO:239	AFTFSSYAMS
	HCDR2	SEQ ID NO:109	SISSGGSTSYPDSVKG	SEQ ID NO:240	SISSGGSTS
	HCDR3	SEQ ID NO:110	GSPYWYFDV	SEQ ID NO:110	GSPYWYFDV
	LCDR1	SEQ ID NO:111	KASQNVGISVA	SEQ ID NO:111	KASQNVGISVA
	LCDR2	SEQ ID NO:112	SASYRYS	SEQ ID NO:112	SASYRYS
	LCDR3	SEQ ID NO:113	QQYNRYPT	SEQ ID NO:113	QQYNRYPT
M16	HCDR1	SEQ ID NO:108	SYAMS	SEQ ID NO:239	AFTFSSYAMS
	HCDR2	SEQ ID NO:109	SISSGGSTSYPDSVKG	SEQ ID NO:240	SISSGGSTS
	HCDR3	SEQ ID NO:110	GSPYWYFDV	SEQ ID NO:110	GSPYWYFDV
	LCDR1	SEQ ID NO:111	KASQNVGISVA	SEQ ID NO:111	KASQNVGISVA
	LCDR2	SEQ ID NO:112	SASYRYS	SEQ ID NO:112	SASYRYS
	LCDR3	SEQ ID NO:118	QQYNRDPT	SEQ ID NO:118	QQYNRDPT
M17	HCDR1	SEQ ID NO:121	SYNIH	SEQ ID NO:241	GYTFASYNIH
	HCDR2	SEQ ID NO:122	SIYPGNGDPSYNQKFKG	SEQ ID NO:242	SIYPGNGDPS
	HCDR3	SEQ ID NO:93	G**DG**YDRLDY	SEQ ID NO:93	GDGYDRLDY
	LCDR1	SEQ ID NO:123	KASQNVGTYVV	SEQ ID NO:123	KASQNVGTYVV
	LCDR2	SEQ ID NO:95	SASYRFS	SEQ ID NO:95	SASYRFS
	LCDR3	SEQ ID NO:124	HQYNNYPHT	SEQ ID NO:124	HQYNNYPHT
M18	HCDR1	SEQ ID NO:129	SYWVN	SEQ ID NO:243	GYTFTSYWVN
	HCDR2	SEQ ID NO:130	RIHPYDSETHYNQKFKD	SEQ ID NO:244	RIHPYDSETH
	HCDR3	SEQ ID NO:131	WTARAASAMDY	SEQ ID NO:131	WTARAASAMDY
	LCDR1	SEQ ID NO:132	SANSSVSYMY	SEQ ID NO:132	SANSSVSYMY

	LCDR2	SEQ ID NO:133	RTSNLAS	SEQ ID NO:133	RTSNLAS
	LCDR3	SEQ ID NO:134	QQYHSFPLT	SEQ ID NO:134	QQYHSFPLT
M19	HCDR1	SEQ ID NO:91	SYNMH	SEQ ID NO:236	GYTFSSYNMH
	HCDR2	SEQ ID NO:92	SIYPGNGDTSYNQKFKG	SEQ ID NO:237	SIYPGNGDTS
	HCDR3	SEQ ID NO:93	GDGYDRLDY	SEQ ID NO:93	GDGYDRLDY
	LCDR1	SEQ ID NO:139	KASQNVGTNVV	SEQ ID NO:139	KASQNVGTNVV
	LCDR2	SEQ ID NO:112	SASYRYS	SEQ ID NO:112	SASYRYS
	LCDR3	SEQ ID NO:96	QQYKSYPHT	SEQ ID NO:96	QQYKSYPHT
M20	HCDR1	SEQ ID NO:143	IYSVH	SEQ ID NO:245	GFSLSIYSVH
	HCDR2	SEQ ID NO:144	MIWSGGNTDYNSTLKS	SEQ ID NO:246	MIWSGGNTD
	HCDR3	SEQ ID NO:145	NWRNDTHLYYVMDY	SEQ ID NO:145	NWRNDTHLYYVMDY
	LCDR1	SEQ ID NO:146	HASQNINVWLN	SEQ ID NO:146	HASQNINVWLN
	LCDR2	SEQ ID NO:147	KTSTLHT	SEQ ID NO:147	KTSTLHT
	LCDR3	SEQ ID NO:148	QQGQSYPFT	SEQ ID NO:148	QQGQSYPFT
M21	HCDR1	SEQ ID NO:81	SDYAWN	SEQ ID NO:234	GYSITSDYAWN
	HCDR2	SEQ ID NO:153	YISYSGSTTYNPSLKS	SEQ ID NO:247	YISYSGSTT
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY	SEQ ID NO:154	WGTIYYRGYEGFAY
	LCDR1	SEQ ID NO:155	KASQSVNNDVA	SEQ ID NO:155	KASQSVNNDVA
	LCDR2	SEQ ID NO:156	YASNRFT	SEQ ID NO:156	YASNRFT
	LCDR3	SEQ ID NO:157	QQDYSSPWT	SEQ ID NO:157	QQDYSSPWT
M22	HCDR1	SEQ ID NO:162	RYSVH	SEQ ID NO:248	GFSLSRYSVH
	HCDR2	SEQ ID NO:163	MIWSGENTDYNSALKS	SEQ ID NO:249	MIWSGENTD
	HCDR3	SEQ ID NO:164	NWRNDTHLYYAMDY	SEQ ID NO:164	NWRNDTHLYYAMDY
	LCDR1	SEQ ID NO:146	HASQNINVWLN	SEQ ID NO:146	HASQNINVWLN
	LCDR2	SEQ ID NO:165	KSSNLHT	SEQ ID NO:165	KSSNLHT
	LCDR3	SEQ ID NO:166	QQGQGFPFT	SEQ ID NO:166	QQGQGFPFT
M23	HCDR1	SEQ ID NO:143	IYSVH	SEQ ID NO:245	GFSLSIYSVH
	HCDR2	SEQ ID NO:144	MIWSGGNTDYNSTLKS	SEQ ID NO:246	MIWSGGNTD
	HCDR3	SEQ ID NO:171	NWRNDTHLYYALDY	SEQ ID NO:171	NWRNDTHLYYALDY
	LCDR1	SEQ ID NO:146	HASQNINVWLN	SEQ ID NO:146	HASQNINVWLN
	LCDR2	SEQ ID NO:147	KTSTLHT	SEQ ID NO:147	KTSTLHT
	LCDR3	SEQ ID NO:148	QQGQSYPFT	SEQ ID NO:148	QQGQSYPFT
M24	HCDR1	SEQ ID NO:176	RYSIH	SEQ ID NO:250	GFSLSRYSIH

	HCDR2	SEQ ID NO:177	MIWGGGNTDYNSALKS	SEQ ID NO:251	MIWGGGNTD
	HCDR3	SEQ ID NO:164	NWRNDTHLYYAMDY	SEQ ID NO:164	NWRNDTHLYYAMDY
	LCDR1	SEQ ID NO:146	HASQNINVWLN	SEQ ID NO:146	HASQNINVWLN
	LCDR2	SEQ ID NO:178	KAANLHT	SEQ ID NO:178	KAANLHT
	LCDR3	SEQ ID NO:148	QQGQSYPFT	SEQ ID NO:148	QQGQSYPFT
M25	HCDR1	SEQ ID NO:183	SYWIQ	SEQ ID NO:252	GYTFTSYWIQ
	HCDR2	SEQ ID NO:184	AIYPGDGGTRYTQKFKG	SEQ ID NO:253	AIYPGDGGTR
	HCDR3	SEQ ID NO:185	LYSNYYIDS	SEQ ID NO:185	LYSNYYIDS
	LCDR1	SEQ ID NO:186	KASQDINSYLS	SEQ ID NO:186	KASQDINSYLS
	LCDR2	SEQ ID NO:187	RADRLVE	SEQ ID NO:187	RADRLVE
	LCDR3	SEQ ID NO:188	LQYDEFPNT	SEQ ID NO:188	LQYDEFPNT
M26	HCDR1	SEQ ID NO:193	SYGVH	SEQ ID NO:254	GFSLTSYGVH
	HCDR2	SEQ ID NO:194	VIWAGGRTIYNPALMS	SEQ ID NO:255	VIWAGGRTI
	HCDR3	SEQ ID NO:195	DLYGGAYGDY	SEQ ID NO:195	DLYGGAYGDY
	LCDR1	SEQ ID NO:196	KASQDVSTTVA	SEQ ID NO:196	KASQDVSTTVA
	LCDR2	SEQ ID NO:57	SASYRYT	SEQ ID NO:57	SASYRYT
	LCDR3	SEQ ID NO:197	QQHYRSPLT	SEQ ID NO:197	QQHYRSPLT
M27	HCDR1	SEQ ID NO:202	IYSIH	SEQ ID NO:256	GFSLSIYSIH
	HCDR2	SEQ ID NO:144	MIWSGGNTDYNSTLKS	SEQ ID NO:246	MIWSGGNTD
	HCDR3	SEQ ID NO:145	NWRNDTHLYYVMDY	SEQ ID NO:145	NWRNDTHLYYVMDY
	LCDR1	SEQ ID NO:146	HASQNINVWLN	SEQ ID NO:146	HASQNINVWLN
	LCDR2	SEQ ID NO:203	KTSTLHI	SEQ ID NO:203	KTSTLHI
	LCDR3	SEQ ID NO:148	QQGQSYPFT	SEQ ID NO:148	QQGQSYPFT
M28	HCDR1	SEQ ID NO:208	NYRMN	SEQ ID NO:257	GYTFTNYRMN
	HCDR2	SEQ ID NO:209	WINTYSGVPIYADDFKG	SEQ ID NO:258	WINTYSGVPI
	HCDR3	SEQ ID NO:210	TLYDGYSLYYVMDY	SEQ ID NO:210	TLYDGYSLYYVMDY
	LCDR1	SEQ ID NO:211	HASQNINGWLS	SEQ ID NO:211	HASQNINGWLS
	LCDR2	SEQ ID NO:212	KASNLHT	SEQ ID NO:212	KASNLHT
	LCDR3	SEQ ID NO:213	QQGQSHPLT	SEQ ID NO:213	QQGQSHPLT

Example 4: Construction, expression and purification of antibodies

4.1 Plasmid construction

The VH coding sequence of the 28 monoclonal Fab sequences was selected to be respectively

connected with the coding sequence for the heavy chain constant region of human IgG1 (SEQ ID NO:223) to obtain the heavy chain coding sequence for the human-mouse chimeric antibody, and the VL coding sequence of the Fab sequences was respectively connected to the coding sequence for the Kappa-type (SEQ ID NO:224) of the human light chain constant region (CL) to obtain the light chain coding sequence for the human-mouse chimeric antibody. The coding sequences for the antibody heavy and light chains were respectively inserted into a proprietary eukaryotic expression vector plasmid (PCDNA 3.4), transformed into E. coli DH5α, and cultured overnight at 37 ℃. Plasmid extraction was performed using an endotoxin-free plasmid extraction kit (GenScript Biotech) to obtain endotoxin-free antibody plasmid for eukaryotic expression.

4.2 expression and purification of antibodies

Antibody expression: the full-length antibody sequence obtained above was expressed by Expi293F transient expression system (Thermo Fisher, A14635) or ExpiCHO-S transient expression system (Thermo Fisher, A29133). For specific methods, refer to the corresponding kit operation instructions of the supplier.

Antibody purification: supernatants were collected and antibody affinity purification was performed using Protein A Magnetic Beads (GenScript Biotech). Protein A Magnetic Beads were added to the supernatant and incubated at room temperature for 2 hours. After incubation, Protein A Magnetic Beads were equilibrated with 10 column volumes of Binding buffer (PBS). The Protein A Magnetic Beads were eluted with an Elution buffer (0.1M Glycine, pH 2.5), the eluate was collected and pH adjusted by using Neutralizing buffer (0.1M Tris pH 9.0) at 1/10 volumes to neutral. After elution, Protein A Magnetic Beads were equilibrated with 10 column volumes of Binding buffer. The eluted and neutralized antibodies were placed in a dialysis bag and dialyzed with Dialysis buffer (PBS) for 2 hours at room temperature, then dialyzed with replaced Dialysis buffer for 16 hours at 2-8°C. The antibodies were transferred from the dialysis bag to a centrifuge tube and the volume was recorded.

Example 5: Detection of physicochemical properties of antibodies

In this example, the relative molecular weights and purities of the candidate antibodies were determined by SDS-PAGE and SEC-HPLC.

SDS-PAGE assay of antibodies

Preparation of non-reducing solution: 3 μg of each obtained antibody was respectively added to 2×SDS loading buffer, heated in a dry bath at 99 ℃ for 5 min, cooled to room temperature, and subjected to centrifugation at 12000 rpm for 5 min to obtain a supernatant.

Preparation of reducing solution: 3 μg of each obtained antibody was respectively added to 2×SDS loading buffer with 5 mM DTT, heated in a dry bath at 99 ℃ for 5 min, cooled to room

temperature, and subjected to instantaneous centrifugation. The supernatant was subjected to gel electrophoresis using Bis-tris 4-15% gradient gel (Genscript) and the protein bands were visualized by Coomassie blue staining.

Protein gels with developed protein bands (destained with destaining solution until the gel background was clear) were photographed using the Odyssey 9140 two-color infrared laser imaging system and the purity of the reduced and non-reduced bands was calculated by the own software.

The test results showed that the bands of the respective antibodies in the non-reduced gel were around 150 kD, the bands in the reduced gel were around 55 kD and around 25 kD, and the expected sizes were met, as reported in TABLE 3.

TABLE 3 Expression amount and physicochemical properties of candidate antibody

Clone ID	Volume of transfection (mL)	Total antibody amount (mg)	Antibody purity (SDS-PAGE)
M1	35	0.36	99%
M2	35	0.35	99%
M3	35	0.21	99%
M4	35	0.07	99%
M5	35	0.11	99%
M6	35	0.64	99%
M7	35	0.12	99%
M8	35	0.32	99%
M9	35	0.43	99%
M10	35	0.56	99%
M11	35	0.09	99%
M12	35	0.10	99%
M13	35	0.08	98%
M14	35	1.18	99%
M15	35	0.49	98%
M16	35	0.14	97%
M17	35	0.50	99%
M18	35	1.51	96%
M19	35	0.32	99%
M20	35	0.26	99%
M21	35	1.01	99%
M22	35	0.36	99%
M23	35	0.72	99%
M24	35	1.00	99%
M25	35	0.23	99%
M26	35	0.50	99%
M27	35	0.29	99%

Example 6: Detection of antigen binding activity of antibodies

In this example, the binding of the expressed antibody to human Mucin17 antigen protein huMucin17-His was detected based on the ELISA method, and the binding of the expressed antibody to cells huMucin17-CHO K1 overexpressing human Mucin17 was also detected based on the FACS method.

6.1 Detection of the binding capacity of antibodies to the antigen protein huMucin17-His based on ELISA

A 96-well ELISA plate was coated with 0.5 μg/mL of human Mucin17 antigen protein (30 μL /well) overnight at 4 ℃. The next day, the plate was washed 3 times with PBST and blocked with 5% skim milk for 2 h. After washing the plate 3 times with PBST, each antibody and positive control antibody Tab1 which were diluted in gradient (1ug/ml, 3-fold gradient dilution, 9 concentration points) were added and incubated for 1 h. After washing the plate 3 times with PBST, the secondary antibody Goat-anti-human Fc-HRP (Abcam, Ab97225) was added and incubated for 30 min. After incubation, the plate was washed 6 times with PBST and TMB was added for color development. The color was developed at 25°C for 15 min. 1M HCl was added to terminate the reaction, and the absorbance was read at OD450 using a microplate reader.

As shown in FIG. 1-2, all the antibodies obtained by the application have good binding capacity with the antigenic protein huMucin17.

6.2 Detection of the binding capacity of antibodies to huMucin17-CHO K1 cells based on FACS

In this example, the binding activity of the antibody was evaluated using human Mucin17 over-expressing cell huMucin17-CHO K1.

The specific method comprises: huMucin17-CHO K1 cells in the logarithmic growth phase were prepared into single cell suspensions with density adjusted to 2×10^6 cells/mL, added at 50 μL per well to a 96-well round bottom plate, centrifuged at 300 g at 4 ℃ to remove the supernatant. The detection antibody and the positive control antibody Tab 1 were respectively added into the corresponding wells, mixed well and incubated for 40 min at 4 ℃. Washing the incubated cell mixture for 3 times, adding 100 μL of diluted secondary antibody Goat F(ab')2 Anti-Human IgG-Fc, incubating for 30 min at 4 ℃ in a dark place, washing for 3 times, detecting by a flow cytometer, and reading a fluorescence intensity value (MFI).

The results are shown in TABLE 4, all tested antibodies had good binding ability to huMucin17-CHO K1 cells overexpressing antigens

TABLE 4 FACS detection of the binding of recombinant antibody and huMucin17-CHO K1 cells

Clone ID	Antibody concentration (nM)	CHO-K1 cells (MFI)	huMucin17-CHO K1 cells (MFI)	fold decrease of signal
M1	100 nM	120	20051	167.1
	10 nM	89.4	57344	641.4
	1 nM	90.1	14944	165.9
M2	100 nM	154	28346	184.1
	10 nM	94.6	57398	606.7
	1 nM	88.8	22943	258.4
M3	100 nM	120	9692	80.8
	10 nM	97.1	44351	456.8
	1 nM	93.2	25206	270.5
M5	100 nM	125	33611	268.9
	10 nM	94.9	43576	459.2
	1 nM	91.7	13916	151.8
M6	100 nM	113	29478	260.9
	10 nM	92.3	37243	403.5
	1 nM	90.6	11844	130.7
M7	100 nM	195	9569	49.1
	10 nM	102	24275	238
	1 nM	91	11159	122.6
M10	100 nM	131	14205	108.4
	10 nM	89.3	5518	61.8
	1 nM	90.3	1159	12.8
M11	100 nM	149	47318	317.6
	10 nM	96.9	77179	796.5
	1 nM	87.7	20242	230.8
M12	100 nM	151	24464	162
	10 nM	104	4325	41.6
	1 nM	89.6	835	9.3
M14	100 nM	97.4	41190	422.9
	10 nM	92.1	11781	127.9
	1 nM	85.4	1636	19.2
M15	100 nM	259	21198	81.8
	10 nM	109	28808	264.3
	1 nM	86.6	6220	71.8
M16	100 nM	457	27441	60
	10 nM	150	10438	69.6
	1 nM	87.7	2338	26.7
M18	100 nM	86.2	48351	560.9
	10 nM	83.9	147418	1757.1
	1 nM	78.1	16559	212
IgG1	100 nM	93.9	127	1.4

	10 nM	84.4	112	1.3
	1 nM	78	106	1.4
Tab1	100 nM	107	85537	799.4
	10 nM	89.3	75087	840.8
	1 nM	79.8	10063	126.1
PBS	NA	78	112	1.4
M20	50 nM	65.9	122449	1858.1
	5 nM	67.2	36452	542.4
	0.5 nM	62.5	4886	78.2
M21	50 nM	65.6	92608	1411.7
	5 nM	69	60937	883.1
	0.5 nM	66.6	4839	72.7
M22	50 nM	69.7	31058	445.6
	5 nM	70.9	31122	439
	0.5 nM	66.3	6934	104.6
M23	50 nM	73.3	102484	1398.1
	5 nM	74.3	66979	901.5
	0.5 nM	67.8	5684	83.8
M24	50 nM	77	123262	1600.8
	5 nM	75.1	17344	230.9
	0.5 nM	69	4888	70.8
M25	50 nM	76	59188	778.8
	5 nM	72.2	26154	362.2
	0.5 nM	69.7	7285	104.5
M26	50 nM	74.3	43319	583
	5 nM	75	13782	183.8
	0.5 nM	66.4	3833	57.7
M27	50 nM	71.7	144485	2015.1
	5 nM	75	70739	943.2
	0.5 nM	68.6	7049	102.8
IgG1	50 nM	69.5	100	1.4
	5 nM	69.3	95.1	1.4
	0.5 nM	76.9	94.4	1.2
Tab1	50 nM	72.4	72612	1002.9
	5 nM	74.5	70163	941.8
	0.5 nM	74.1	13120	177.1
PBS	NA	71.6	61.1	0.9

Example 7: Species Cross-Reactivity Testing of Antibodies

In this example, the cross-reactivity of each antibody obtained in this application on human and monkey species antigen was detected. The antibody prepared in Example 4 and the CHO K1 cell line

expressing monkey Mucin17 were used to determine the binding ability. For specific operation methods, refer to Example 6.

As shown in FIG. 3, all antibodies obtained in this application can bind to cell lines expressing monkey proteins, showing good human monkey cross-reactivity.

Example 8: Detection of antibody affinity

In this example, the affinity of the antibody obtained according to the present application and the positive control antibody Tab-1 to the antigenic protein huMucin17-His was detected on the basis of a Biacore equipment. The anti-Mucin17 antibody samples were diluted to 10 ug/mL using running buffer HBS-EP + (10mM HEPES, 150mM NaCl, 3mM EDTA and 0.05% P20, pH 7.4) (BR 100826, GE), respectively, and human Mucin17 antigenic protein was diluted to between 0.03125 nM and 2 nM with HBS-EP + buffer in a 2-fold gradient. The anti-Mucin 17 antibody was affinity-captured using Protein A biosensor chip (BR100354, GE) with a capture time of 60s and a flow rate of 30 μL/min. And samples of human Mucin17 diluted to different concentrations from zero to the highest concentration were sequentially injected, with binding time of 120s, dissociation time of 360s and flow rate of 30 uL/min. The reaction signal was detected in real time using a Biacore X100 instrument to obtain binding and dissociation curves. After dissociation was completed in each experimental cycle, the Protein A biosensor chip was washed and regenerated with 10mM Glycine-HCl (pH1.5) (29127558, GE), with regeneration time of 30s and flow rate of 30 uL/min. And parameter fitting: the experiment is operated in a single circulation mode, the analysis time is used as an abscissa, and the response value is used as an ordinate. And after double-reference subtraction is carried out on the obtained data, fitting is carried out through BIAcore X100 (GE) analysis software, the used fitting model is a 1:1 Langmuir binding model, and affinity indexes such as association constant and dissociation constant of the model are determined. The results are shown in TABLE 5. The antibodies obtained in the present application have higher affinity than the positive control antibody Tab1.

TABLE 5 KD values of the antibodies

Clone ID	ka (1/Ms)	kd (1/s)	KD (M)
M2	1505992	0.000679	4.51E-10
M11	268485.6	0.001788	6.66E-09
M18	760010.8	0.001679	2.21E-09
M20	1141416	0.001264	1.11E-09
M21	111017.4	0.001368	1.23E-08
M22	1459630	0.00309	2.12E-09
M23	1443877	0.002999	2.08E-09
M24	2927275	0.010404	3.55E-09
M25	1489585	0.002639	1.77E-09
M26	333926.7	0.001269	3.80E-09
M27	843844.7	0.001579	1.87E-09
Tab1	360533.2	0.002499	6.93E-09

Example 9: Detection of antibody endocytosis

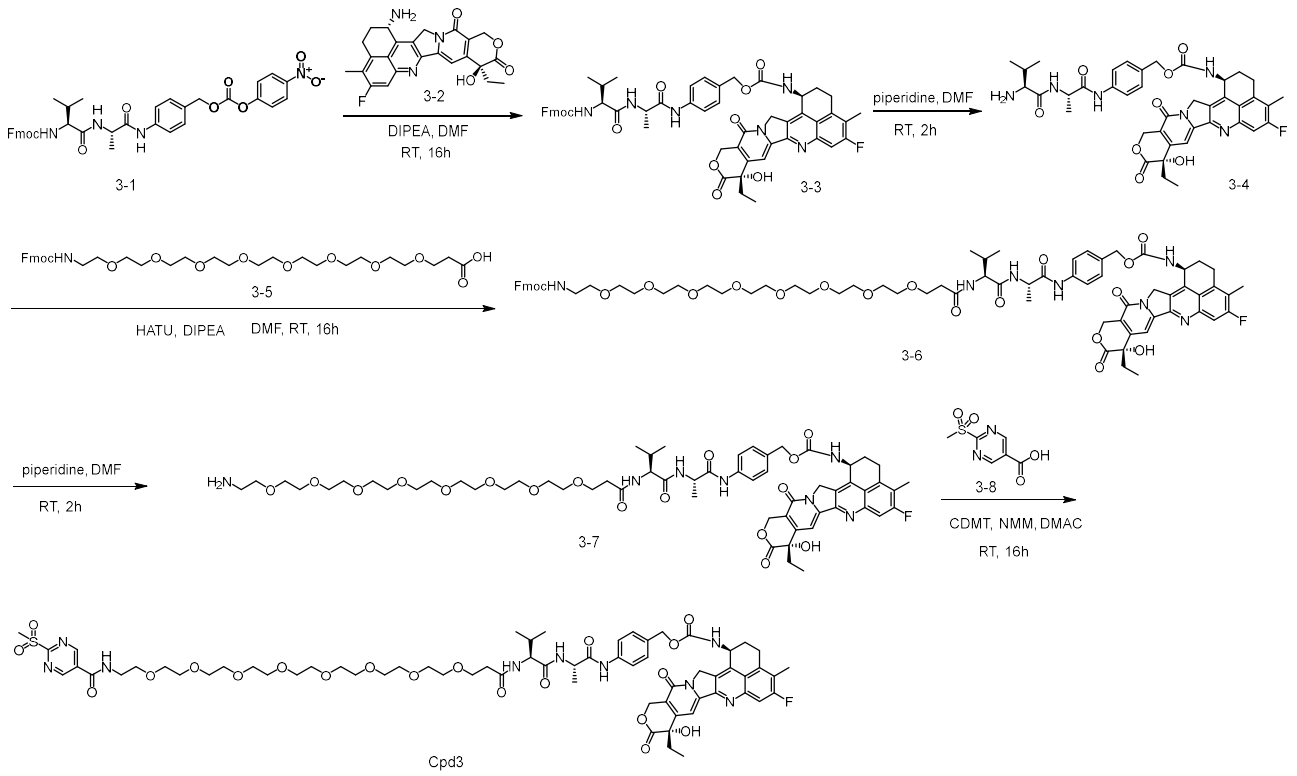
Incucyte (Sartorius, Incucyte S3) was used to detect the ability of recombinant antibodies to be endocytosed by target cells (huMucin17-CHO K1). Target cells were digested, collected and resuspended in assay buffer, and cell suspensions were transferred to 96-well assay plates at 5000 cells per well. The plates were incubated overnight in a cell culture incubator (37℃/5% CO_2). Test sample/reference sample working solution and labeling reagent working solution (4 ×) were prepared using the assay buffer. The sample/reference working solution and the labeling reagent working solution were mixed at a molar ratio of 1:3 and a volume ratio of 1:1, and incubated in a cell culture incubator (37℃/5% CO_2) for 15 minutes to allow them to be sufficiently conjugated. The conjugation mixture working solution was transferred to the corresponding well of the 96-well assay plate. The plates were incubated in a cell culture incubator (37℃/5% CO_2) for a period of time, and images were taken at designated time points using an Incucyte instrument that matched the detection wavelength.

The original experimental data and results are analyzed and exported through the Incucyte® Live-Cell Analysis System. The analytical results are expressed as: Total Red Object Integrated Intensity (GCU × μm^2/Image). The raw data were further analyzed and plotted using Microsoft Office Excel 2016 and GraphPad Prism 6 software. The experimental results are shown in FIG. 5, which shows that the tested molecules all have good endocytosis effects, and the antibody endocytosis increases with time.

Example 10: preparation method of linker-payload

The preparation of the linkers and payloads used in the present invention, such as deruxtecan, GGFG-Dxd, Dxd, GGFG-Exd, and Val-Ala-PAB, refers to WO2014057687, WO1997046260, and CN101795711, which are incorporated herein by reference in their entirety.

Linker-payload Cpd3 used in the present invention and the preparation method thereof are as follows:



Step 1: (9H-fluoren-9-yl)methyl ((S)-3-methyl-1-(((S)-1-((4-((((4-nitrophenoxy)carbonyl) oxy)methyl)phenyl) amino)-1-oxopropan-2-yl)amino)-1-oxobutan-2-yl)carbamate (**3-1**, 2.5 g, 3.6 mmol), (1S,9S)-1-amino-9- ethyl-5-fluoro-9-hydroxy-4-methyl-1,2,3,9,12,15-hexahydro-10H,13H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinoline-10,13-dione (**3-2**, 1.6 g, 3.6 mmol), N,N-diisopropylethylamine (965 mg, 7.5 mmol) were dissloved in anhydrous N,N-dimethylformamide (20 mL), the reaction solution was stirred at room temperature for 16 hours. LCMS monitored the reaction was complete, 4-((S)-2-((S)-2-((((9H-fluoren-9-yl) methoxy)carbonyl)amino)-3-methylbutanamido)propanamido)benzyl ((1S,9S)-9-ethyl-5-fluoro-9-hydroxy- 4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7] indolizino[1,2-b]quinolin-1-yl)carbamate (**3-3**) was obtained. LCMS (ESI) m/z: 977.3 $[M+H]^+$.

Step 2: To the reaction solution of step 1 was added hexahydropyridine (464 mg, 5.4 mmol) directly, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was separated and purified by C18 column chromatography directly to obtain 4-((S)-2-((S)-2-amino-3-methylbutanamido) propanamido)benzyl ((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl- 10,13-dioxo-2,3,9,10,13,15 -hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl) carbamate (**3-4**) (1.8g). LCMS (ESI) m/z: 755.2 $[M+H]^+$.

Step 3: 1-(9H-fluoren-9-yl)-3-oxo-2,7,10,13,16,19,22,25,28-nonaoxa-4-azahentriacontan-31-oic acid (**3-5**, 1.8 g, 2.38 mmol), 4-((S)-2-((S)-2-amino-3-methylbutanamido)propanamido)benzyl ((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl- 10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de] pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)carbamate (**3-4**, 1.8 g, 2.38 mmol), N,N-diisopropylethylamine (614 mg, 4.76 mmol) were dissloved in anhydrous

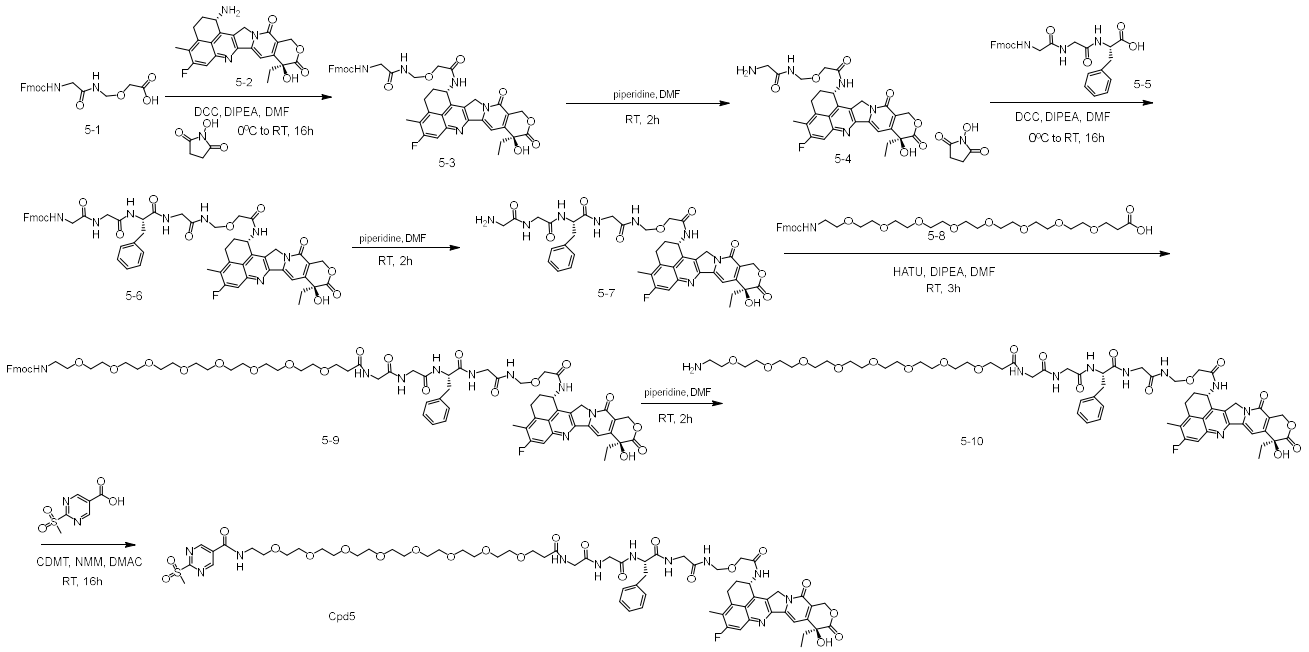
N,N-dimethylformamide (10 mL), then the reaction was stirred at room temperature for 3 h. LCMS monitored the reaction was complete, 4-((33S,36S)-1-(9H-fluoren-9-yl)-33-isopropyl-36-methyl-3,31,34-trioxo-2,7,10,13,16,19,22,25,28-nonaoxa-4,32,35-triazaheptatriacontan-37-amido)benzyl ((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)carbamate (**3-6**) was obtained. LCMS (ESI) m/z: 1400.5 $[M+H]^+$.

Step 4: To the reaction solution of step 3 was added hexahydropyridine (409 mg, 4.76 mmol) directly, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was separated and purified by C18 column chromatography directly to obtain 4-((29S,32S)-1-amino-29-isopropyl-32-methyl-27,30 -dioxo-3,6,9,12,15,18,21,24-octaoxa-28,31-diaza-tritriacontan-33-amido)benzyl((1S,9S)-9-ethyl-5-fl uoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7] indolizino[1,2-b]quinolin-1-yl)carbamate (**3-7**) (1.2g). LCMS (ESI) m/z: 1178.4 $[M+H]^+$.

Step 5: 4-((29S,32S)-1-amino-29-isopropyl-32-methyl-27,30-dioxo-3,6,9,12,15,18,21,24-octaoxa-28,31-diaza-tritriacontan-33-amido)benzyl ((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15- hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino [1,2-b]quinolin-1-yl)carbamate (**3-7**, 20 mg, 0.017 mmol), 2-(methylsulfonyl)pyrimidine-5-carboxylic acid (**3-8**, 13.7 mg, 0.068 mmol), 4-(4,6-dimethoxytriazin-2-yl)-4-methylmorpholinium tetrafluoroborate (22.3 mg, 0.068 mmol) were dissloved in anhydrous N,N-dimethylacetamide (3 mL), the reaction solution was stirred at room temperature for 16 hours. The reaction was separated and purified by C18 column chromatography to obtain 4-((31S,34S)-31-isopropyl-34-methyl-1-(2-(methylsulfonyl)pyrimidin-5-yl)-1,29,32-trioxo-5,8,11,14,17,20,23,26- octaoxa-2,30,33-triazapentatriacontan-35-amido)benzyl ((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13- dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)carbamate (i.e., **Cpd3**, 2.3 mg, yield: 10%).

^{1}H NMR (400 MHz, DMSO-d6) δ 9.95 (s, 1H), 9.37 (s, 1H), 9.14 (s, 1H), 8.46 (s, 1H), 8.21 (d, *J* = 6.8 Hz, 1H), 8.06 (d, *J* = 7.8 Hz, 1H), 7.89 (d, *J* = 8.3 Hz, 1H), 7.78 (d, *J* = 10.9 Hz, 1H), 7.60 (d, *J* = 8.4 Hz, 2H), 7.36 (d, *J* = 8.1 Hz, 2H), 7.31 (s, 1H), 6.53 (s, 1H), 5.45 (s, 2H), 5.28 (s, 3H), 5.08 (s, 2H), 4.42 – 4.34 (m, 1H), 4.22 – 4.17 (m, 1H), 3.62 – 3.53 (m, 10H), 3.52 – 3.46 (m, 28H), 2.38 (s, 3H), 2.33 (s, 1H), 2.20 (s, 3H), 2.01 – 1.81 (m, 4H), 1.30 (d, *J* = 7.0 Hz, 3H), 0.90 – 0.80 (m, 9H) .

Linker-payload Cpd5 used in the present invention and the preparation method thereof are as follows:



Step 1: 1-(9H-fluoren-9-yl)-3,6-dioxo-2,9-dioxa-4,7-diazaundecan-11-oic acid (**5-1**, 440 mg, 1.15 mmol), (1S,9S)-1-amino-9-ethyl-5-fluoro-9-hydroxy-4-methyl-1,2,3,9,12,15-hexahydro-10H,13H-benzo[de] pyrano [3',4':6,7]indolizino[1,2-b]quinoline-10,13-dione (500 mg, 1.15 mmol) were dissloved in anhydrous N,N-dimethylformamide (20 mL), N,N'-dicyclohexyl carbodiimide (308 mg, 1.5 mmol), N-hydroxysuccinimide (132 mg, 1.15 mmol) and N,N-diisopropylethylamine (148 mg, 1.15 mmol) were added under an ice-bath, then the reaction solution was stirred at room temperature for 16 hours. LCMS monitored the reaction was complete, the reaction was extracted with ethyl acetate and water, the organic phase was concentrated, the residue was purified on silica gel column with methanol and dichloromethane (1: 20) to obtain (9H-fluoren-9-yl)methyl (2-(((2-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12 H-benzo[de] pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-2-oxoethoxy)methyl)amino)-2-oxoethyl)carbamate (**5-3**, 650 mg). LCMS (ESI) m/z: 802.3 $[M+H]^+$.

Step 2: (9H-fluoren-9-yl)methyl (2-(((2-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b] quinolin-1-yl)amino)-2-oxoethoxy)methyl)amino)-2-oxoethyl)carbamate (**5-3**, 650 mg, 0.81 mmol) was dissloved in N,N-dimethylformamide (10 mL), then hexahydropyridine (69 mg, 5.4 mmol) was added, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was seperated and purified by C18 column chromatography directly to obtain 2-amino-N-((2-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydr o-1H,12H- benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-2-oxoethoxy)methyl) acetamide (**5-4**, 420 mg). LCMS (ESI) m/z: 580.2 $[M+H]^+$.

Step 3: 2-Amino-N-((2-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-2-oxoethoxy)methyl)-acetamide (**5-4**, 420 mg, 0.73 mmol), (((9H-fluoren-9-yl)methoxy)carbonyl)glycylglycyl-L-phenylalanine (**5-5**, 370 mg, 0.73 mmol) were dissloved in anhydrous N,N-dimethylformamide (10 mL), N,N'-dicyclohexyl carbodiimide (195 mg, 0.95 mmol), N-hydroxysuccinimide (84 mg, 0.73 mmol) and N,N-diisopropylethylamine (94 mg, 0.73 mmol) were added under an ice-bath, then the reaction solution was stirred at room temperature for 16 hours. LCMS monitored the reaction was complete, the reaction was extracted with ethyl acetate and water, the organic phase was concentrated, the residue was purified on silica gel column with methanol and dichloromethane (1: 15) to obtain (9H-fluoren-9-yl)methyl ((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1,6,9,12,15- pentaoxo-3-oxa-5,8,11,14-tetraazahexadecan-16-yl)carbamate (**5-6**, 550 mg). LCMS (ESI) m/z: 1063.5 $[M+H]^+$.

Step 4: (9H-fluoren-9-yl)methyl ((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl- 10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino [1,2-b]quinolin-1-yl)amino)- 1,6,9,12,15-pentaoxo-3-oxa-5,8,11,14-tetraazahexadecan-16-yl) carbamate (**5-6**, 550 mg, 0.52 mmol) was dissloved in N,N-dimethylformamide (5 mL), then hexahydropyridine (44 mg, 0.52 mmol) was added, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was seperated and purified by C18 column chromatography directly to obtain ((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H- benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1,6,9,12,15-pentaoxo-3-oxa-5,8,11,14-tetraaza- hexadecan-16-yl)amine (**5-7**, 400 mg). LCMS (ESI) m/z: 841.4 $[M+H]^+$.

Step 5: 1-(9H-fluoren-9-yl)-3-oxo-2,7,10,13,16,19,22,25,28-nonaoxa-4-aza-hentriacontan-31-oic acid (347 mg, 0.52 mmol), HATU (274 mg, 0.72 mmol) and N,N-diisopropylethylamine (124 mg, 0.96 mmol) were dissloved in anhydrous N,N-dimethylformamide (5 mL), then the reaction was stirred at room temperature for 1 h, then ((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H- benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1,6,9,12,15-pentaoxo-3-oxa-5,8,11,14-tetraaza- hexadecan-16-yl)amine (**5-7**, 400 mg, 0.48 mmol) was added, then the reaction was stirred at room temperature for 16 h. LCMS monitored the reaction was complete, the reaction solution was purified by C18 column chromatography directly to obtain (9H-fluoren-9-yl)methyl ((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H- benzo[de]pyrano[3',4':6,7]indolizino[1,2-b] quinolin-1-yl)amino)-1,6,9,12,15,18-hexaoxo- 3,21,24,27,30,33,36,39,42-nonaoxa-5,8,11,14,17-

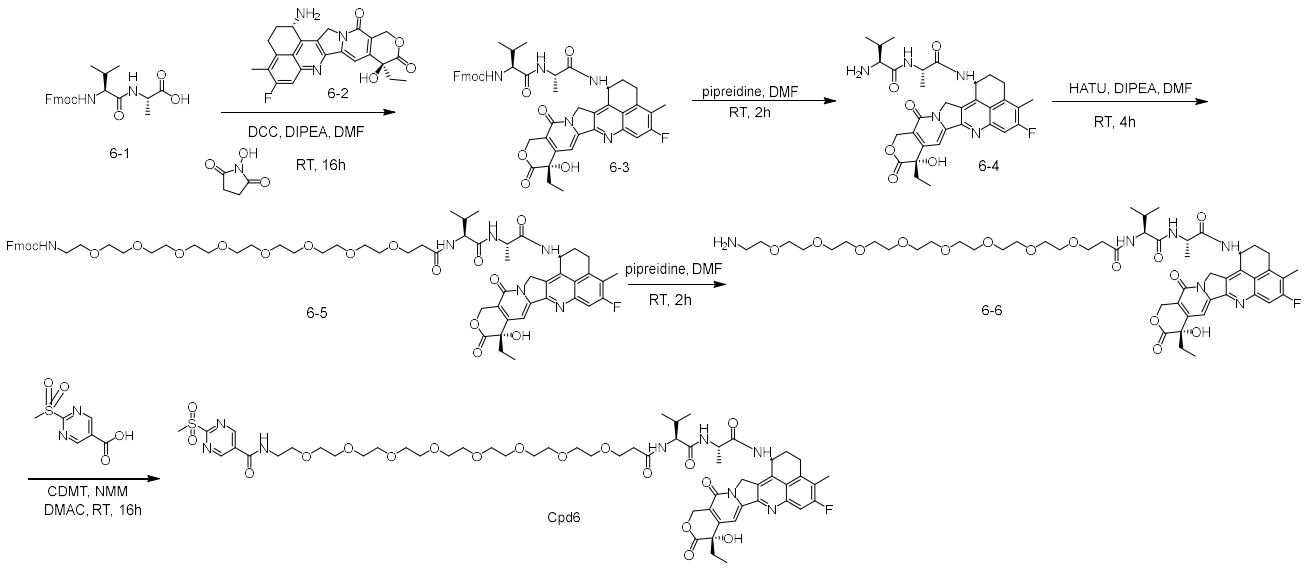
pentaaza-tetratetracontan-44-yl)carbamate (**5-9**, 350 mg). LCMS (ESI) m/z: 1486.6 $[M+H]^+$.

Step 6: (9H-fluoren-9-yl)methyl ((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl- 10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7] indolizino[1,2-b]quinolin-1-yl)amino)- 1,6,9,12,15,18-hexaoxo-3,21,24,27,30,33,36,39,42-nonaoxa-5,8,11,14,17-pentaazatetratetracontan-44-yl)carbamate (**5-9**, 350 mg, 0.24 mmol) was dissloved in N,N-dimethylformamide (5 mL), then hexahydropyridine (20 mg, 0.24 mmol) was added, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was seperated and purified by C18 column chromatography directly to obtain 1-amino-N-((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7] indolizino[1,2-b]quinolin-1-yl)amino)-1,6,9,12,15- pentaoxo-3-oxa-5,8,11,14-tetraaza-hexadecan-16-yl)-3,6,9,12,15,18,21,24-octaoxa-heptacosan-27-amide (**5-10**, 200 mg). LCMS (ESI) m/z: 1264.6 $[M+H]^+$.

Step 7: 1-Amino-N-((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino [1,2-b]quinolin-1-yl)amino)-1,6,9,12,15- pentaoxo-3-oxa-5,8,11,14-tetraaza-hexadecan-16-yl) -3,6,9,12,15,18,21,24-octaoxa-heptacosan-27-amide (**5-10**, 100 mg, 0.079 mmol), 2-(methylsulfonyl)pyrimidine-5-carboxylic acid (64 mg, 0.3 mmol), 2-chloro-4,6-dimethoxy-1,3,5-triazine (53 mg, 0.3 mmol), N-methylmorpholine (182 mg, 1.8 mmol) were dissloved in anhydrous N,N-dimethylacetamide (5 mL), the reaction solution was stirred at room temperature for 16 hours. Separated and purified by C18 column chromatography to obtain N-((S)-10-benzyl-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexa hydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1,6,9,12,15,18-hexa oxo- 3,21,24,27,30,33,36,39,42-nonaoxa-5,8,11,14,17-pentaaza-tetratetracontan-44-yl)-2-(methylsulfonyl)pyrimidine-5-carboxamide (i.e. **Cpd5**, 5mg). LCMS (ESI) m/z: 1448.6 $[M+H]^+$.

^{1}H NMR (400 MHz, DMSO-d6) δ 9.37 (d, *J* = 2.1 Hz, 2H), 9.12 (s, 1H), 8.63 (s, 1H), 8.51 (d, *J* = 8.6 Hz, 1H), 8.29 (s, 1H), 8.21 – 8.07 (m, 2H), 7.99 (s, 1H), 7.78 (d, *J* = 10.9 Hz, 1H), 7.31 (s, 1H), 7.21 (t, *J* = 15.2 Hz, 5H), 6.52 (s, 1H), 5.60 (s, 1H), 5.42 (s, 2H), 5.20 (s, 2H), 4.64 (d, *J* = 6.3 Hz, 2H), 4.47 (s, 1H), 4.02 (s, 2H), 3.76 – 3.66 (m, 4H), 3.59 – 3.53 (m, 8H), 3.51 – 3.45 (m, 29H), 2.39 (s, 5H), 2.18 (s, 2H), 2.00 (d, *J* = 7.9 Hz, 1H), 1.84 (dd, *J* = 15.4, 7.8 Hz, 2H), 1.33 – 1.20 (m, 5H), 1.12 (d, *J* = 6.6 Hz, 1H), 0.87 (t, *J* = 6.3 Hz, 3H) .

Linker-payload Cpd6 used in the present invention and the preparation method thereof are as follows:



Step 1: (((9H-fluoren-9-yl)methoxy)carbonyl)-L-valyl-L-alanine (**6-1**, 943 mg, 2.3 mmol), (1S,9S)-1-amino-9-ethyl-5-fluoro-9-hydroxy-4-methyl-1,2,3,9,12,15-hexahydro-10H,13H-benzo[de] pyrano [3',4':6,7]indolizino[1,2-b]quinoline-10,13-dione (1 g, 2.3 mmol) were dissloved in anhydrous N,N-dimethylformamide (20 mL), then N,N'-dicyclohexyl carbodiimide (616 mg, 3 mmol), N-hydroxysuccinimide (264 mg, 2.3 mmol) and N,N-diisopropylethylamine (297 mg, 2.3 mmol) were added under an ice-bath, then the reaction solution was stirred at room temperature for 16 hours. LCMS monitored the reaction was complete, the reaction was extracted with ethyl acetate and water, the organic phase was concentrated, the resiude was purified on silica gel column with methanol and dichloromethane (1: 20) to obtain (9H-fluoren-9-yl)methyl ((S)-1-(((S)-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro -1H,12H- benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1-oxopropan-2-yl)amino) -3-methyl-1-oxobutan-2-yl)carbamate (**6-3**, 730 mg). LCMS (ESI) m/z: 828.3 $[M+H]^+$.

Step 2: (9H-fluoren-9-yl)methyl ((S)-1-(((S)-1-(((1S,9S)-9-ethyl-5-fluoro-9 -hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7] indolizino[1,2-b]quinolin-1-yl)amino)-1-oxopropan-2-yl)amino)-3-methyl-1-oxobutan-2-yl)carbamat e (**6-3**, 730 mg, 0.88 mmol) was dissloved in N,N-dimethylformamide (10 mL), then hexahydropyridine (75 mg, 0.88 mmol) was added, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was seperated and purified by C18 column chromatography directly to obtain (S)-2-amino-N-((S)-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-he xahydro- 1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1-oxopropan-2-yl)-3-methylbutanamide (**6-4**, 450 mg). LCMS (ESI) m/z: 606.2 $[M+H]^+$.

Step 3: 1-(9H-fluoren-9-yl)-3-oxo-2,7,10,13,16,19,22,25,28-nonaoxa-4-azahentriacontan -31-oic acid (592 mg, 0.89 mmol), HATU (422 mg, 1.11 mmol) and N,N-diisopropylethylamine (143 mg, 1.11 mmol) were dissloved in anhydrous N,N-dimethylformamide (5 mL), then the reaction was

stirred at room temperature for 1 h, then (S)-2-amino-N-((S)-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro- 1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1-oxopropan-2-yl)-3-methylbutanamide (450 mg, 0.74 mmol) was added, then the reaction was stirred at room temperature for 4h. LCMS monitored the reaction was complete, the reaction solution was purified by C18 column chromatography directly to obtain (9H-fluoren-9-yl)methyl (29S,32S)-33-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-29-isopropyl-32-methyl- 27,30,33-trioxo-3,6,9,12,15,18,21,24-octaoxa-28,31-diazatritriacontyl)carbamate (**6-5**, 400 mg). LCMS (ESI) m/z: 1251.6 $[M+H]^+$.

Step 4: (9H-fluoren-9-yl)methyl ((29S,32S)-33-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-29-isopropyl- 32-methyl-27,30,33-trioxo-3,6,9,12,15,18,21,24-octaoxa-28,31-diazatritriacontyl)carbamate (**6-5**, 400 mg, 0.32 mmol) was dissloved in N,N-dimethylformamide (5 mL), then hexahydropyridine (27 mg, 0.32 mmol) was added, the reaction solution was stirred at room temperature for 2 hours. LCMS monitored the reaction of the raw material was complete, the reaction solution was seperated and purified by C18 column chromatography directly to obtain 1-amino-N-((S)-1-(((S)-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro- 1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1-oxopropan-2-yl)amino)-3-methyl-1- oxobutan-2-yl)-3,6,9,12,15,18,21,24-octaoxaheptacosan-27-amide (**6-6**, 210 mg). LCMS (ESI) m/z: 1029.6 $[M+H]^+$.

Step 5: 1-Amino-N-((S)-1-(((S)-1-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo- 2,3,9,10,13,15-hexahydro-1H,12H-benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-1-oxopropan-2-yl)amino)-3-methyl-1-oxobutan-2-yl)-3,6,9,12,15,18,21,24-octaoxaheptacosan-27-amide (**6-6**, 100 mg, 0.097 mmol), 2-(methylsulfonyl)pyrimidine-5-carboxylic acid (78 mg, 0.39 mmol), 2-chloro-4,6-dimethoxy-1,3,5-triazine (68 mg, 0.39 mmol) and N-methylmorpholine (59 mg, 0.582 mmol) were dissloved in anhydrous N,N-dimethylacetamide (5 mL), the reaction solution was stirred at room temperature for 16 hours. The reaction was separated and purified by C18 column chromatography to obtain N-((29S,32S)-33-(((1S,9S)-9-ethyl-5-fluoro-9-hydroxy-4-methyl-10,13-dioxo-2,3,9,10,13,15-hexahydro-1H,12H- benzo[de]pyrano[3',4':6,7]indolizino[1,2-b]quinolin-1-yl)amino)-29-isopropyl-32-methyl-27,30,33-trioxo- 3,6,9,12,15,18,21,24-octaoxa-28,31-diazatritriacontyl)-2-(methylsulfonyl)pyrimidine-5-carboxamide (i.e., **Cpd6**, 11.5 mg). LCMS (ESI) m/z: 1213.6 $[M+H]^+$

^{1}H NMR (400 MHz, DMSO-d6) δ 9.36 (s, 2H), 9.13 (s, 1H), 8.41 (d, J = 8.9 Hz, 1H), 8.10 (d, J = 6.9 Hz, 1H), 7.86 (d, J = 8.4 Hz, 1H), 7.79 (d, J = 11.0 Hz, 1H), 7.30 (s, 1H), 6.53 (s, 1H), 5.54 (s,

1H), 5.42 (s, 2H), 5.24 (d, *J* = 18.9 Hz, 1H), 5.11 (d, *J* = 19.0 Hz, 1H), 4.32 – 4.21 (m, 1H), 4.17 – 4.06 (m, 1H), 3.58 – 3.52 (m, 8H), 3.48 (s, 25H), 3.44 (s, 6H), 2.40 (s, 3H), 2.29 (dd, *J* = 13.7, 7.1 Hz, 1H), 2.13 (s, 2H), 1.91 (ddd, *J* = 23.2, 22.6, 7.6 Hz, 4H), 1.27 (d, *J* = 7.0 Hz, 3H), 0.87 (t, *J* = 7.4 Hz, 3H), 0.83 – 0.72 (m, 6H) .

Example 11: Preparation and identification of MUC17-ADC

The antibody stock solution was taken from the refrigerator (-80 °C), added to a centrifuge tube after thawing, and then PB (20 mM, pH 7.2, 751 uL) buffer, DTPA-3Na (10 mM, 375 uL), TCEP (10 mM, 94 uL) solution were added, and the mixture was reacted at 25 °C for 2 h. Then, the linker-payload described in Example 10, such as Cpd3 was added, and reacted at 25 °C for 2 h. After the reaction was complete, the reaction was added to an ultrafiltration centrifuge tube (30 KD) and dialyzed with His/His-HCl (10 mM, pH 5.5) to obtain the ADC stock solution (DAR: 7.5~8.5, SEC purity≥95%).

As an example, the linker-payload used in the above experiment is Cpd3 described in Example 10. The antibody stock solution can be any clone of M1~M27; the linker-payload may be a combination of linker and camptothecins that are common in the art, including but not limited to deruxtecan, Cpd3, Cpd5, Cpd6, etc.

Using clone M26, the above experiments were carried out with other linker-payloads. Each ADC sample was identified, and the test results are shown in Table 6 below.

Table 6. Test results of ADC samples

Antibody	Linker-Payload	Test results of ADCs		
		DAR	SEC purity	Free drug
M26	Cpd3	7.8	96.6%	0.53%
M26	Cpd5	7.8	97.7%	0.002%
M26	Cpd6	7.9	97.%	Not detectable

Example 12: Detection of ADC activity

An animal efficacy evaluation experiment is carried out by using Balb/c nude mice (source: Shanghai Lingchang Biotechnology Co., Ltd.) with the weight of 18-20g, and the animals are housed in separate cages, with 5 mice in each cage, in a barrier environment (independent ventilation system). All the cages, padding and drinking water are sterilized before use. After 7 days of adaptive feeding of mice, 100ul of a suspension of 10×10^6 GSU tumor cells (Riken, RCB2278) was mixed with Matrigel at a ratio of 1:1 and inoculated subcutaneously on the right upper back of the mouse.

The body weight was measured using a scale, the long and short diameters of the tumor were measured with an electronic digital caliper (manual caliper, OMC Fontana) to calculate the tumor volume (mm^3). Tumor volume (mm^3) = 1/2× long diameter (mm) × [short diameter (mm)]^2, measured 2 times per week. 7 days after inoculation, when the mean tumor volume reached 279 mm^3,

the 36 experimental animals were randomly divided into 6 groups, and the test ADC drug or control PBS was administered via tail vein injection on the day of the experiment as the following dose.

Experimental group one: PBS control group (Vehicle Single), a single dose at the same dose as ADC.

Experimental group two: M21-Deruxtecan, 3mg/kg, single dose.

Experimental group three: M26-Deruxtecan, 3mg/kg, single dose.

Experimental group four: M26-Cpd 3, 3mg/kg, single dose.

Experimental group five: M26-Cpd 5, 3mg/kg, single dose.

Experimental group six: M26-Cpd 6, 3mg/kg, single dose.

All data are presented as mean values. All data were analyzed using Microsoft Excel 2016. The tumor inhibition rate in the mice is shown in the following TABLE 7.

Tumor Growth Inhibition (TGI) refers to the rate of tumor growth inhibition. TGI is commonly used to assess the effect of certain treatments or interventions on tumor growth. Specifically, TGI can be calculated by the following formula:

TGI = (1- tumor weight of treatment group / tumor weight of control group) ×100%.

In the present application, TGI of other groups are calculated based on experimental group one.

TABLE 7. Tumor inhibition rate of ADC in mice

	TGI (%)									
	Measurement (day)									
	3	7	10	14	17	21	24	29	32	36
M21-Deruxtecan	34.16%	63.58%	67.44%	65.82%	60.85%	61.66%	58.57%	54.88%	53.45%	50.87%
M26-Deruxtecan	40.24%	71.95%	75.86%	81.59%	81.71%	79.41%	72.29%	67.48%	66.51%	62.40%
M26-Cpd3	29.86%	67.67%	77.94%	87.25%	91.00%	95.29%	95.58%	96.24%	96.81%	96.40%
M26-Cpd5	36.52%	73.95%	71.65%	72.25%	63.59%	71.57%	72.49%	64.49%	69.56%	63.85%

The results of the experiments are shown in FIG. 4 and TABLE 7, which indicate that M21 and M26 antibodies can significantly inhibit tumor growth after being conjugated to Deruxtecan or Cpd3, Cpd5. Wherein the effect of M26-Cpd3 ADC in inhibiting tumor growth is better than that of M26-Deruxtcan ADC, and the effect of M26-Cpd5 ADC in inhibiting tumor growth is similar to that of M26-Deruxtcan ADC. No weight loss was observed in all experimental animals during the experiment period.

Example 13: Humanization of chimeric antibodies and characterization of humanized

antibodies

A. Humanization of chimeric antibodies

Humanization method: the parent antibody structure was modeled by computer-assisted homology modeling. Selecting a human natural germline sequence with high homology to the parent sequence. The humanized antibody was designed using CDR grafting technique. Briefly, the CDRs of a parent antibody are grafted into a human natural germline sequence to obtain a humanized chimeric antibody of the parent antibody. Comparing the different amino acid residues of the chimeric antibody and the parent antibody, and judging the key points that will affect the subsequent affinity based on the classic residues, interaction loop regions, core regions, mutation hotspots, etc., and selecting proper sites for back mutation to obtain humanized antibodies. Randomly pairing the heavy and light chains of humanized antibodies for antibody production and identification.

Screening for humanized molecule: the humanization sequence design for chimeric antibody M21 was performed according to the humanization design principle described above and the method disclosed in Example 4. The VH coding sequence of the humanized antibody is connected with the coding sequence of a heavy chain constant region of human IgG1 to obtain a heavy chain coding sequence, the VL coding sequence of the humanized antibody is connected with the coding sequence of a Kappa subtype of a human light chain constant region to obtain a light chain coding sequence, and then the coding sequences of the heavy chain and the light chain are respectively inserted into a eukaryotic expression vector PCDNA3.4 for combined expression, purification and detection. Finally obtaining the humanized antibody: M21-01, M21-02, M21-03, M21-04, M21-05, M21-06, M21-07, M21-08, M21-09, M21-10, M21-11, M21-12, M21-13, M21-14, M21-15, M21-16, M21-17 and M21-18.

B: Characterization of humanized antibodies

B.1 ELISA: a 96-well ELISA plate was coated with 1 μg/mL of human Mucin17 antigen protein (100 μL/well) and incubated overnight at 4 ℃. The following day, the well plates were washed 3 times with PBST, blocked with 1% bovine serum albumin in PBST for 1 h, washed 3 times with PBST, and then each humanized antibody was added in a gradient (10nM, 5 folds gradient dilution, 7 concentration points) and incubated for 1 h at 37 ℃. After 3 washes with PBST, a secondary antibody anti-human IgG-HRP (Sigma, Cat#A 0170) was added and incubated for 45 min. After incubation was complete, the plate was washed 3 times with PBST and developed with TMB. Color development was carried out for 15min at 25 ℃, 1M HCl was added to terminate the reaction, and the absorbance was read by a microplate reader at OD450. The results for ELISA are shown in TABLE 8 below.

TABLE 8 Results for ELISA of humanized antibody

Antibody ID	EC50 (nM)	Span	Top
M21-01	0.04	2.84	2.96
M21-02	0.04	2.80	2.92

M21-03	0.04	2.81	2.93
M21-04	0.06	2.83	2.95
M21-05	0.03	2.82	2.94
M21-06	0.04	2.85	2.98
M21-07	0.04	2.85	2.96
M21-08	0.04	2.80	2.91
M21-09	0.03	2.78	2.90
M21-10	0.07	2.82	2.94
M21-11	0.06	2.81	2.92
M21-12	0.04	2.81	2.97
M21-13	0.05	2.86	2.96
M21-14	0.04	2.81	2.93
M21-15	0.05	2.82	2.93
M21-16	0.05	2.80	2.91
M21-17	0.05	2.81	2.92
M21-18	0.04	2.84	2.95

B.2 FACS binding activity: HEK293 cells highly expressing huMucin17 protein were constructed using conventional methods. The huMucin17-HEK293 cells in the logarithmic growth phase were prepared as single cell suspensions, adjusted to a density of 2×10^6 cells/mL, added at 100 μL per well to a 96-well round bottom plate, centrifuged at 300 g at 4 ℃ and removing the supernatant. And the antibodies to be detected were respectively added into the corresponding wells, mixed well and incubated for 1h at 4 ℃. After incubation, the cell mixture was washed 3 times, 100 μL of a diluted secondary antibody, Goat $F(ab')_2$ Anti-Human IgG-Fc (source: Jackson, Cat#109-136-098) was added, incubated at 4 ℃ for 30 min in the dark, and after 3 washes, the mean fluorescence intensity (MFI) was read by a flow cytometer. The results of FACS detection are shown in FIGS. 6A-6B, in which the prefix "Hu" in the antibody name indicates the humanized antibody, "Hu 112" indicates the humanized antibody of chimeric antibody M21, and the suffix indicates the sequence number of the humanized antibody derived from chimeric antibody M21, the number correspond to the corresponding clones obtained in section A of this Example.

B.3 Endocytosis activity assay: GSU cells (Riken, RC2278) were incubated with primary antibody (100 nM) for 30min at 4 ℃ and washed 2 times; after incubating the cells at 4 ℃ and/or 37 ℃ for 0/2/4/6 hours, respectively, the cells were fixed with 2% PFA on ice for 10min, washed 2 times; adding a fluorescent secondary antibody (Alexa 488 Goat Anti-Human IgG, Fc γ fragment specific, Jackson, Cat#109-545-098) and incubating for 1 hour on ice in dark; FACS analysis was performed, and the results are shown in TABLE 9 below, showing that all humanized antibodies showed significant internalization.

TABLE 9 Results of endocytosis activity of humanized antibodies

	Mean Fluorescence Intensity（MFI）			
Primary antibody\Temperature	0h	2h	4h	6h
M21-02(BM1) 4℃	69761	60039	59899	57930
M21-08(BM5) 4℃	97037	83744	85543	82218
M21-09(BM7) 4℃	96920	85913	85856	83309
M21-17(BM5) 4℃	107024	87374	87316	83002
M21-18(BM7) 4℃	102275	87679	88865	83017
M21-chimeric 4℃	91994	82083	84288	77434
hIgG1 4℃	14427	13969	13026	11290
M21-02(BM1) 37℃	69761	44231	40809	38751
M21-08(BM5) 37℃	97037	71290	66809	61201
M21-09(BM7) 37℃	96920	74974	67745	60827
M21-17(BM5) 37℃	107024	75265	70651	60294
M21-18(BM7) 37℃	102275	76206	71486	63393
M21-chimeric 37℃	91994	70571	65942	59646
hIgG1 37℃	14427	8445	7495	7023

B.4 BiaCore affinity detection: affinity analysis was performed using BIAcore 8K, according to the method disclosed in Example 8, the flow cell and sample chamber temperature were set to 25 ℃, and the results are shown in TABLE 10 below.

TABLE 10. Results for humanized antibody affinity assay

Capture 1 Solution	Analyte 1 Solution	Kinetics/Affinity Chi² (RU²)	ka (1/Ms)	kd (1/s)	KD (M)
2μg/mL M21-02(BM1)	32350-A-his	1.52E-01	6.11E+04	9.40E-04	1.54E-08
2μg/mL M21-03(BM3)	32350-A-his	5.04E-01	6.74E+04	8.90E-04	1.32E-08
2μg/mL M21-05(BM3)	32350-A-his	9.43E-02	5.44E+04	9.65E-04	1.77E-08
2μg/mL M21-08(BM5)	32350-A-his	4.92E-01	5.82E+04	1.20E-04	2.06E-09
2μg/mL M21-09(BM7)	32350-A-his	1.18E-01	7.90E+04	1.44E-04	1.82E-09
2μg/mL M21-14(BM3)	32350-A-his	1.12E-01	4.69E+04	1.05E-03	2.24E-08
2μg/mL M21-17(BM5)	32350-A-his	9.28E-01	6.53E+04	1.27E-04	1.95E-09
2μg/mL M21-18(BM7)	32350-A-his	2.03E-01	7.54E+04	1.97E-04	2.61E-09
2μg/mL M21-chimeric	32350-A-his	2.88E-01	5.78E+04	1.28E-04	2.21E-09
2μg/mL hIgG1(LL, DEL)	32350-A-his	N/A	N/A	N/A	N/A

Example 14: Binding of humanized antibodies or antibody drug conjugates to tumor cells

A. Construction of antibody drug conjugate for humanized antibody

Antibody drug conjugates of humanized antibodies were prepared according to the method of Example 11 using clone M21-17 and a linker-toxin.

As an example, the linker-toxin used in the above experiments was Cpd3 described in Example 10. Linker-toxins may be combinations of linkers with camptothecin compounds which are common in the art, including but not limited to deruxtecan, Cpd3, Cpd5, Cpd6, and the like.

B. Validation and characterization of antibody drug conjugates

Each ADC sample was verified and the test results are shown in the TABLE below.

Name of antibody	Linker-Payload	ADC test result	
		DAR (DAR)	SEC purity
M21-17	Cpd 3	7.87	97.7%

C. Binding of humanized antibodies and conjugates thereof to tumor cells

Experimental method: GSU cells (Riken, RC2278) or NUGC4 cells (Nanjing Cobioer Biosciences Co., Ltd.) in logarithmic growth phase were prepared as single cell suspension, adjusted to a density of 2×10^6 cells/mL, added to a 96-well round bottom plate at 100 μL per well, centrifuged at 300 g at 4 ℃ and the supernatant was removed. The antibody to be detected, ADC, or positive control AMG199 antibody (commercially available) was added to the corresponding wells, mixed well and incubated for 30 min at 4 ℃. After incubation, the cell mixture was washed for 3 times, 100 μL of diluted secondary antibody Goat Anti-Human IgG (Jackson 109-136-098) was added and incubated for 30 min at 4 ℃ in the dark, and after 3 washes, the mean fluorescence intensity (MFI) was read by a flow cytometer.,

The experimental results show that the maximum MFI value of the binding of the candidate molecules to the cells is higher than that of the positive control molecules on the detected tumor cell strains. TABLE 11 shows the binding data of the humanized antibodies and their ADCs to the tumor cells (GSU and NUGC4).

TABLE 11. Binding activity of target antibody to tumor cells

Tumor cell	Antibody/protein	Maximum MFI	EC_{50} (nM)
GSU	M21-17	41210	1.18
	M21-17-Cpd3	40219	1.64
	AMG199-IgG1 Fc	35092	0.30
NUGC4	M21-17	2751	3.97
	M21-17-Cpd3	3060	8.12

	AMG199-IgG1 Fc	2069	0.67

Example 15: Study of *in Vitro* tumor cell killing by antibody-drug conjugates

Experimental method: each suspension of the CHO-K1 cells highly expressing MUC17 in logarithmic growth phase and tumor cells (NUGC4, GSU and SW480 cells, wherein GSU cells express the highest amount of MUC17, MUCG4 expresses medium amount of MUC17, and SW480 expresses relatively low amount of MUC17) was adjusted to the cell density of 1.5×10^4/ml to prepare cell working solution, and adding the cell working solution into a 96-well cell culture plate at 100 μL per well. The cell culture plates were incubated overnight at 37 ℃ in a 5% CO_2 cell incubator. ADC samples M21-17-Cpd3 to be detected were added to the corresponding wells and incubated for 5 days in a cell incubator. The cell culture plate was left at room temperature for 10min, equilibrated to room temperature. 75 uL of solution in Luminescent Cell Viability Assay Kit (Promega) was added to wells, mixed for 2 minutes at room temperature using an orbital oscillator and incubated for 10 minutes at room temperature. Using an microplate reader to read the fluorescence signal value, then calculating the cell viability.

Experimental result: the *in vitro* cell killing capacity of the candidate ADC molecule is positively correlated with the expression of the MUC17 molecule on the cell surface, and the higher the expression is, the higher the killing effect of the ADC. The results of cell killing of the antibody drug conjugate M21-17-Cpd3 in three tumor cell lines are shown in FIG. 7.

Example 16: Bystander killing effect of antibody drug conjugate on tumor cells

This Example investigated whether the ADC has a bystander killing effect. The bystander killing effect refers to the killing effect of the ADC drugs on cells around or adjacent to target antigen positive cells.

Antigen-highly-expressing cells (positive cells: NUGC4 or GSU) and negative cells (MDA-MB-468 (National Collection of Authenticated Cell Cultures) or HCC827 cells (Nanjing Cobioer Biosciences Co., Ltd.)) were mixed at a cell density of 1×10^5/ml, respectively, to prepare mixed cell working solutions, and the mixed cell working solutions were added to 12-well cell culture plates at 1 ml/well, and incubated overnight at 37 ℃ under 5% CO_2 conditions. ADC samples M21-17-Cpd3 to be detected were added to the corresponding wells and incubated for 5 days in a cell incubator. After digestion and centrifugation of the cells, the cells were resuspended and counted, and the cells were transferred to a 96-well plate for flow cytometry analysis. The ratio of the two types of cells was counted, and then the number of live cells of the two types of cells was calculated separately, and a bar graph was drawn using GraphPad software.

The bystander killing effect of M21-17-Cpd3 was detected by co-culturing target-negative cells with positive cells and detecting the number of surviving negative cells. The results are shown in

Figures 8A-8C, and the results show that the antibody drug conjugate of the present invention has a bystander killing effect, wherein the molecule M21-Dxd refers to the antibody conjugate formed by conjugation M21 antibody to the toxin linker (Dxd) of DS8201.

Example 17: Verification of anti-tumor effect of humanized ADCs on human gastric cancer GSU transplanted tumor model

The anti-tumor activity of the antibody drug conjugate M21-17-Cpd 3 of the present application was detected using the experimental method described in Example 12.

The experimental design is as follows:

Experimental group one: PBS control group, a single dose at the same dose as ADC..

Experimental group two: M21-17-Cpd3, 0.3 mg/kg, single dose.

Experimental group three: M21-17-Cpd3, 1 mg/kg, single dose.

Experimental group four: M21-17-Cpd3, 10 mg/kg, single dose.

Experimental group five: M21-17-Cpd3, 30 mg/kg, single dose.

Experimental group six: M21-17-Cpd3, 10 mg/kg, QW*3.

All data are presented as average values. The *in vivo* efficacy index of the mice is shown in the following TABLE 12.

TABLE 12. *In vivo* potency of humanized ADCs in mice (GSU cells)

Experimental group	TGI (%)	T/C (%)	PRR	IR (%)
1	-	-	-	-
2	10.63	89.37	0/6	8.58
3	48.87	51.13	0/6	41.03
4	81.41	18.59	3/6	76.73
5	96.45	3.55	6/6	96.25
6	99.17	0.83	6/6	97.83

Note: Complete Response (CR) refers to Tumor Volume (TV) =0 mm^3; Partial Response (PR) refers to at least a 30% reduction in tumor volume relative to baseline; Complete Response Rate (CRR) refers to the proportion of subjects who completely eradicate the tumor, i.e. CR/number of animals used in the experiment; Partial Response Rate (PRR) refers to the proportion of subjects with partially reduced tumors after treatment, i.e., PR/CR/number of animals used in the experiment; TGI refers to tumor growth inhibition rate; T/C refers relative tumor proliferation rate, T/C (%) = T/C×100 (T: average tumor volume of a treatment group; C: average tumor volume of a solvent control group); IR refers to tumor weight inhibition rate, IR (%) = [1- (average tumor weight of a treatment group/average tumor weight of solvent control group)] ×100.

The experimental results shows that a single dose of 0.3-30 mg/kg M21-17-Cpd3 could inhibit the growth of GSU transplanted tumors in a dose-dependent manner; the tumor volume measurement data for each experimental group is shown in FIG. 9. No weight loss was observed in all experimental animals during the experimental period.

Example 18: Verification of anti-tumor effect of humanized ADCs on human gastric cancer NUGC-4 transplanted tumor model

The anti-tumor activity of the antibody drug conjugate M21-17-Cpd3 of the present application was detected using the experimental method described in Example 12.

The experimental design is as follows:

Experimental group one: PBS control group, a single dose at the same dose as ADC.

Experimental group two: M21-17-Cpd3, 1 mg/kg, single dose.

Experimental group three: M21-17-Cpd3, 3 mg/kg, single dose.

Experimental group four: M21-17-Cpd3, 10 mg/kg, single dose.

Experimental group five: M21-17-Cpd3, 30 mg/kg, single dose.

Experimental group six: M21-17-Cpd3, 10 mg/kg, QW*3.

All data are presented as average values. The *in vivo* efficacy index of the mice is shown in the following TABLE 13.

TABLE 13. *In vivo* efficacy of humanized ADCs in mice (NUGC4 cells)

Experimental group	TGI (%)	T/C (%)	PRR	IR (%)
1	-	-	-	-
2	38.33	61.67	0/6	36.74
3	49.92	50.08	0/6	48.25
4	74.20	25.80	0/6	70.90
5	96.24	3.76	6/6	94.20
6	96.14	3.86	6/6	93.37

Note: Complete Response (CR) refers to Tumor Volume (TV) =0 mm^3; partial Response (PR) refers to at least a 30% reduction in tumor volume relative to baseline; complete Response Rate (CRR) refers to the proportion of subjects who completely eradicate the tumor, i.e. CR/number of animals used in the experiment; partial Response Rate (PRR) refers to the proportion of subjects with partially reduced tumors after treatment, i.e., PR/CR/number of animals used in the experiment; TGI refers to tumor growth inhibition rate; T/C refers relative tumor proliferation rate, T/C (%) = T/C×100 (T: average tumor volume of a treatment group; C: average tumor volume of a solvent control group); IR refers tumor weight inhibition rate, IR (%) = [1- (average tumor weight of a treatment group/average tumor weight of solvent control group)] ×100.

The experimental result shows that 1-30 mg/kg of M21-17-Cpd 3 can inhibit the growth of the NUGC-4 transplanted tumor in a dose-dependent manner by single administration; the tumor volume measurement data for each experimental group is shown in fig. 10.

Example 19: Verification of anti-tumor effect of humanized ADCs on human colon cancer SW480 transplanted tumor model

The anti-tumor activity of the antibody drug conjugate M21-17-Cpd3 of the present application was detected using the experimental method described in Example 12. SW480 cells were purchased from ATCC, CCL-228.

The experimental design is as follows:

Experimental group one: PBS control group, a single dose at the same dose as ADC.

Experimental group two: M21-17-Cpd3, 3 mg/kg, single dose.

Experimental group three: M21-17-Cpd3, 10 mg/kg, single dose.

Experimental group four: M21-17-Cpd3, 30 mg/kg, single dose.

Experimental group five: M21-17-Cpd3, 3 mg/kg, QW*3.

Experimental group six: M21-17-Cpd3, 10 mg/kg, QW*3.

All data are presented as average values. The *in vivo* efficacy index of the mice is shown in the following TABLE 14.

TABLE 14. *In vivo* efficacy of humanized ADCs in mice (SW480 cells)

Experimental group	TGI (%)	T/C (%)	PRR	IR (%)
1	-	-	-	-
2	44.76	55.24	0/6	41.39%
3	63.03	36.97	0/6	62.72%
4	88.74	11.26	0/6	87.40%
5	26.09	73.91	0/6	27.25%
6	80.07	19.93	1/6	77.72%

Note: Complete Response (CR) refers to Tumor Volume (TV) =0 mm^3; Partial Response (PR) refers to at least a 30% reduction in tumor volume relative to baseline; Complete Response Rate (CRR) refers to the proportion of subjects who completely eradicate the tumor, i.e. CR/number of animals used in the experiment; Partial Response Rate (PRR) refers to the proportion of subjects with partially reduced tumors after treatment, i.e., PR/CR/number of animals used in the experiment; TGI refers to tumor growth inhibition rate; T/C refers relative tumor proliferation rate, T/C (%) = T/C×100 (T: average tumor volume of a treatment group; C: average tumor volume of a solvent control group); IR refers to tumor weight inhibition rate, IR (%) = [1- (average tumor weight of a

treatment group/average tumor weight of solvent control group)] ×100.

The experimental result shows that a single dose of 3-30 mg/kg M21-17-Cpd3 could inhibit the growth of SW480 transplanted tumor in a dose-dependent manner; the tumor volume measurement data for each experimental group is shown in FIG. 11.

Example 20: Validation for plasma stability of linker-toxin Cpd3

The test ADC molecule M21-17-Cpd3 (concentration of 0.2 mg/mL) was incubated in plasma of different species (human/monkey/rat/mouse) for 21 days at 37 ℃, during which the concentration of free drug (e.g., Cpd3 or Dxd) in plasma at different time points was detected by LC-MS/Ms. The control sample of this Example was DS-8201 (commercially available). TABLE 15 below sets forth the experimental parameters for M21-17-Cpd3 (analyte Cpd3) and control DS-8201 (analyte Dxd).

The release rate (%) refers to the falling-off rate of the free drug in the plasma obtained by measuring the content of the free drug in the plasma after the ADC and the plasma have been incubated for a certain time and calculating according to the ratio of the content of the free drug in the plasma to the total amount of the drug in the ADC.

TABLE 14. Stability of ADC in plasma

Test ADC molecules	Analyte	Time (day)	Release rate%			
			Mouse	PBS	Monkey	Human
M21-17-Cpd3	Cpd3	0	0.137	0.021	0.024	0.047
		3	0.723	0.033	0.057	0.116
		7	1.120	0.041	0.064	0.134
		14	1.188	0.088	0.104	0.184
		21	1.152	0.074	0.107	0.391
DS-8201	Dxd	0	0.014	0.008	0.013	0.010
		3	0.078	0.043	0.250	0.423
		7	0.152	0.085	0.462	0.783
		14	0.261	0.169	0.938	1.325
		21	0.327	0.283	1.218	2.104

The experimental results show that the humanized antibody M21-17 conjugated with Cpd3 (DAR8) has good plasma stability and has stability in the plasma of different species. Cpd3 showed very high stability in humans and monkeys and was superior to the linker-toxin Dxd of the control DS-8201.

Example 21: Verification of the conjugation properties of the linker-toxin Cpd3

Cpd3 was used for conjugation with her2 antibody Trastuzumab, and the conjugation efficiency and quality criteria of the antibody drug conjugate were verified.

Using commercially available her2 antibody Trastuzumab, conventional antibody drug conjugate preparation method similar to example 11 was adopted to replace the solution of Trastuzumab with a buffer of 20 mM His, pH 6.0, and the concentration was measured with a ultraviolet spectrophotometer at 16.95 mg/mL. A new stock solution of TCEP (5 mmol/L) was prepared with 20 mM His, pH 6.0. His, antibody and TCEP were added to an EP tube in this order to give a final antibody reaction concentration of 6.0 mg/mL, wherein the amount of TCEP added was 10 molar equivalents (relative to the antibody concentration), and the mixture was incubated for 2 hours at 25 ℃ (Taking 4.8mg/mL antibody stock solution as an example, add 450.8 ul His, 283.19 ul antibody, 65.97 ul TCEP in sequence respectively.); after incubation for 1h at 25 ℃, the buffer of the reaction mixture was replaced with 20 mM His pH 6.0 using a desalting column to remove unconjugated small molecule drug, and stored at 4 ℃. The final samples were pooled and concentrated, and the absorption of ADC and LP (linker-toxin) at 280nm and 365nm were detected. The final sample was sterile filtered through a 0.22um filter to obtain Trastuzumab-Cpd3. The antibody drug conjugates produced were characterized as follows.

Sample analysis:

1. SEC analysis: 100% buffer A was run at 0.8ml/min for 20 minutes. (Buffer: 100 mM PB, 15% IPA, pH 6.8).

2. Reversed-Phase Analysis (RP) of ADC: 27% –50% buffer B was run at 1.0ml/min for 40 min. (Buffer A: 0.05% TFA, water; Buffer B: 0.05% TFA, acetonitrile) .

3. Hydrophobic interaction analysis (HIC) of ADC: 0% –100% Buffer B was run at 0.5ml/min for 35 minutes (Buffer A: 1.5 M $(NH_4)_2SO_4$, 25 mM PB, pH 7.0; Buffer B: 25 mM PB, 20% IPA, pH 7.0) .

4. Free small molecule assay of ADC (C18): performing ultraviolet full wavelength scanning on the linker-toxin (L-D) by using an ultraviolet spectrophotometer to determine any maximum absorption wavelength of the L-D except 280 nm; the standard substance was diluted in a gradient manner, loaded 10 ul of each concentration, sequentially loaded 1 ug, 0.5 ug, 0.3 ug, 0.1 ug, 0.05 ug and 0.02ug of final sample, and simultaneously detecting the absorption of multiple wavelengths, to prepare a standard curve of L-D. (Buffer A: 0.05% TFA, water; Buffer B: 0.05% TFA, acetonitrile) .

5. Endotoxin detection: (1) preparing standard curve: dissolving endotoxin standard substance with 1 ml water for injection, and treating for 10 min with vortex oscillator to prepare 10 EU/ml. Diluting the standard substance with water for injection in a gradient manner to 1 EU/ml, 0.1 EU/ml and 0.01 EU/ml in sequence, and setting a positive reference of 0.5 EU/ml; (2) treating a sample:

diluting the sample 20 times with water for injection and treating for 30 s with vortex oscillator, (3) loading: sequentially adding the standard substance, the positive reference substance and the detection sample into a sterile enzyme-free and pyrogen-free 96-well plate, sequentially adding 100 ul of Tachypleus Amebocyte Lysate into the other plate, using a multichannel pipettor to draw 100 ul of samples to be detected, and adding the samples to be detected into a detection plate containing the Tachypleus Amebocyte Lysate, and arranging 2 replicate wells for each sample; (4) detecting: the wavelength at 405 nm is dynamically detected for 90 min.

The results of the experiments are shown in TABLE 15 below and in FIG. 12-14. The prepared Her-2-Cpd3 ADC has the SEC purity of 98%, the RP-DAR value of 7.9, the free toxin content < 5%, the recovery rate of 67%, the HIC-DAR value of 7.95 and the endotoxin of 0.01 EU/mg.

TABLE 15. ADC sample detection results

Name of antibody	Linker-Payload	ADC detection result			
		DAR	SEC purity	Endotoxin (EU/mg)	Conc. (mg/ml)
Trastuzumab	Cpd3	7.90	98.43 %	0.01	6.18

Experimental conclusion: Cpd3 as a linker-toxin has high conjugation efficiency and mild reaction conditions. Therefore, Cpd3 as a hydrophilic linker-toxin can be used to prepare ADCs with high DAR values and excellent purity.

Various modifications of the application in addition to those described herein will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. Each reference (including all patents, patent applications, journal articles, books, and any other publications) cited in this disclosure is hereby incorporated by reference in its entirety.

Sequence

M1	HCDR1 (Kabat)	SEQ ID NO:1	SYWMN
	HCDR2 (Kabat)	SEQ ID NO:2	QIYPGDGDARYNGKFNG
	HCDR3 (Kabat)	SEQ ID NO:3	SMGLGLDY
	LCDR1 (Kabat)	SEQ ID NO:4	RSSQSLVHSNGNTYLH
	LCDR2 (Kabat)	SEQ ID NO:5	KVSNRFS
	LCDR3 (Kabat)	SEQ ID NO:6	SQTTHVPPYT
	VH	SEQ ID NO:7	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPG QGLEWIGQIYPGDGDARYNGKFNGKATLTTDKSSSTAYMQLSS LTSEDSAVYFCTRSMGLGLDYWGQGTTLTVSS
	VL	SEQ ID NO:8	DVVMTQTPLSLPVSLGHQASISCRSSQSLVHSNGNTYLHWYLQ KPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDL GVYFCSQTTHVPPYTFGGGTKLEIK
	heavy chain	SEQ ID NO:9	QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPG QGLEWIGQIYPGDGDARYNGKFNGKATLTTDKSSSTAYMQLSS LTSEDSAVYFCTRSMGLGLDYWGQGTTLTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
	light chain	SEQ ID NO:10	DVVMTQTPLSLPVSLGHQASISCRSSQSLVHSNGNTYLHWYLQ KPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDL GVYFCSQTTHVPPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKS GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG EC
M2	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:12	HIYWDDDKRYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:13	RAPYFDSPFAY
	LCDR1 (Kabat)	SEQ ID NO:14	KSSQSVLYSSNQKNYLA
	LCDR2 (Kabat)	SEQ ID NO:15	WASTRES
	LCDR3 (Kabat)	SEQ ID NO:16	HQYLSSLT
	VH	SEQ ID NO:17	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK

			GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT ADTATYYCARRAPYFDSPFAYWGQGTLVTVSA
	VL	SEQ ID NO:18	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWY QQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQA EDLAVYYCHQYLSSLTFGAGTMLELK
	heavy chain	SEQ ID NO:19	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT ADTATYYCARRAPYFDSPFAYWGQGTLVTVSAASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
	light chain	SEQ ID NO:20	NIMMTQSPSSLAVSAGEKVTMSCKSSQSVLYSSNQKNYLAWY QQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQA EDLAVYYCHQYLSSLTFGAGTMLELKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M3	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:12	HIYWDDDKRYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:21	TIPTVVFDY
	LCDR1 (Kabat)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (Kabat)	SEQ ID NO:15	WASTRES
	LCDR3 (Kabat)	SEQ ID NO:23	QQYYSYRT
	VH	SEQ ID NO:24	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVD TADTATYYCARTIPTVVFDYWGQGTTLTVSS
	VL	SEQ ID NO:25	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWY QQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKA EDLAVYYCQQYYSYRTFGGGTKLEIK
	heavy chain	SEQ ID NO:26	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT ADTATYYCARTIPTVVFDYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN

			HYTQKSLSLSPGK
	light chain	SEQ ID NO:27	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQ QKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAE DLAVYYCQQYYSYRTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M4	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:12	HIYWDDDKRYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:21	TIPTVVFDY
	LCDR1 (Kabat)	SEQ ID NO:28	HASQVISSNIG
	LCDR2 (Kabat)	SEQ ID NO:29	HGTNLED
	LCDR3 (Kabat)	SEQ ID NO:30	VRYAQFPWT
	VH	SEQ ID NO:24	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT ADTATYYCARTIPTVVFDYWGQGTTLTVSS
	VL	SEQ ID NO:31	DILMTQSPSSMSVSLGDAVSITCHASQVISSNIGWLQQKPGKSF KGLIYHGTNLEDGVPSRFSGSGSGADYSLTISSLESEDFADYYC VRYAQFPWTFGGGTKLEIK
	heavy chain	SEQ ID NO:26	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT ADTATYYCARTIPTVVFDYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:32	DILMTQSPSSMSVSLGDAVSITCHASQVISSNIGWLQQKPGKSF KGLIYHGTNLEDGVPSRFSGSGSGADYSLTISSLESEDFADYYC VRYAQFPWTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M5	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:12	HIYWDDDKRYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:33	TTTTVVFDY
	LCDR1 (Kabat)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2	SEQ ID NO:15	WASTRES

	(Kabat)		
	LCDR3 (Kabat)	SEQ ID NO:23	QQYYSYRT
	VH	SEQ ID NO:34	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLRITSVD TADSATYHCARTTTTVVFDYWGQGTTLTVSS
	VL	SEQ ID NO:35	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWY QQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKA EDLAVYYCQQYYSYRTFGGGTKLEIK
	heavy chain	SEQ ID NO:36	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLRITSVDT ADSATYHCARTTTTVVFDYWGQGTTLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:37	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQ QKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAE DLAVYYCQQYYSYRTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M6	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:12	HIYWDDDKRYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:38	NYAGYFDY
	LCDR1 (Kabat)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (Kabat)	SEQ ID NO:39	WASTRDS
	LCDR3 (Kabat)	SEQ ID NO:23	QQYYSYRT
	VH	SEQ ID NO:40	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVD TADTATYYCARNYAGYFDYWGQGTTLTVSS
	VL	SEQ ID NO:41	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWY QQKPGQSPKLLIYWASTRDSGVPDRFTGSGSGTDFTLTISSVKA EDLAVYYCQQYYSYRTFGGGTRLEIK
	heavy chain	SEQ ID NO:42	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT ADTATYYCARNYAGYFDYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV

			VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:43	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQ QKPGQSPKLLIYWASTRDSGVPDRFTGSGSGTDFTLTISSVKAE DLAVYYCQQYYSYRTFGGGTRLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M7	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:44	HIYWDDDKHYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:45	TITTVVFDY
	LCDR1 (Kabat)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (Kabat)	SEQ ID NO:15	WASTRES
	LCDR3 (Kabat)	SEQ ID NO:46	LQYYSYRT
	VH	SEQ ID NO:47	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKHYNPSLKSRLTISKDTSRNQVFLKIPSVD TADTATYYCARTITTVVFDYWGQGTTLTVSS
	VL	SEQ ID NO:48	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWY QQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKA EDLAVYYCLQYYSYRTFGGGTKLEIK
	heavy chain	SEQ ID NO:49	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKHYNPSLKSRLTISKDTSRNQVFLKIPSVDT ADTATYYCARTITTVVFDYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:50	DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSSNQKNYLAWYQ QKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAE DLAVYYCLQYYSYRTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M8	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:44	HIYWDDDKHYNPSLKS

	HCDR3 (Kabat)	SEQ ID NO:45	TITTVVFDY
	LCDR1 (Kabat)	SEQ ID NO:51	HASQDIRSNIG
	LCDR2 (Kabat)	SEQ ID NO:29	HGTNLED
	LCDR3 (Kabat)	SEQ ID NO:52	VQYAQFSWT
	VH	SEQ ID NO:47	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKHYNPSLKSRLTISKDTSRNQVFLKIPSVD TADTATYYCARTITTVVFDYWGQGTTLTVSS
	VL	SEQ ID NO:53	DILMTQSPSSMSVSLGDTVSITCHASQDIRSNIGWLQQKPGKSF KGLIYHGTNLEDGVPSRFSGSGSGADYSLTISSLESEDFADYYC VQYAQFSWTFGGGSKLEIK
	heavy chain	SEQ ID NO:49	QVTLKESGPGILQSSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKHYNPSLKSRLTISKDTSRNQVFLKIPSVDT ADTATYYCARTITTVVFDYWGQGTTLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:54	DILMTQSPSSMSVSLGDTVSITCHASQDIRSNIGWLQQKPGKSF KGLIYHGTNLEDGVPSRFSGSGSGADYSLTISSLESEDFADYYC VQYAQFSWTFGGGSKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M9	HCDR1 (Kabat)	SEQ ID NO:11	TSGMGVS
	HCDR2 (Kabat)	SEQ ID NO:12	HIYWDDDKRYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:55	MRIITTAFDY
	LCDR1 (Kabat)	SEQ ID NO:56	KASQDVSPAVA
	LCDR2 (Kabat)	SEQ ID NO:57	SASYRYT
	LCDR3 (Kabat)	SEQ ID NO:58	QQHYSTPFT
	VH	SEQ ID NO:59	QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVD TADTATYYCARMRIITTAFDYWGQGTTLTVSS
	VL	SEQ ID NO:60	DIVMTQSHKFMSTSVGDRVSITCKASQDVSPAVAWYQQKPGQ SPKLLIYSASYRYTGVPDRFTGSGSGTDFTFTISSVQAEDLAVY YCQQHYSTPFTFGSGTKLEIK
	heavy chain	SEQ ID NO:61	QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVSWIRQPSGK GLEWLAHIYWDDDKRYNPSLKSRLTISKDTSRNQVFLKITSVDT

			ADTATYYCARMRIITTAFDYWGQGTTLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:62	DIVMTQSHKFMSTSVGDRVSITCKASQDVSPAVAWYQQKPGQS PKLLIYSASYRYTGVPDRFTGSGSGTDFTFTISSVQAEDLAVYY CQQHYSTPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M10	HCDR1 (Kabat)	SEQ ID NO:63	TYGVH
	HCDR2 (Kabat)	SEQ ID NO:64	VIWRGGSTDYNAAFMT
	HCDR3 (Kabat)	SEQ ID NO:65	AGTTEPPFAY
	LCDR1 (Kabat)	SEQ ID NO:66	KSSQSLLYSRNQKNYLA
	LCDR2 (Kabat)	SEQ ID NO:67	WASTGES
	LCDR3 (Kabat)	SEQ ID NO:68	QQYYSYPYT
	VH	SEQ ID NO:69	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTTYGVHWVRQSPGK GLEWLGVIWRGGSTDYNAAFMTRLSITKDNSKSQVFFKMNSL QPDDTAVYYCARAGTTEPPFAYWGQGTLVTVSA
	VL	SEQ ID NO:70	DIVMSQSPSSLPVSVGEKVTMSCKSSQSLLYSRNQKNYLAWFQ QKPGQSPKLLIYWASTGESGVPDRFTGSGSGTDFTLTISSVKAE DLAVYYCQQYYSYPYTFGGGTKLEIK
	heavy chain	SEQ ID NO:71	QVQLKQSGPGLVQPSQSLSITCTVSGFSLTTYGVHWVRQSPGK GLEWLGVIWRGGSTDYNAAFMTRLSITKDNSKSQVFFKMNSL QPDDTAVYYCARAGTTEPPFAYWGQGTLVTVSAASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:72	DIVMSQSPSSLPVSVGEKVTMSCKSSQSLLYSRNQKNYLAWFQ QKPGQSPKLLIYWASTGESGVPDRFTGSGSGTDFTLTISSVKAE DLAVYYCQQYYSYPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M11	HCDR1	SEQ ID NO:1	SYWMN

	(Kabat)		
	HCDR2 (Kabat)	SEQ ID NO:73	QIYPGDGDTNYNGKFKG
	HCDR3 (Kabat)	SEQ ID NO:74	SMSYSDY
	LCDR1 (Kabat)	SEQ ID NO:75	KSSQSLLYTTNQKNYLA
	LCDR2 (Kabat)	SEQ ID NO:15	WASTRES
	LCDR3 (Kabat)	SEQ ID NO:76	QQYSSYPRT
	VH	SEQ ID NO:77	QVQLQQSGAELVRPGSSVKISCKASGYEFSSYWMNWVKQRPG QGLEWIGQIYPGDGDTNYNGKFKGKATLTADKSSSKAYMQFS SLTSEDSAVYFCARSMSYSDYWGQGTTLTVSS
	VL	SEQ ID NO:78	DIVMSQSPSSLAVSVGEKANMSCKSSQSLLYTTNQKNYLAWY QQKPGQAPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKA EDLAIYYCQQYSSYPRTFGGGTKLEIK
	heavy chain	SEQ ID NO:79	QVQLQQSGAELVRPGSSVKISCKASGYEFSSYWMNWVKQRPG QGLEWIGQIYPGDGDTNYNGKFKGKATLTADKSSSKAYMQFSS LTSEDSAVYFCARSMSYSDYWGQGTTLTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:80	DIVMSQSPSSLAVSVGEKANMSCKSSQSLLYTTNQKNYLAWYQ QKPGQAPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAE DLAIYYCQQYSSYPRTFGGGTKLEIKRTVAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR GEC
M12	HCDR1 (Kabat)	SEQ ID NO:81	SDYAWN
	HCDR2 (Kabat)	SEQ ID NO:82	FISYSGGTIYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:83	NNGYGFDY
	LCDR1 (Kabat)	SEQ ID NO:84	SVSSSISYIH
	LCDR2 (Kabat)	SEQ ID NO:85	DTSKLTS
	LCDR3 (Kabat)	SEQ ID NO:86	QQWSTYPLT
	VH	SEQ ID NO:87	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPG NKLEWMGFISYSGGTIYNPSLKSRFSITRDTSKNLFFLQLKSVTS EDTATYYCSRNNGYGFDYWGQGTSLTVSS
	VL	SEQ ID NO:88	QIVLTQSPAIMSASPGERVTMTCSVSSSISYIHWYQQKSGTSPK

			RWIYDTSKLTSGVPARFSGSGSGTSYSLTISNMEAEDAATYYC QQWSTYPLTFGAGTKLELK
	heavy chain	SEQ ID NO:89	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGN KLEWMGFISYSGGTIYNPSLKSRFSITRDTSKNLFFLQLKSVTSE DTATYYCSRNNGYGFDYWGQGTSLTVSSASTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:90	QIVLTQSPAIMSASPGERVTMTCSVSSSISYIHWYQQKSGTSPKR WIYDTSKLTSGVPARFSGSGSGTSYSLTISNMEAEDAATYYCQQ WSTYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M13	HCDR1 (Kabat)	SEQ ID NO:91	SYNMH
	HCDR2 (Kabat)	SEQ ID NO:92	SIYPGNGDTSYNQKFKG
	HCDR3 (Kabat)	SEQ ID NO:93	GDGYDRLDY
	LCDR1 (Kabat)	SEQ ID NO:94	RASQNVGTNVV
	LCDR2 (Kabat)	SEQ ID NO:95	SASYRFS
	LCDR3 (Kabat)	SEQ ID NO:96	QQYKSYPHT
	VH	SEQ ID NO:97	QVQLQQPGAELVKPGASVRMSCKASGYTFSSYNMHWVKQTP GQGLDWIGSIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQL SSLTSEDSAVYYCAKGDGYDRLDYWGQGTSVTVSS
	VL	SEQ ID NO:98	DIVMTQSQKFMSTSVGDRVSVTCRASQNVGTNVVWYQQKPG QSPKPLIFSASYRFSGVPDRFTGSVSGTDFTLTISNVQSEDLAEY FCQQYKSYPHTFGGGTKLEIR
	heavy chain	SEQ ID NO:99	QVQLQQPGAELVKPGASVRMSCKASGYTFSSYNMHWVKQTP GQGLDWIGSIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLS SLTSEDSAVYYCAKGDGYDRLDYWGQGTSVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:100	DIVMTQSQKFMSTSVGDRVSVTCRASQNVGTNVVWYQQKPG QSPKPLIFSASYRFSGVPDRFTGSVSGTDFTLTISNVQSEDLAEY FCQQYKSYPHTFGGGTKLEIRRTVAAPSVFIFPPSDEQLKSGTAS

			VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M14	HCDR1 (Kabat)	SEQ ID NO:81	SDYAWN
	HCDR2 (Kabat)	SEQ ID NO:101	YISYSGYTTYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:83	NNGYGFDY
	LCDR1 (Kabat)	SEQ ID NO:102	SASSSVSYMH
	LCDR2 (Kabat)	SEQ ID NO:103	DTSKLAS
	LCDR3 (Kabat)	SEQ ID NO:86	QQWSTYPLT
	VH	SEQ ID NO:104	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPG NKLEWMGYISYSGYTTYNPSLKSRFSFTRDTSKNQFFLQLNSV TTEDTGTYYCATNNGYGFDYWGQGATLTVSS
	VL	SEQ ID NO:105	QIALTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAGTYY CQQWSTYPLTFGAGTKLELK
	heavy chain	SEQ ID NO:106	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGN KLEWMGYISYSGYTTYNPSLKSRFSFTRDTSKNQFFLQLNSVTT EDTGTYYCATNNGYGFDYWGQGATLTVSSASTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:107	QIALTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSP KRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAGTYYC QQWSTYPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M15	HCDR1 (Kabat)	SEQ ID NO:108	SYAMS
	HCDR2 (Kabat)	SEQ ID NO:109	SISSGGSTSYPDSVKG
	HCDR3 (Kabat)	SEQ ID NO:110	GSPYWYFDV
	LCDR1 (Kabat)	SEQ ID NO:111	KASQNVGISVA
	LCDR2 (Kabat)	SEQ ID NO:112	SASYRYS
	LCDR3 (Kabat)	SEQ ID NO:113	QQYNRYPT
	VH	SEQ ID NO:114	EVKLVESGGGLVKPRGSLKLSCAASAFTFSSYAMSWVRQTPEK RLEWVASISSGGSTSYPDSVKGRFTISRDNARNILYLQMSSLRS

			EDTAMYYCARGSPYWYFDVWGAGTTVTVSS
	VL	SEQ ID NO:115	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGISVAWYQQKSGQ SPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYF CQQYNRYPTFGGGTKLEIK
	heavy chain	SEQ ID NO:116	EVKLVESGGGLVKPRGSLKLSCAASAFTFSSYAMSWVRQTPEK RLEWVASISSGGSTSYPDSVKGRFTISRDNARNILYLQMSSLRSE DTAMYYCARGSPYWYFDVWGAGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:117	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGISVAWYQQKSGQ SPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYF CQQYNRYPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M16	HCDR1 (Kabat)	SEQ ID NO:108	SYAMS
	HCDR2 (Kabat)	SEQ ID NO:109	SISSGGSTSYPDSVKG
	HCDR3 (Kabat)	SEQ ID NO:110	GSPYWYFDV
	LCDR1 (Kabat)	SEQ ID NO:111	KASQNVGISVA
	LCDR2 (Kabat)	SEQ ID NO:112	SASYRYS
	LCDR3 (Kabat)	SEQ ID NO:118	QQYNRDPT
	VH	SEQ ID NO:114	EVKLVESGGGLVKPRGSLKLSCAASAFTFSSYAMSWVRQTPEK RLEWVASISSGGSTSYPDSVKGRFTISRDNARNILYLQMSSLRS EDTAMYYCARGSPYWYFDVWGAGTTVTVSS
	VL	SEQ ID NO:119	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGISVAWYQQKSGQ SPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAEYF CQQYNRDPTFGGGTKLEIK
	heavy chain	SEQ ID NO:116	EVKLVESGGGLVKPRGSLKLSCAASAFTFSSYAMSWVRQTPEK RLEWVASISSGGSTSYPDSVKGRFTISRDNARNILYLQMSSLRSE DTAMYYCARGSPYWYFDVWGAGTTVTVSSASTKGPSVFPLAP SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK
	light chain	SEQ ID NO:120	MDIVMTQSQKFMSTSVGDRVSVTCKASQNVGISVAWYQQKSG

			QSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSEDLAE YFCQQYNRDPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M17	HCDR1 (Kabat)	SEQ ID NO:121	SYNIH
	HCDR2 (Kabat)	SEQ ID NO:122	SIYPGNGDPSYNQKFKG
	HCDR3 (Kabat)	SEQ ID NO:93	GDGYDRLDY
	LCDR1 (Kabat)	SEQ ID NO:123	KASQNVGTYVV
	LCDR2 (Kabat)	SEQ ID NO:95	SASYRFS
	LCDR3 (Kabat)	SEQ ID NO:124	HQYNNYPHT
	VH	SEQ ID NO:125	QVQLQQPGTELVKPGASVKMSCKASGYTFASYNIHWVKQTPG QGLEWIASIYPGNGDPSYNQKFKGKATLTADTSSSTAYMQLSS LTSEDSAVYYCAKGDGYDRLDYWGQGTSVTVSS
	VL	SEQ ID NO:126	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTYVVWYQQKPG QSPKPLIYSASYRFSEVPDRFTGSGSGTDFTLTISNVQSEDLAEY FCHQYNNYPHTFGGGTKLEVK
	heavy chain	SEQ ID NO:127	QVQLQQPGTELVKPGASVKMSCKASGYTFASYNIHWVKQTPG QGLEWIASIYPGNGDPSYNQKFKGKATLTADTSSSTAYMQLSSL TSEDSAVYYCAKGDGYDRLDYWGQGTSVTVSSASTKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE ALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:128	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTYVVWYQQKPG QSPKPLIYSASYRFSEVPDRFTGSGSGTDFTLTISNVQSEDLAEY FCHQYNNYPHTFGGGTKLEVKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M18	HCDR1 (Kabat)	SEQ ID NO:129	SYWVN
	HCDR2 (Kabat)	SEQ ID NO:130	RIHPYDSETHYNQKFKD
	HCDR3 (Kabat)	SEQ ID NO:131	WTARAASAMDY
	LCDR1 (Kabat)	SEQ ID NO:132	SANSSVSYMY
	LCDR2 (Kabat)	SEQ ID NO:133	RTSNLAS
	LCDR3 (Kabat)	SEQ ID NO:134	QQYHSFPLT

	VH	SEQ ID NO:135	QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWVNWVKQRP EQGLEWIGRIHPYDSETHYNQKFKDKAILTVDKSSSTAYMQLS SLTSEDSAVYYCARWTARAASAMDYWGQGSSVTVSS
	VL	SEQ ID NO:136	QIVLTQSPAIMSASPGEKVTISCSANSSVSYMYWYQQKPGSSPK PWIYRTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQ QYHSFPLTFGAGTKLELK
	heavy chain	SEQ ID NO:137	QVQLQQPGAELVRPGASVKLSCKASGYTFTSYWVNWVKQRPE QGLEWIGRIHPYDSETHYNQKFKDKAILTVDKSSSTAYMQLSSL TSEDSAVYYCARWTARAASAMDYWGQGSSVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:138	QIVLTQSPAIMSASPGEKVTISCSANSSVSYMYWYQQKPGSSPK PWIYRTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQ QYHSFPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M19	HCDR1 (Kabat)	SEQ ID NO:91	SYNMH
	HCDR2 (Kabat)	SEQ ID NO:92	SIYPGNGDTSYNQKFKG
	HCDR3 (Kabat)	SEQ ID NO:93	GDGYDRLDY
	LCDR1 (Kabat)	SEQ ID NO:139	KASQNVGTNVV
	LCDR2 (Kabat)	SEQ ID NO:112	SASYRYS
	LCDR3 (Kabat)	SEQ ID NO:96	QQYKSYPHT
	VH	SEQ ID NO:97	QVQLQQPGAELVKPGASVRMSCKASGYTFSSYNMHWVKQTP GQGLDWIGSIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQL SSLTSEDSAVYYCAKGDGYDRLDYWGQGTSVTVSS
	VL	SEQ ID NO:140	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVVWYQHKPG QSPKALIFSASYRYSGVPDRFTGSVSGTDFTLTISNVQSEDLAEY FCQQYKSYPHTFGGGTKLEIR
	heavy chain	SEQ ID NO:141	QVQLQQPGAELVKPGASVRMSCKASGYTFSSYNMHWVKQTP GQGLDWIGSIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLS SLTSEDSAVYYCAKGDGYDRLDYWGQGTSVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH

			EALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:142	DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVVWYQHKPG QSPKALIFSASYRYSGVPDRFTGSVSGTDFTLTISNVQSEDLAEY FCQQYKSYPHTFGGGTKLEIRRTVAAPSVFIFPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY SLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M20	HCDR1 (Kabat)	SEQ ID NO:143	IYSVH
	HCDR2 (Kabat)	SEQ ID NO:144	MIWSGGNTDYNSTLKS
	HCDR3 (Kabat)	SEQ ID NO:145	NWRNDTHLYYVMDY
	LCDR1 (Kabat)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (Kabat)	SEQ ID NO:147	KTSTLHT
	LCDR3 (Kabat)	SEQ ID NO:148	QQGQSYPFT
	VH	SEQ ID NO:149	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSVHWVRQPPGKG LEWLGMIWSGGNTDYNSTLKSRLSIRKDNSKSQIFLKMNSLQT DDTAMYYCARNWRNDTHLYYVMDYWGQGTSVTVSS
	VL	SEQ ID NO:150	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPENIP KLLIFKTSTLHTGVPSRFSGSGSGTGFTLTISSLQPEDFATYYCQ QGQSYPFTFGSGTKLEIK
	heavy chain	SEQ ID NO:151	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSVHWVRQPPGKG LEWLGMIWSGGNTDYNSTLKSRLSIRKDNSKSQIFLKMNSLQT DDTAMYYCARNWRNDTHLYYVMDYWGQGTSVTVSSASTKG PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:152	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPENIP KLLIFKTSTLHTGVPSRFSGSGSGTGFTLTISSLQPEDFATYYCQQ GQSYPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M21	HCDR1 (Kabat)	SEQ ID NO:81	SDYAWN
	HCDR2 (Kabat)	SEQ ID NO:153	YISYSGSTTYNPSLKS
	HCDR3 (Kabat)	SEQ ID NO:154	WGTIYYRGYEGFAY
	LCDR1 (Kabat)	SEQ ID NO:155	KASQSVNNDVA
	LCDR2 (Kabat)	SEQ ID NO:156	YASNRFT

	LCDR3 (Kabat)	SEQ ID NO:157	QQDYSSPWT
	VH	SEQ ID NO:158	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPG NKLEWMGYISYSGSTTYNPSLKSRISITRDTSKNQFFLQLNSVT TEDTATYYCARWGTIYYRGYEGFAYWGQGTLVTVSA
	VL	SEQ ID NO:159	NIVMTQTPKFLLVSAGDRVTITCKASQSVNNDVAWYQQKPGQ SPKVLIYYASNRFTGVPDRFTGSGFGTDFTLTISTVQAEDLAVY FCQQDYSSPWTFGGGTKLEIK
	heavy chain	SEQ ID NO:160	DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGN KLEWMGYISYSGSTTYNPSLKSRISITRDTSKNQFFLQLNSVTTE DTATYYCARWGTIYYRGYEGFAYWGQGTLVTVSAASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:161	NIVMTQTPKFLLVSAGDRVTITCKASQSVNNDVAWYQQKPGQS PKVLIYYASNRFTGVPDRFTGSGFGTDFTLTISTVQAEDLAVYFC QQDYSSPWTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M22	HCDR1 (Kabat)	SEQ ID NO:162	RYSVH
	HCDR2 (Kabat)	SEQ ID NO:163	MIWSGENTDYNSALKS
	HCDR3 (Kabat)	SEQ ID NO:164	NWRNDTHLYYAMDY
	LCDR1 (Kabat)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (Kabat)	SEQ ID NO:165	KSSNLHT
	LCDR3 (Kabat)	SEQ ID NO:166	QQGQGFPFT
	VH	SEQ ID NO:167	QVQLKESGPGLVAPSQSLSITCSVSGFSLSRYSVHWVRQPPGKA LEWLGMIWSGENTDYNSALKSRLSISKDNSKSQVFLKMNSLQT DDTALYYCARNWRNDTHLYYAMDYWGQGTSVTVSS
	VL	SEQ ID NO:168	DIQMNQSPSSLSASLGDTIAITCHASQNINVWLNWYQQKPGNF PKLLIYKSSNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYC QQGQGFPFTFGSGTKLEIK
	heavy chain	SEQ ID NO:169	QVQLKESGPGLVAPSQSLSITCSVSGFSLSRYSVHWVRQPPGKA LEWLGMIWSGENTDYNSALKSRLSISKDNSKSQVFLKMNSLQT DDTALYYCARNWRNDTHLYYAMDYWGQGTSVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

			KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:170	DIQMNQSPSSLSASLGDTIAITCHASQNINVWLNWYQQKPGNF PKLLIYKSSNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQ QGQGFPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M23	HCDR1 (Kabat)	SEQ ID NO:143	IYSVH
	HCDR2 (Kabat)	SEQ ID NO:144	MIWSGGNTDYNSTLKS
	HCDR3 (Kabat)	SEQ ID NO:171	NWRNDTHLYYALDY
	LCDR1 (Kabat)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (Kabat)	SEQ ID NO:147	KTSTLHT
	LCDR3 (Kabat)	SEQ ID NO:148	QQGQSYPFT
	VH	SEQ ID NO:172	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSVHWVRQPPGKG LEWLGMIWSGGNTDYNSTLKSRLSIRKDNSKSQIFLKMNSLQT DDTAMYYCARNWRNDTHLYYALDYWGQGTSVTVSS
	VL	SEQ ID NO:173	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPENIP KLLIYKTSTLHTGVPSRFSGSGSGTGFTLTINSLQPEDFATYYCQ QGQSYPFTFGSGTKLEIK
	heavy chain	SEQ ID NO:174	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSVHWVRQPPGKG LEWLGMIWSGGNTDYNSTLKSRLSIRKDNSKSQIFLKMNSLQT DDTAMYYCARNWRNDTHLYYALDYWGQGTSVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:175	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPENIP KLLIYKTSTLHTGVPSRFSGSGSGTGFTLTINSLQPEDFATYYCQ QGQSYPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M24	HCDR1 (Kabat)	SEQ ID NO:176	RYSIH
	HCDR2 (Kabat)	SEQ ID NO:177	MIWGGGNTDYNSALKS
	HCDR3 (Kabat)	SEQ ID NO:164	NWRNDTHLYYAMDY
	LCDR1 (Kabat)	SEQ ID NO:146	HASQNINVWLN

	LCDR2 (Kabat)	SEQ ID NO:178	KAANLHT
	LCDR3 (Kabat)	SEQ ID NO:148	QQGQSYPFT
	VH	SEQ ID NO:179	QVQLKESGPGLVAPSQSLSITCTVSGFSLSRYSIHWVRQPPGRG LEWLGMIWGGGNTDYNSALKSRLSISKDNSKSQVFLKMNSLQ PDDTAMYYCARNWRNDTHLYYAMDYWGQGTSVTVSS
	VL	SEQ ID NO:180	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPGNV PKLLIYKAANLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYC QQGQSYPFTFGSGTKLEIK
	heavy chain	SEQ ID NO:181	QVQLKESGPGLVAPSQSLSITCTVSGFSLSRYSIHWVRQPPGRGL EWLGMIWGGGNTDYNSALKSRLSISKDNSKSQVFLKMNSLQP DDTAMYYCARNWRNDTHLYYAMDYWGQGTSVTVSSASTKGP SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:182	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPGNV PKLLIYKAANLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYC QQGQSYPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M25	HCDR1 (Kabat)	SEQ ID NO:183	SYWIQ
	HCDR2 (Kabat)	SEQ ID NO:184	AIYPGDGGTRYTQKFKG
	HCDR3 (Kabat)	SEQ ID NO:185	LYSNYYIDS
	LCDR1 (Kabat)	SEQ ID NO:186	KASQDINSYLS
	LCDR2 (Kabat)	SEQ ID NO:187	RADRLVE
	LCDR3 (Kabat)	SEQ ID NO:188	LQYDEFPNT
	VH	SEQ ID NO:189	QVQFHQSGAELARPGASVKMSCKASGYTFTSYWIQWVKQRPG QGLEWIGAIYPGDGGTRYTQKFKGRATLTADKSSSTAYMQLSS LTSEDSAVYYCATLYSNYYIDSWGQGTSVTVSS
	VL	SEQ ID NO:190	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSP KTLIYRADRLVEGVPSRFSGSGSGQDYSLTISSLEHEDMGIYYC LQYDEFPNTFGGGTKLEIK
	heavy chain	SEQ ID NO:191	QVQFHQSGAELARPGASVKMSCKASGYTFTSYWIQWVKQRPG QGLEWIGAIYPGDGGTRYTQKFKGRATLTADKSSSTAYMQLSSL TSEDSAVYYCATLYSNYYIDSWGQGTSVTVSSASTKGPSVFPLA PSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV

			VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPGK
	light chain	SEQ ID NO:192	DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSP KTLIYRADRLVEGVPSRFSGSGSGQDYSLTISSLEHEDMGIYYC LQYDEFPNTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M26	HCDR1 (Kabat)	SEQ ID NO:193	SYGVH
	HCDR2 (Kabat)	SEQ ID NO:194	VIWAGGRTIYNPALMS
	HCDR3 (Kabat)	SEQ ID NO:195	DLYGGAYGDY
	LCDR1 (Kabat)	SEQ ID NO:196	KASQDVSTTVA
	LCDR2 (Kabat)	SEQ ID NO:57	SASYRYT
	LCDR3 (Kabat)	SEQ ID NO:197	QQHYRSPLT
	VH	SEQ ID NO:198	QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPPGK GLEWLGVIWAGGRTIYNPALMSRLSISKDTSKSQVFLKMNSLQ TDDTAMYYCARDLYGGAYGDYWGQGTTLTVSS
	VL	SEQ ID NO:199	DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQ SPKLLIYSASYRYTGLPDRFTGSGSGTDFTFTISSVQAEDLAVY YCQQHYRSPLTFGAGTKLELK
	heavy chain	SEQ ID NO:200	QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPPGKG LEWLGVIWAGGRTIYNPALMSRLSISKDTSKSQVFLKMNSLQT DDTAMYYCARDLYGGAYGDYWGQGTTLTVSSASTKGPSVFPL APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVE PKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK
	light chain	SEQ ID NO:201	DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQS PKLLIYSASYRYTGLPDRFTGSGSGTDFTFTISSVQAEDLAVYYC QQHYRSPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M27	HCDR1 (Kabat)	SEQ ID NO:202	IYSIH
	HCDR2 (Kabat)	SEQ ID NO:144	MIWSGGNTDYNSTLKS
	HCDR3 (Kabat)	SEQ ID NO:145	NWRNDTHLYYVMDY

	LCDR1 (Kabat)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (Kabat)	SEQ ID NO:203	KTSTLHI
	LCDR3 (Kabat)	SEQ ID NO:148	QQGQSYPFT
	VH	SEQ ID NO:204	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSIHWVRQPPGKGL EWLGMIWSGGNTDYNSTLKSRLSIRKDNSKSQIFLKMNSLQTD DTAMYYCARNWRNDTHLYYVMDYWGQGTSVTVSS
	VL	SEQ ID NO:205	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPENIP KLLIYKTSTLHIGVPSRFSGSGSGTGFTLTISSLQPEDFATYYCQ QGQSYPFTFGSGTKLEIK
	heavy chain	SEQ ID NO:206	QVQLKESGPGLVAPSQSLSITCTVSGFSLSIYSIHWVRQPPGKGL EWLGMIWSGGNTDYNSTLKSRLSIRKDNSKSQIFLKMNSLQTD DTAMYYCARNWRNDTHLYYVMDYWGQGTSVTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:207	DIQMNQSPSSLSASLGDTITITCHASQNINVWLNWYQQKPENIP KLLIYKTSTLHIGVPSRFSGSGSGTGFTLTISSLQPEDFATYYCQQ GQSYPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
M28	HCDR1 (Kabat)	SEQ ID NO:208	NYRMN
	HCDR2 (Kabat)	SEQ ID NO:209	WINTYSGVPIYADDFKG
	HCDR3 (Kabat)	SEQ ID NO:210	TLYDGYSLYYVMDY
	LCDR1 (Kabat)	SEQ ID NO:211	HASQNINGWLS
	LCDR2 (Kabat)	SEQ ID NO:212	KASNLHT
	LCDR3 (Kabat)	SEQ ID NO:213	QQGQSHPLT
	VH	SEQ ID NO:214	QIQLVQSGPELKKPGETVKISCKASGYTFTNYRMNWVKQAPG KDLKWMGWINTYSGVPIYADDFKGRFAFSLETSANTAYLQINN LKNEDTATYFCARTLYDGYSLYYVMDYWGQGTSVTVSS
	VL	SEQ ID NO:215	DIQMNQSPSSLSASLGDTITITCHASQNINGWLSWYQQKPGNVP KLLIYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQ QGQSHPLTFGAGTKLELK
	heavy chain	SEQ ID NO:216	QIQLVQSGPELKKPGETVKISCKASGYTFTNYRMNWVKQAPG KDLKWMGWINTYSGVPIYADDFKGRFAFSLETSANTAYLQINN LKNEDTATYFCARTLYDGYSLYYVMDYWGQGTSVTVSSASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS

			GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:217	DIQMNQSPSSLSASLGDTITITCHASQNINGWLSWYQQKPGNVP KLLIYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQ QGQSHPLTFGAGTKLELKRTVAAPSVFIFPPSDEQLKSGTASVV CLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Tab1	heavy chain	SEQ ID NO:218	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPG KCLEWIGDIDASGSTKYNPSLKSRVTISLDTSKNQFSLKLNSVT AADTAVYFCARKKYSTVWSYFDNWGQGTLVTVSSASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH EALHNHYTQKSLSLSPGK
	light chain	SEQ ID NO:219	SYELTQPSSVSVPPGQTASITCSGDKLGDKYASWYQQKPGQSPV LVIYQDRKRPSGVPERFSGSNSGNTATLTISGTQAMDEADYYCQ AWGSSTAVFGCGTKLTVLGQPKAAPSVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAAS SYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
Mucin 17 mice Fc		SEQ ID NO:220	RTTTCFGDGCQNTASRCKNGGTWDGLKCQCPNLYYGELCEEV VSSIDIGPPETISAQMELTVTVTSVKFTEELKNHSSQEFQEFKQT FTEQMNIVYSGIPEYVGVNITKLRLGSVVVEHDVLLRTKYTPEY KTVLDNATEVVKEKITKVTTQQIMINDICSDMMCFNTTGTQVQ NITVTQYDPEEDCRKMAKEYGDYFVVEYRDQKPYCISPCEPGF SVSKNCNLGKCQMSLSGPQCLCVTTETHWYSGETCNQGTQKS LVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVV DISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPI MHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKN TQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNH HTEKSLSHSPGK
humanMucin17 truncated sequence（4131-4414aa）		SEQ ID NO:221	RTTTCFGDGCQNTASRCKNGGTWDGLKCQCPNLYYGELCEEV VSSIDIGPPETISAQMELTVTVTSVKFTEELKNHSSQEFQEFKQT FTEQMNIVYSGIPEYVGVNITKLRLGSVVVEHDVLLRTKYTPEY KTVLDNATEVVKEKITKVTTQQIMINDICSDMMCFNTTGTQVQ NITVTQYDPEEDCRKMAKEYGDYFVVEYRDQKPYCISPCEPGF SVSKNCNLGKCQMSLSGPQCLCVTTETHWYSGETCNQGTQKS LVYGLVGAGVVLMLIILVALLMLVF
Monkey Mucin17 truncated sequence（856-1213aa）		SEQ ID NO:222	RTTTCVGDQCSRCKNGGFWDGLKCQCLTPYYGESCEEVVNSI DIAPPETVSAQMELTVTVTSVKFTDELKNHSSQEFREFNKTFTE QMNIVYSGIPEYVGVNITNLRLGSVVVEHDVLLRTKYTPEYKT

			ALDNATEVVKQKITKVTTEQIMTNDNCSALMCFNTTGTQVQNI TVTQYDPVEECRQKAEEYGDYFLVEYRDQKPYCISPCESGFNA SKNCNHGKCQMSQNGARCLCVTTETHWYSGEDCNQGTQKSL VYGLVGAGVVLVLIILVALLMLIFHSKREVKRQKYRLSQWYKW QEENGGPTPGTFQNIGFDICQDDDSIHLESIYSNFQPSLRHIDPET KIQIQRPQVKTSF
Human IgG1 heavy chain constant region		SEQ ID NO:223	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK
Human light chain constant region (Kappa)		SEQ ID NO:224	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKV DNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA CEVTHQGLSSPVTKSFNRGEC
M21-02	VH	SEQ ID NO:259	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:263	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQP PKLLIYYASNRFTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QQDYSSPWTFGGGTKVEIK
	HCDR1	SEQ ID NO:81	SDYAWN
	HCDR2	SEQ ID NO:153	YISYSGSTTYNPSLKS
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY
	LCDR1	SEQ ID NO:155	KASQSVNNDVA
	LCDR2	SEQ ID NO:156	YASNRFT
	LCDR3	SEQ ID NO:157	QQDYSSPWT
M21-08	VH	SEQ ID NO:259	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:260	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQS PKVLIYYASNRFTGVPDRFSGSGFGTDFTLTISSLQAEDVAVYFC QQDYSSPWTFGGGTKVEIK
	HCDR1	SEQ ID NO:81	SDYAWN
	HCDR2	SEQ ID NO:153	YISYSGSTTYNPSLKS
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY
	LCDR1	SEQ ID NO:155	KASQSVNNDVA
	LCDR2	SEQ ID NO:156	YASNRFT
	LCDR3	SEQ ID NO:157	QQDYSSPWT
M21-09	VH	SEQ ID NO:261	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGN GLEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTA ADTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:260	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQS PKVLIYYASNRFTGVPDRFSGSGFGTDFTLTISSLQAEDVAVYFC QQDYSSPWTFGGGTKVEIK
	HCDR1	SEQ ID NO:81	SDYAWN
	HCDR2	SEQ ID NO:153	YISYSGSTTYNPSLKS
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY

	LCDR1	SEQ ID NO:155	KASQSVNNDVA
	LCDR2	SEQ ID NO:156	YASNRFT
	LCDR3	SEQ ID NO:157	QQDYSSPWT
M21-17	VH	SEQ ID NO:259	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:262	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKS PKVLIYYASNRFTGVPSRFSGSGFGTDFTLTISSLQPEDFATYFCQ QDYSSPWTFGGGTKVEIK
	HCDR1	SEQ ID NO:81	SDYAWN
	HCDR2	SEQ ID NO:153	YISYSGSTTYNPSLKS
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY
	LCDR1	SEQ ID NO:155	KASQSVNNDVA
	LCDR2	SEQ ID NO:156	YASNRFT
	LCDR3	SEQ ID NO:157	QQDYSSPWT
M21-18	VH	SEQ ID NO:261	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGN GLEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTA ADTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:262	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKS PKVLIYYASNRFTGVPSRFSGSGFGTDFTLTISSLQPEDFATYFCQ QDYSSPWTFGGGTKVEIK
	HCDR1	SEQ ID NO:81	SDYAWN
	HCDR2	SEQ ID NO:153	YISYSGSTTYNPSLKS
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY
	LCDR1	SEQ ID NO:155	KASQSVNNDVA
	LCDR2	SEQ ID NO:156	YASNRFT
	LCDR3	SEQ ID NO:157	QQDYSSPWT
M21-01	VH	SEQ ID NO:264	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISVDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:263	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQP PKLLIYYASNRFTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QQDYSSPWTFGGGTKVEIK
M21-03	VH	SEQ ID NO:261	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGN GLEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTA ADTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:263	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQP PKLLIYYASNRFTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC QQDYSSPWTFGGGTKVEIK
M21-04	VH	SEQ ID NO:264	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISVDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:265	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQS PKLLIYYASNRFTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC QQDYSSPWTFGGGTKVEIK
M21-05	VH	SEQ ID NO:259	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:265	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQS PKLLIYYASNRFTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC

			QQDYSSPWTFGGGTKVEIK
M21-06	VH	SEQ ID NO:261	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGN GLEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTA ADTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:265	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQS PKLLIYYASNRFTGVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC QQDYSSPWTFGGGTKVEIK
M21-07	VH	SEQ ID NO:264	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISVDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:260	DIVMTQSPDSLAVSLGERATINCKASQSVNNDVAWYQQKPGQS PKVLIYYASNRFTGVPDRFSGSGFGTDFTLTISSLQAEDVAVYFC QQDYSSPWTFGGGTKVEIK
M21-10	VH	SEQ ID NO:264	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISVDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:266	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKA PKLLIYYASNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ QDYSSPWTFGGGTKVEIK
M21-11	VH	SEQ ID NO:259	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:266	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKA PKLLIYYASNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ QDYSSPWTFGGGTKVEIK
M21-12	VH	SEQ ID NO:261	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGN GLEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTA ADTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:266	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKA PKLLIYYASNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ QDYSSPWTFGGGTKVEIK
M21-13	VH	SEQ ID NO:264	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISVDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:267	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKS PKLLIYYASNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQ QDYSSPWTFGGGTKVEIK
M21-14	VH	SEQ ID NO:259	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK GLEWIGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:267	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKS PKLLIYYASNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQ QDYSSPWTFGGGTKVEIK
M21-15	VH	SEQ ID NO:261	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGN GLEWMGYISYSGSTTYNPSLKSRVTISRDTSKNQFSLKLSSVTA ADTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:267	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKS PKLLIYYASNRFTGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQ QDYSSPWTFGGGTKVEIK
M21-	VH	SEQ ID NO:264	DVQLQESGPGLVKPSETLSLTCTVSGYSITSDYAWNWIRQPPGK

16			GLEWIGYISYSGSTTYNPSLKSRVTISVDTSKNQFSLKLSSVTAA DTAVYYCARWGTIYYRGYEGFAYWGQGTLVTVSS
	VL	SEQ ID NO:262	DIQMTQSPSSLSASVGDRVTITCKASQSVNNDVAWYQQKPGKS PKVLIYYASNRFTGVPSRFSGSGFGTDFTLTISSLQPEDFATYFCQ QDYSSPWTFGGGTKVEIK
M1	HCDR1 (AbM)	SEQ ID NO:225	GYAFSSYWMN
	HCDR2 (AbM)	SEQ ID NO:226	QIYPGDGDAR
	HCDR3 (AbM)	SEQ ID NO:3	SMGLGLDY
	LCDR1 (AbM)	SEQ ID NO:4	RSSQSLVHSNGNTYLH
	LCDR2 (AbM)	SEQ ID NO:5	KVSNRFS
	LCDR3 (AbM)	SEQ ID NO:6	SQTTHVPPYT
M2	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:228	HIYWDDDKR
	HCDR3 (AbM)	SEQ ID NO:13	RAPYFDSPFAY
	LCDR1 (AbM)	SEQ ID NO:14	KSSQSVLYSSNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:15	WASTRES
	LCDR3 (AbM)	SEQ ID NO:16	HQYLSSLT
M3	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:228	HIYWDDDKR
	HCDR3 (AbM)	SEQ ID NO:21	TIPTVVFDY
	LCDR1 (AbM)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:15	WASTRES
	LCDR3 (AbM)	SEQ ID NO:23	QQYYSYRT
M4	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:228	HIYWDDDKR
	HCDR3 (AbM)	SEQ ID NO:21	TIPTVVFDY
	LCDR1 (AbM)	SEQ ID NO:28	HASQVISSNIG
	LCDR2	SEQ ID NO:29	HGTNLED

	(AbM)		
	LCDR3 (AbM)	SEQ ID NO:30	VRYAQFPWT
M5	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:228	HIYWDDDKR
	HCDR3 (AbM)	SEQ ID NO:33	TTTTVVFDY
	LCDR1 (AbM)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:15	WASTRES
	LCDR3 (AbM)	SEQ ID NO:23	QQYYSYRT
M6	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:228	HIYWDDDKR
	HCDR3 (AbM)	SEQ ID NO:38	NYAGYFDY
	LCDR1 (AbM)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:39	WASTRDS
	LCDR3 (AbM)	SEQ ID NO:23	QQYYSYRT
M7	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:229	HIYWDDDKH
	HCDR3 (AbM)	SEQ ID NO:45	TITTVVFDY
	LCDR1 (AbM)	SEQ ID NO:22	KSSQSLLYSSNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:15	WASTRES
	LCDR3 (AbM)	SEQ ID NO:46	LQYYSYRT
M8	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:229	HIYWDDDKH
	HCDR3 (AbM)	SEQ ID NO:45	TITTVVFDY
	LCDR1 (AbM)	SEQ ID NO:51	HASQDIRSNIG
	LCDR2 (AbM)	SEQ ID NO:29	HGTNLED
	LCDR3	SEQ ID NO:52	VQYAQFSWT

	(AbM)		
M9	HCDR1 (AbM)	SEQ ID NO:227	GFSLSTSGMGVS
	HCDR2 (AbM)	SEQ ID NO:228	HIYWDDDKR
	HCDR3 (AbM)	SEQ ID NO:55	MRIITTAFDY
	LCDR1 (AbM)	SEQ ID NO:56	KASQDVSPAVA
	LCDR2 (AbM)	SEQ ID NO:57	SASYRYT
	LCDR3 (AbM)	SEQ ID NO:58	QQHYSTPFT
M10	HCDR1 (AbM)	SEQ ID NO:230	GFSLTTYGVH
	HCDR2 (AbM)	SEQ ID NO:231	VIWRGGSTD
	HCDR3 (AbM)	SEQ ID NO:65	AGTTEPPFAY
	LCDR1 (AbM)	SEQ ID NO:66	KSSQSLLYSRNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:67	WASTGES
	LCDR3 (AbM)	SEQ ID NO:68	QQYYSYPYT
M11	HCDR1 (AbM)	SEQ ID NO:232	GYEFSSYWMN
	HCDR2 (AbM)	SEQ ID NO:233	QIYPGDGDTN
	HCDR3 (AbM)	SEQ ID NO:74	SMSYSDY
	LCDR1 (AbM)	SEQ ID NO:75	KSSQSLLYTTNQKNYLA
	LCDR2 (AbM)	SEQ ID NO:15	WASTRES
	LCDR3 (AbM)	SEQ ID NO:76	QQYSSYPRT
M12	HCDR1 (AbM)	SEQ ID NO:234	GYSITSDYAWN
	HCDR2 (AbM)	SEQ ID NO:235	FISYSGGTI
	HCDR3 (AbM)	SEQ ID NO:83	NNGYGFDY
	LCDR1 (AbM)	SEQ ID NO:84	SVSSSISYIH
	LCDR2 (AbM)	SEQ ID NO:85	DTSKLTS
	LCDR3 (AbM)	SEQ ID NO:86	QQWSTYPLT
M13	HCDR1	SEQ ID NO:236	GYTFSSYNMH

	(AbM)		
	HCDR2 (AbM)	SEQ ID NO:237	SIYPGNGDTS
	HCDR3 (AbM)	SEQ ID NO:93	GDGYDRLDY
	LCDR1 (AbM)	SEQ ID NO:94	RASQNVGTNVV
	LCDR2 (AbM)	SEQ ID NO:95	SASYRFS
	LCDR3 (AbM)	SEQ ID NO:96	QQYKSYPHT
M14	HCDR1 (AbM)	SEQ ID NO:234	GYSITSDYAWN
	HCDR2 (AbM)	SEQ ID NO:238	YISYSGYTT
	HCDR3 (AbM)	SEQ ID NO:83	NNGYGFDY
	LCDR1 (AbM)	SEQ ID NO:102	SASSSVSYMH
	LCDR2 (AbM)	SEQ ID NO:103	DTSKLAS
	LCDR3 (AbM)	SEQ ID NO:86	QQWSTYPLT
M15	HCDR1 (AbM)	SEQ ID NO:239	AFTFSSYAMS
	HCDR2 (AbM)	SEQ ID NO:240	SISSGGSTS
	HCDR3 (AbM)	SEQ ID NO:110	GSPYWYFDV
	LCDR1 (AbM)	SEQ ID NO:111	KASQNVGISVA
	LCDR2 (AbM)	SEQ ID NO:112	SASYRYS
	LCDR3 (AbM)	SEQ ID NO:113	QQYNRYPT
M16	HCDR1 (AbM)	SEQ ID NO:239	AFTFSSYAMS
	HCDR2 (AbM)	SEQ ID NO:240	SISSGGSTS
	HCDR3 (AbM)	SEQ ID NO:110	GSPYWYFDV
	LCDR1 (AbM)	SEQ ID NO:111	KASQNVGISVA
	LCDR2 (AbM)	SEQ ID NO:112	SASYRYS
	LCDR3 (AbM)	SEQ ID NO:118	QQYNRDPT
M17	HCDR1 (AbM)	SEQ ID NO:241	GYTFASYNIH
	HCDR2	SEQ ID NO:242	SIYPGNGDPS

	(AbM)		
	HCDR3 (AbM)	SEQ ID NO:93	GDGYDRLDY
	LCDR1 (AbM)	SEQ ID NO:123	KASQNVGTYVV
	LCDR2 (AbM)	SEQ ID NO:95	SASYRFS
	LCDR3 (AbM)	SEQ ID NO:124	HQYNNYPHT
M18	HCDR1 (AbM)	SEQ ID NO:243	GYTFTSYWVN
	HCDR2 (AbM)	SEQ ID NO:244	RIHPYDSETH
	HCDR3 (AbM)	SEQ ID NO:131	WTARAASAMDY
	LCDR1 (AbM)	SEQ ID NO:132	SANSSVSYMY
	LCDR2 (AbM)	SEQ ID NO:133	RTSNLAS
	LCDR3 (AbM)	SEQ ID NO:134	QQYHSFPLT
M19	HCDR1 (AbM)	SEQ ID NO:236	GYTFSSYNMH
	HCDR2 (AbM)	SEQ ID NO:237	SIYPGNGDTS
	HCDR3 (AbM)	SEQ ID NO:93	GDGYDRLDY
	LCDR1 (AbM)	SEQ ID NO:139	KASQNVGTNVV
	LCDR2 (AbM)	SEQ ID NO:112	SASYRYS
	LCDR3 (AbM)	SEQ ID NO:96	QQYKSYPHT
M20	HCDR1 (AbM)	SEQ ID NO:245	GFSLSIYSVH
	HCDR2 (AbM)	SEQ ID NO:246	MIWSGGNTD
	HCDR3 (AbM)	SEQ ID NO:145	NWRNDTHLYYVMDY
	LCDR1 (AbM)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (AbM)	SEQ ID NO:147	KTSTLHT
	LCDR3 (AbM)	SEQ ID NO:148	QQGQSYPFT
M21	HCDR1 (AbM)	SEQ ID NO:234	GYSITSDYAWN
	HCDR2 (AbM)	SEQ ID NO:247	YISYSGSTT
	HCDR3	SEQ ID NO:154	WGTIYYRGYEGFAY

	(AbM)		
	LCDR1 (AbM)	SEQ ID NO:155	KASQSVNNDVA
	LCDR2 (AbM)	SEQ ID NO:156	YASNRFT
	LCDR3 (AbM)	SEQ ID NO:157	QQDYSSPWT
M22	HCDR1 (AbM)	SEQ ID NO:248	GFSLSRYSVH
	HCDR2 (AbM)	SEQ ID NO:249	MIWSGENTD
	HCDR3 (AbM)	SEQ ID NO:164	NWRNDTHLYYAMDY
	LCDR1 (AbM)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (AbM)	SEQ ID NO:165	KSSNLHT
	LCDR3 (AbM)	SEQ ID NO:166	QQGQGFPFT
M23	HCDR1 (AbM)	SEQ ID NO:245	GFSLSIYSVH
	HCDR2 (AbM)	SEQ ID NO:246	MIWSGGNTD
	HCDR3 (AbM)	SEQ ID NO:171	NWRNDTHLYYALDY
	LCDR1 (AbM)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (AbM)	SEQ ID NO:147	KTSTLHT
	LCDR3 (AbM)	SEQ ID NO:148	QQGQSYPFT
M24	HCDR1 (AbM)	SEQ ID NO:250	GFSLSRYSIH
	HCDR2 (AbM)	SEQ ID NO:251	MIWGGGNTD
	HCDR3 (AbM)	SEQ ID NO:164	NWRNDTHLYYAMDY
	LCDR1 (AbM)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (AbM)	SEQ ID NO:178	KAANLHT
	LCDR3 (AbM)	SEQ ID NO:148	QQGQSYPFT
M25	HCDR1 (AbM)	SEQ ID NO:252	GYTFTSYWIQ
	HCDR2 (AbM)	SEQ ID NO:253	AIYPGDGGTR
	HCDR3 (AbM)	SEQ ID NO:185	LYSNYYIDS
	LCDR1	SEQ ID NO:186	KASQDINSYLS

	(AbM)		
	LCDR2 (AbM)	SEQ ID NO:187	RADRLVE
	LCDR3 (AbM)	SEQ ID NO:188	LQYDEFPNT
M26	HCDR1 (AbM)	SEQ ID NO:254	GFSLTSYGVH
	HCDR2 (AbM)	SEQ ID NO:255	VIWAGGRTI
	HCDR3 (AbM)	SEQ ID NO:195	DLYGGAYGDY
	LCDR1 (AbM)	SEQ ID NO:196	KASQDVSTTVA
	LCDR2 (AbM)	SEQ ID NO:57	SASYRYT
	LCDR3 (AbM)	SEQ ID NO:197	QQHYRSPLT
M27	HCDR1 (AbM)	SEQ ID NO:256	GFSLSIYSIH
	HCDR2 (AbM)	SEQ ID NO:246	MIWSGGNTD
	HCDR3 (AbM)	SEQ ID NO:145	NWRNDTHLYYVMDY
	LCDR1 (AbM)	SEQ ID NO:146	HASQNINVWLN
	LCDR2 (AbM)	SEQ ID NO:203	KTSTLHI
	LCDR3 (AbM)	SEQ ID NO:148	QQGQSYPFT
M28	HCDR1 (AbM)	SEQ ID NO:257	GYTFTNYRMN
	HCDR2 (AbM)	SEQ ID NO:258	WINTYSGVPI
	HCDR3 (AbM)	SEQ ID NO:210	TLYDGYSLYYVMDY
	LCDR1 (AbM)	SEQ ID NO:211	HASQNINGWLS
	LCDR2 (AbM)	SEQ ID NO:212	KASNLHT
	LCDR3 (AbM)	SEQ ID NO:213	QQGQSHPLT

Claims

1. Anti-MUC17 antibody or antigen-binding fragment thereof, wherein the antibody or antigen-binding fragment thereof comprises heavy chain complementary determining regions (HCDRs) and/or light chain complementary determining regions (LCDRs) selected from the following groups:

(1) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:7 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:8 or variants thereof; or,

(2) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:17 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:18 or variants thereof; or,

(3) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:24 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:25 or variants thereof; or,

(4) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:24 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:31 or variants thereof; or,

(5) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:34 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:35 or variants thereof; or,

(6) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:40 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:41 or variants thereof; or,

(7) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:47 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:48 or variants thereof; or,

(8) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:47 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:53 or variants thereof; or,

(9) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:59 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:60 or variants thereof; or,

(10) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:69 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:70 or variants thereof; or,

(11) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:77 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ

ID NO:78 or variants thereof; or,

(12) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:87 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:88 or variants thereof; or,

(13) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:97 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:98 or variants thereof; or,

(14) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:104 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:105 or variants thereof; or,

(15) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:114 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:115 or variants thereof; or,

(16) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:114 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:119 or variants thereof; or,

(17) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:125 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:126 or variants thereof; or,

(18) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:135 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:136 or variants thereof; or,

(19) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:97 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:140 or variants thereof; or,

(20) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:149 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:150 or variants thereof; or,

(21) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:158 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:159 or variants thereof; or,

(22) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:167 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:168 or variants thereof; or,

(23) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:172 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:173 or variants thereof; or,

(24) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:179 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ

ID NO:180 or variants thereof; or,

(25) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:189 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:190 or variants thereof; or,

(26) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:198 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:199 or variants thereof; or,

(27) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:204 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:205 or variants thereof; or,

(28) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:214 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:215 or variants thereof;

(29) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:259 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:263 or variants thereof;

(30) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:259 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:260 or variants thereof;

(31) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:261 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:260 or variants thereof;

(32) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:259 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:262 or variants thereof;

(33) the 3 CDRs (HCDR1, HCDR2, HCDR3) comprised in VH as shown in SEQ ID NO:261 or variants thereof; and/or the 3 CDRs (LCDR1, LCDR2, LCDR3) comprised in VL as shown in SEQ ID NO:262 or variants thereof.

Wherein the variant of any one of (1) - (33) has one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) as compared to the sequence from which it is derived; preferably, the substitution is a conservative substitution;

Preferably, the CDRs are defined by the Kabat, AbM, Chothia or IMGT numbering system.

2. The anti-MUC17 antibody or antigen-binding fragment thereof of claim 1, comprising complementarity determining regions (CDRs) selected from the group consisting of:

(I) the following 3 HCDRs (HCDR1, HCDR2, HCDR3) of the heavy chain variable regions (VH), and/or the following 3 LCDRs (LCDR1, LCDR2, LCDR3) of the light chain variable regions (VL), wherein the HCDR1, HCDR2, HCDR3, and/or LCDR1, LCDR2, LCDR3 are defined by Kabat

numbering system:

(1) HCDR1 comprising the sequence as shown in SEQ ID NO:1 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:1;

HCDR2 comprising the sequence as shown in SEQ ID NO:2 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:2;

HCDR3 comprising the sequence as shown in SEQ ID NO:3 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:3;

LCDR1 comprising the sequence as shown in SEQ ID NO:4 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:4;

LCDR2 comprising the sequence as shown in SEQ ID NO:5 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:5;

LCDR3 comprising the sequence as shown in SEQ ID NO:6 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:6;

or,

(2) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:13 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:13;

LCDR1 comprising the sequence as shown in SEQ ID NO:14 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:14;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:16 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:16;

or,

(3) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(4) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:28 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:28;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:30 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:30;

or,

(5) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:33 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:33;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(6) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:38 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:38;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:39 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:39;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(7) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:44 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:44;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:46 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:46;

or,

(8) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:44 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:44;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:51 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:51;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:52 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:52;

or,

(9) HCDR1 comprising the sequence as shown in SEQ ID NO:11 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:11;

HCDR2 comprising the sequence as shown in SEQ ID NO:12 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:12;

HCDR3 comprising the sequence as shown in SEQ ID NO:55 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:55;

LCDR1 comprising the sequence as shown in SEQ ID NO:56 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:56;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:58 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:58;

or,

(10) HCDR1 comprising the sequence as shown in SEQ ID NO:63 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:63;

HCDR2 comprising the sequence as shown in SEQ ID NO:64 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:64;

HCDR3 comprising the sequence as shown in SEQ ID NO:65 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:65;

LCDR1 comprising the sequence as shown in SEQ ID NO:66 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:66;

LCDR2 comprising the sequence as shown in SEQ ID NO:67 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:67;

LCDR3 comprising the sequence as shown in SEQ ID NO:68 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:68;

or,

(11) HCDR1 comprising the sequence as shown in SEQ ID NO:1 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:1;

HCDR2 comprising the sequence as shown in SEQ ID NO:73 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:73;

HCDR3 comprising the sequence as shown in SEQ ID NO:74 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:74;

LCDR1 comprising the sequence as shown in SEQ ID NO:75 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:75;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:76 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:76;

or,

(12) HCDR1 comprising the sequence as shown in SEQ ID NO:81 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:81;

HCDR2 comprising the sequence as shown in SEQ ID NO:82 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:82;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:84 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:84;

LCDR2 comprising the sequence as shown in SEQ ID NO:85 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:85;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or,

(13) HCDR1 comprising the sequence as shown in SEQ ID NO:91 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:91;

HCDR2 comprising the sequence as shown in SEQ ID NO:92 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:92;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:94 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:94;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or,

(14) HCDR1 comprising the sequence as shown in SEQ ID NO:81 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:81;

HCDR2 comprising the sequence as shown in SEQ ID NO:101 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:101;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:102 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:102;

LCDR2 comprising the sequence as shown in SEQ ID NO:103 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:103;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or,

(15) HCDR1 comprising the sequence as shown in SEQ ID NO:108 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:108;

HCDR2 comprising the sequence as shown in SEQ ID NO:109 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:109;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:113 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:113;

or,

(16) HCDR1 comprising the sequence as shown in SEQ ID NO:108 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:108;

HCDR2 comprising the sequence as shown in SEQ ID NO:109 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:109;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:118 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:118;

or,

(17) HCDR1 comprising the sequence as shown in SEQ ID NO:121 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:121;

HCDR2 comprising the sequence as shown in SEQ ID NO:122 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:122;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:123 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:123;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:124 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:124;

or,

(18) HCDR1 comprising the sequence as shown in SEQ ID NO:129 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:129;

HCDR2 comprising the sequence as shown in SEQ ID NO:130 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:130;

HCDR3 comprising the sequence as shown in SEQ ID NO:131 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:131;

LCDR1 comprising the sequence as shown in SEQ ID NO:132 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:132;

LCDR2 comprising the sequence as shown in SEQ ID NO:133 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:133;

LCDR3 comprising the sequence as shown in SEQ ID NO:134 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:134;

or,

(19) HCDR1 comprising the sequence as shown in SEQ ID NO:91 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:91;

HCDR2 comprising the sequence as shown in SEQ ID NO:92 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:92;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:139 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:139;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or,

(20) HCDR1 comprising the sequence as shown in SEQ ID NO:143 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:143;

HCDR2 comprising the sequence as shown in SEQ ID NO:144 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:144;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(21) HCDR1 comprising the sequence as shown in SEQ ID NO:81 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:81;

HCDR2 comprising the sequence as shown in SEQ ID NO:153 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:153;

HCDR3 comprising the sequence as shown in SEQ ID NO:154 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:154;

LCDR1 comprising the sequence as shown in SEQ ID NO:155 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:155;

LCDR2 comprising the sequence as shown in SEQ ID NO:156 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:156;

LCDR3 comprising the sequence as shown in SEQ ID NO:157 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:157;

or,

(22) HCDR1 comprising the sequence as shown in SEQ ID NO:162 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:162;

HCDR2 comprising the sequence as shown in SEQ ID NO:163 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:163;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:165 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:165;

LCDR3 comprising the sequence as shown in SEQ ID NO:166 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:166;

or,

(23) HCDR1 comprising the sequence as shown in SEQ ID NO:143 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:143;

HCDR2 comprising the sequence as shown in SEQ ID NO:144 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:144;

HCDR3 comprising the sequence as shown in SEQ ID NO:171 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:171;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(24) HCDR1 comprising the sequence as shown in SEQ ID NO:176 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:176;

HCDR2 comprising the sequence as shown in SEQ ID NO:177 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:177;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:178 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:178;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(25) HCDR1 comprising the sequence as shown in SEQ ID NO:183 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:183;

HCDR2 comprising the sequence as shown in SEQ ID NO:184 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:184;

HCDR3 comprising the sequence as shown in SEQ ID NO:185 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:185;

LCDR1 comprising the sequence as shown in SEQ ID NO:186 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:186;

LCDR2 comprising the sequence as shown in SEQ ID NO:187 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:187;

LCDR3 comprising the sequence as shown in SEQ ID NO:188 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:188;

or,

(26) HCDR1 comprising the sequence as shown in SEQ ID NO:193 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:193;

HCDR2 comprising the sequence as shown in SEQ ID NO:194 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:194;

HCDR3 comprising the sequence as shown in SEQ ID NO:195 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:195;

LCDR1 comprising the sequence as shown in SEQ ID NO:196 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:196;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:197 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:197;

or,

(27) HCDR1 comprising the sequence as shown in SEQ ID NO:202 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:202;

HCDR2 comprising the sequence as shown in SEQ ID NO:144 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:144;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:203 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:203;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(28) HCDR1 comprising the sequence as shown in SEQ ID NO:208 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:208;

HCDR2 comprising the sequence as shown in SEQ ID NO:209 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:209;

HCDR3 comprising the sequence as shown in SEQ ID NO:210 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:210;

LCDR1 comprising the sequence as shown in SEQ ID NO:211 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:211;

LCDR2 comprising the sequence as shown in SEQ ID NO:212 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:212;

LCDR3 comprising the sequence as shown in SEQ ID NO:213 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:213;

Wherein the substitution described in any one of (1) ~ (28) is a conservative substitution;

Or,

(II) The following 3 CDRs (HCDR1, HCDR2, HCDR3) of the heavy chain variable regions (VH), and/or the following 3 CDRs (LCDR1, LCDR2, LCDR3) of the light chain variable regions (VL), wherein the HCDR1, HCDR2, HCDR3, and/or LCDR1, LCDR2, LCDR3 are defined by AbM numbering system:

(1) HCDR1 comprising the sequence as shown in SEQ ID NO:225 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:225;

HCDR2 comprising the sequence as shown in SEQ ID NO:226 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:226;

HCDR3 comprising the sequence as shown in SEQ ID NO:3 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:3;

LCDR1 comprising the sequence as shown in SEQ ID NO:4 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:4;

LCDR2 comprising the sequence as shown in SEQ ID NO:5 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:5;

LCDR3 comprising the sequence as shown in SEQ ID NO:6 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:6;

or,

(2) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:13 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:13;

LCDR1 comprising the sequence as shown in SEQ ID NO:14 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:14;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:16 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:16;

or,

(3) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(4) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:21 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:21;

LCDR1 comprising the sequence as shown in SEQ ID NO:28 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:28;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:30 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:30;

or,

(5) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:33 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:33;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(6) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:38 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:38;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:39 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:39;

LCDR3 comprising the sequence as shown in SEQ ID NO:23 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:23;

or,

(7) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:229 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:229;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:22 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:22;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:46 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:46;

or,

(8) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:229 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:229;

HCDR3 comprising the sequence as shown in SEQ ID NO:45 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:45;

LCDR1 comprising the sequence as shown in SEQ ID NO:51 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:51;

LCDR2 comprising the sequence as shown in SEQ ID NO:29 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:29;

LCDR3 comprising the sequence as shown in SEQ ID NO:52 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:52;

or,

(9) HCDR1 comprising the sequence as shown in SEQ ID NO:227 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:227;

HCDR2 comprising the sequence as shown in SEQ ID NO:228 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:228;

HCDR3 comprising the sequence as shown in SEQ ID NO:55 or a sequence having one or more amino acid substitutions, deletions or additions (e.g. 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:55;

LCDR1 comprising the sequence as shown in SEQ ID NO:56 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:56;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:58 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:58;

or,

(10) HCDR1 comprising the sequence as shown in SEQ ID NO:230 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:230;

HCDR2 comprising the sequence as shown in SEQ ID NO:231 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:231;

HCDR3 comprising the sequence as shown in SEQ ID NO:65 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:65;

LCDR1 comprising the sequence as shown in SEQ ID NO:66 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:66;

LCDR2 comprising the sequence as shown in SEQ ID NO:67 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:67;

LCDR3 comprising the sequence as shown in SEQ ID NO:68 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:68;

or,

(11) HCDR1 comprising the sequence as shown in SEQ ID NO:232 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:232;

HCDR2 comprising the sequence as shown in SEQ ID NO:233 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:233;

HCDR3 comprising the sequence as shown in SEQ ID NO:74 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:74;

LCDR1 comprising the sequence as shown in SEQ ID NO:75 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:75;

LCDR2 comprising the sequence as shown in SEQ ID NO:15 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:15;

LCDR3 comprising the sequence as shown in SEQ ID NO:76 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:76;

or,

(12) HCDR1 comprising the sequence as shown in SEQ ID NO:234 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:234;

HCDR2 comprising the sequence as shown in SEQ ID NO:235 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:235;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:84 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:84;

LCDR2 comprising the sequence as shown in SEQ ID NO:85 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:85;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or,

(13) HCDR1 comprising the sequence as shown in SEQ ID NO:236 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:236;

HCDR2 comprising the sequence as shown in SEQ ID NO:237 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:237;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:94 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:94;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or,

(14) HCDR1 comprising the sequence as shown in SEQ ID NO:234 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:234;

HCDR2 comprising the sequence as shown in SEQ ID NO:238 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:238;

HCDR3 comprising the sequence as shown in SEQ ID NO:83 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:83;

LCDR1 comprising the sequence as shown in SEQ ID NO:102 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:102;

LCDR2 comprising the sequence as shown in SEQ ID NO:103 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:103;

LCDR3 comprising the sequence as shown in SEQ ID NO:86 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:86;

or,

(15) HCDR1 comprising the sequence as shown in SEQ ID NO:239 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:239;

HCDR2 comprising the sequence as shown in SEQ ID NO:240 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:240;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:113 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:113;

or,

(16) HCDR1 comprising the sequence as shown in SEQ ID NO:239 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:239;

HCDR2 comprising the sequence as shown in SEQ ID NO:240 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:240;

HCDR3 comprising the sequence as shown in SEQ ID NO:110 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:110;

LCDR1 comprising the sequence as shown in SEQ ID NO:111 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:111;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:118 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:118;

or,

(17) HCDR1 comprising the sequence as shown in SEQ ID NO:241 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:241;

HCDR2 comprising the sequence as shown in SEQ ID NO:242 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:242;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:123 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:123;

LCDR2 comprising the sequence as shown in SEQ ID NO:95 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:95;

LCDR3 comprising the sequence as shown in SEQ ID NO:124 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:124;

or,

(18) HCDR1 comprising the sequence as shown in SEQ ID NO:243 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:243;

HCDR2 comprising the sequence as shown in SEQ ID NO:244 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:244;

HCDR3 comprising the sequence as shown in SEQ ID NO:131 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:131;

LCDR1 comprising the sequence as shown in SEQ ID NO:132 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:132;

LCDR2 comprising the sequence as shown in SEQ ID NO:133 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:133;

LCDR3 comprising the sequence as shown in SEQ ID NO:134 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:134;

or,

(19) HCDR1 comprising the sequence as shown in SEQ ID NO:236 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:236;

HCDR2 comprising the sequence as shown in SEQ ID NO:237 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:237;

HCDR3 comprising the sequence as shown in SEQ ID NO:93 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:93;

LCDR1 comprising the sequence as shown in SEQ ID NO:139 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:139;

LCDR2 comprising the sequence as shown in SEQ ID NO:112 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:112;

LCDR3 comprising the sequence as shown in SEQ ID NO:96 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:96;

or,

(20) HCDR1 comprising the sequence as shown in SEQ ID NO:245 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:245;

HCDR2 comprising the sequence as shown in SEQ ID NO:246 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:246;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(21) HCDR1 comprising the sequence as shown in SEQ ID NO:234 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:234;

HCDR2 comprising the sequence as shown in SEQ ID NO:247 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:247;

HCDR3 comprising the sequence as shown in SEQ ID NO:154 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:154;

LCDR1 comprising the sequence as shown in SEQ ID NO:155 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:155;

LCDR2 comprising the sequence as shown in SEQ ID NO:156 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:156;

LCDR3 comprising the sequence as shown in SEQ ID NO:157 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:157;

or,

(22) HCDR1 comprising the sequence as shown in SEQ ID NO:248 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:248;

HCDR2 comprising the sequence as shown in SEQ ID NO:249 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:249;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:165 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:165;

LCDR3 comprising the sequence as shown in SEQ ID NO:166 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:166;

or,

(23) HCDR1 comprising the sequence as shown in SEQ ID NO:245 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:245;

HCDR2 comprising the sequence as shown in SEQ ID NO:246 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:246;

HCDR3 comprising the sequence as shown in SEQ ID NO:171 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:171;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:147 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:147;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(24) HCDR1 comprising the sequence as shown in SEQ ID NO:250 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:250;

HCDR2 comprising the sequence as shown in SEQ ID NO:251 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:251;

HCDR3 comprising the sequence as shown in SEQ ID NO:164 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:164;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:178 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:178;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(25) HCDR1 comprising the sequence as shown in SEQ ID NO:252 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:252;

HCDR2 comprising the sequence as shown in SEQ ID NO:253 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:253;

HCDR3 comprising the sequence as shown in SEQ ID NO:185 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:185;

LCDR1 comprising the sequence as shown in SEQ ID NO:186 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:186;

LCDR2 comprising the sequence as shown in SEQ ID NO:187 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:187;

LCDR3 comprising the sequence as shown in SEQ ID NO:188 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:188;

or,

(26) HCDR1 comprising the sequence as shown in SEQ ID NO:254 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:254;

HCDR2 comprising the sequence as shown in SEQ ID NO:255 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:255;

HCDR3 comprising the sequence as shown in SEQ ID NO:195 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:195;

LCDR1 comprising the sequence as shown in SEQ ID NO:196 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:196;

LCDR2 comprising the sequence as shown in SEQ ID NO:57 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:57;

LCDR3 comprising the sequence as shown in SEQ ID NO:197 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:197;

or,

(27) HCDR1 comprising the sequence as shown in SEQ ID NO:256 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:256;

HCDR2 comprising the sequence as shown in SEQ ID NO:246 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:246;

HCDR3 comprising the sequence as shown in SEQ ID NO:145 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:145;

LCDR1 comprising the sequence as shown in SEQ ID NO:146 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:146;

LCDR2 comprising the sequence as shown in SEQ ID NO:203 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:203;

LCDR3 comprising the sequence as shown in SEQ ID NO:148 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:148;

or,

(28) HCDR1 comprising the sequence as shown in SEQ ID NO:257 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:257;

HCDR2 comprising the sequence as shown in SEQ ID NO:258 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:258;

HCDR3 comprising the sequence as shown in SEQ ID NO:210 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:210;

LCDR1 comprising the sequence as shown in SEQ ID NO:211 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:211;

LCDR2 comprising the sequence as shown in SEQ ID NO:212 or a sequence having one or more

amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:212;

LCDR3 comprising the sequence as shown in SEQ ID NO:213 or a sequence having one or more amino acid substitutions, deletions or additions (e.g., 1, 2 or 3 amino acid substitutions, deletions or additions) compared to the sequence of SEQ ID NO:213;

Wherein the substitution described in any one of (1) to (28) is a conservative substitution.

3. The anti-MUC17 antibody or antigen-binding fragment thereof of claim 1 or 2, wherein the antibody or antigen-binding fragment thereof comprises:

(I) a heavy chain variable region (VH) comprising an amino acid sequence selected from:

(1) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:7, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:7, or consists of SEQ ID NO:7;

(2) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:17, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:17, or consists of SEQ ID NO:17;

(3) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:24, or consists of SEQ ID NO:24;

(4) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:34, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:34, or consists of SEQ ID NO:34;

(5) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:40, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:40, or consists of SEQ ID NO:40;

(6) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:47, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:47, or consists of SEQ ID NO:47;

(7) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:59, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:59, or consists of SEQ ID NO:59;

(8) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:69, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:69, or consists of SEQ ID NO:69;

(9) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:77, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:77, or consists of SEQ ID NO:77;

(10) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:87, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:87, or consists of SEQ ID NO:87;

(11) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:97, or consists of SEQ ID NO:97;

(12) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:104, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:104, or consists of SEQ ID NO:104;

(13) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:114, or consists of SEQ ID NO:114;

(14) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:125, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:125, or consists of SEQ ID NO:125;

(15) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:135, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:135, or consists of SEQ ID NO:135;

(16) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:149, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:149, or consists of SEQ ID NO:149;

(17) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:158, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:158, or consists of SEQ ID NO:158;

(18) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:167, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:167, or consists of SEQ ID NO:167;

(19) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:172, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:172, or consists of SEQ ID NO:172;

(20) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:179, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:179, or consists of SEQ ID NO:179;

(21) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:189, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:189, or consists of SEQ ID NO:189;

(22) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:198, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:198, or consists of SEQ ID NO:198;

(23) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:204, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:204, or consists of SEQ ID NO:204;

(24) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:214, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:214, or consists of SEQ ID NO:214;

(25) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259;

(26) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; or

(27) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264;

and/or,

(II) a light chain variable region (VL):

(1) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:8, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:8, or consists of SEQ ID NO:8;

(2) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:18, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:18, or consists of SEQ ID NO:18;

(3) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:25, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:25, or consists of SEQ ID NO:25;

(4) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:31, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:31, or consists of SEQ ID NO:31;

(5) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:35, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:35, or consists of SEQ ID NO:35;

(6) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:41, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:41, or consists of SEQ ID NO:41;

(7) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:48, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:48, or consists of SEQ ID NO:48;

(8) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:53, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:53, or consists of SEQ ID NO:53;

(9) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:60, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:60, or consists of SEQ ID NO:60;

(10) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:70, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:70, or consists of SEQ ID NO:70;

(11) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:78, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:78, or consists of SEQ ID NO:78;

(12) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:88, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:88, or consists of SEQ ID NO:88;

(13) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:98, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:98, or consists of SEQ ID NO:98;

(14) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:105, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:105, or consists of SEQ ID NO:105;

(15) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:115, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:115, or consists of SEQ ID NO:115;

(16) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:119, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:119, or consists of SEQ ID NO:119;

(17) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:126, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:126, or consists of SEQ ID NO:126;

(18) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:136, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:136, or consists of SEQ ID NO:136;

(19) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:140, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:140, or consists of SEQ ID NO:140;

(20) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:150, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:150, or consists of SEQ ID NO:150;

(21) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:159, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:159, or consists of SEQ ID NO:159;

(22) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:168, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:168, or consists of SEQ ID NO:168;

(23) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:173, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:173, or consists of SEQ ID NO:173;

(24) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:180, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:180, or consists of SEQ ID NO:180;

(25) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:190, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:190, or consists of SEQ ID NO:190;

(26) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:199, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:199, or consists of SEQ ID NO:199;

(27) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:205, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:205, or consists of SEQ ID NO:205;

(28) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:215, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:215, or consists of SEQ ID NO:215;

(29) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(30) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(31) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262;

(32) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(33) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266; or

(34) the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO:267.

4. The anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-3, comprising a heavy chain variable region (VH) and a light chain variable region (VL), wherein:

(1) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:7, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:7, or consists of SEQ ID NO:7; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:8, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:8, or consists of SEQ ID NO:8;

(2) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:17, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:17, or consists of SEQ ID NO:17; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:18, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:18, or consists of SEQ ID NO:18;

(3) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:24, or consists of SEQ ID NO:24; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:25, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:25, or consists of

SEQ ID NO:25;

(4) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:24, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:24, or consists of SEQ ID NO:24; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:31, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:31, or consists of SEQ ID NO:31;

(5) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:34, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:34, or consists of SEQ ID NO:34; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:35, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:35, or consists of SEQ ID NO:35;

(6) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:40, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:40, or consists of SEQ ID NO:40; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:41, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:41, or consists of SEQ ID NO:41;

(7) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:47, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:47, or consists of SEQ ID NO:47; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:48, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:48, or consists of SEQ ID NO:48;

(8) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:47, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:47, or consists of SEQ ID NO:47; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:53, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:53, or consists of SEQ ID NO:53;

(9) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:59, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:59, or consists of SEQ ID NO:59; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:60, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:60, or consists of SEQ ID NO:60;

(10) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:69, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:69, or consists of SEQ ID NO:69; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:70, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:70, or consists of SEQ ID NO:70;

(11) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:77, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:77, or consists of SEQ ID NO:77; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:78, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:78, or consists of SEQ ID NO:78;

(12) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:87, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:87, or consists of SEQ ID NO:87; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:88, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:88, or consists of SEQ ID NO:88;

(13) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:97, or consists of SEQ ID NO:97; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:98, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:98, or consists of SEQ ID NO:98;

(14) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:104, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:104, or consists of SEQ ID NO:104; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:105, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:105, or consists of SEQ ID NO:105;

(15) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:114, or consists of SEQ ID NO:114; the light chain variable region comprises the amino acid sequence as shown in

SEQ ID NO:115, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:115, or consists of SEQ ID NO:115;

(16) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:114, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:114, or consists of SEQ ID NO:114; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:119, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:119, or consists of SEQ ID NO:119;

(17) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:125, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:125, or consists of SEQ ID NO:125; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:126, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:126, or consists of SEQ ID NO:126;

(18) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:135, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:135, or consists of SEQ ID NO:135; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:136, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:136, or consists of SEQ ID NO:136;

(19) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:97, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:97, or consists of SEQ ID NO:97; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:140, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:140, or consists of SEQ ID NO:140;

(20) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:149, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:149, or consists of SEQ ID NO:149; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:150, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:150, or consists of SEQ ID NO:150;

(21) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:158, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:158, or consists of

SEQ ID NO:158; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:159, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:159, or consists of SEQ ID NO:159;

(22) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:167, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:167, or consists of SEQ ID NO:167; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:168, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:168, or consists of SEQ ID NO:168;

(23) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:172, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:172, or consists of SEQ ID NO:172; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:173, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:173, or consists of SEQ ID NO:173;

(24) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:179, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:179, or consists of SEQ ID NO:179; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:180, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:180, or consists of SEQ ID NO:180;

(25) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:189, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:189, or consists of SEQ ID NO:189; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:190, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:190, or consists of SEQ ID NO:190;

(26) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:198, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:198, or consists of SEQ ID NO:198; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:199, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:199, or consists of SEQ ID NO:199;

(27) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:204, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:204, or consists of SEQ ID NO:204; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:205, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:205, or consists of SEQ ID NO:205;

(28) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:214, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:214, or consists of SEQ ID NO:214; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:215, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:215, or consists of SEQ ID NO:215;

(29) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(30) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(31) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(32) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262;

(33) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID

NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262;

(34) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(35) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:263, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:263, or consists of SEQ ID NO:263;

(36) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(37) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(38) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:265, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:265, or consists of SEQ ID NO:265;

(39) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:260, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:260, or consists of SEQ ID NO:260;

(40) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266;

(41) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266;

(42) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:266, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:266, or consists of SEQ ID NO:266;

(43) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO:267;

(44) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:259, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:259, or consists of SEQ ID NO:259; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO:267;

(45) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:261, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:261, or consists of SEQ ID NO:261; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:267, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:267, or consists of SEQ ID NO:267;

(46) the heavy chain variable region comprises the amino acid sequence as shown in SEQ ID NO:264, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:264, or consists of SEQ ID NO:264; the light chain variable region comprises the amino acid sequence as shown in SEQ ID NO:262, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:262, or consists of SEQ ID NO:262.

5. The anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-4, further comprising: a heavy chain constant region of a human immunoglobulin or a variant thereof, and a light chain constant region of a human immunoglobulin or a variant thereof, wherein the variant has one or more amino acid substitutions, deletions, or additions (e.g., substitutions, deletions, or additions of up to 20, up to 15, up to 10, or up to 5 amino acids; e.g., substitutions, deletions, or additions of 1, 2, 3, 4, or 5 amino acids) as compared to the wild-type sequence from which it is derived; the heavy chain constant region is an IgG heavy chain constant region, e.g., an IgG1, IgG2, IgG3, or IgG4 heavy chain constant region; the light chain constant region is selected from a kappa or lambda light chain constant region; for example, the heavy chain constant region comprises the sequence as shown in SEQ ID NO:223, or consists of the sequence; for example, the light chain constant region comprises the sequence as shown in SEQ ID NO:224, or consists of the sequence.

6. The anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-5, which is a murine, chimeric, or humanized antibody.

7. The anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-6, comprising a heavy chain and a light chain, wherein:

(1) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:9, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:9, or consists of SEQ ID NO:9; the light chain comprises an amino acid sequence as shown in SEQ ID NO:10, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:10, or consists of SEQ ID NO:10;

(2) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:19, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or

more sequence identity to the amino acid sequence of SEQ ID NO:19, or consists of SEQ ID NO:19; the light chain comprises the amino acid sequence as shown in SEQ ID NO:20, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:20, or consists of SEQ ID NO:20;

(3) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:26, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:26, or consists of SEQ ID NO:26; the light chain comprises the amino acid sequence as shown in SEQ ID NO:27, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:27, or consists of SEQ ID NO:27;

(4) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:26, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:26, or consists of SEQ ID NO:26; the light chain comprises the amino acid sequence as shown in SEQ ID NO:32, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:32, or consists of SEQ ID NO:32;

(5) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:36, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:36, or consists of SEQ ID NO:36; the light chain comprises the amino acid sequence as shown in SEQ ID NO:37, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:37, or consists of SEQ ID NO:37;

(6) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:42, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:42, or consists of SEQ ID NO:42; the light chain comprises the amino acid sequence as shown in SEQ ID NO:43, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:43, or consists of SEQ ID NO:43;

(7) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:49, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:49, or consists of SEQ ID NO:49; the light chain comprises the amino acid sequence as shown in SEQ ID NO:50, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:50, or consists of SEQ ID NO:50;

(8) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:49, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:49, or consists of SEQ ID NO:49; the light chain comprises the amino acid sequence as shown in SEQ ID NO:54, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:54, or consists of SEQ ID NO:54;

(9) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:61, or an

amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:61, or consists of SEQ ID NO:61; the light chain comprises the amino acid sequence as shown in SEQ ID NO:62, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:62, or consists of SEQ ID NO:62;

(10) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:71, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:71, or consists of SEQ ID NO:71; the light chain comprises the amino acid sequence as shown in SEQ ID NO:72, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:72, or consists of SEQ ID NO:72;

(11) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:79, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:79, or consists of SEQ ID NO:79; the light chain comprises the amino acid sequence as shown in SEQ ID NO:80, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:80, or consists of SEQ ID NO:80;

(12) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:89, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:89, or consists of SEQ ID NO:89; the light chain comprises the amino acid sequence as shown in SEQ ID NO:90, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:90, or consists of SEQ ID NO:90;

(13) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:99, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:99, or consists of SEQ ID NO:99; the light chain comprises the amino acid sequence as shown in SEQ ID NO:100, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:100, or consists of SEQ ID NO:100;

(14) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:106, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:106, or consists of SEQ ID NO:106; the light chain comprises the amino acid sequence as shown in SEQ ID NO:107, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:107, or consists of SEQ ID NO:107;

(15) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:116, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:116, or consists of SEQ ID NO:116; the light chain comprises the amino acid sequence as shown in SEQ ID NO:117, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or

more sequence identity to the amino acid sequence of SEQ ID NO:117, or consists of SEQ ID NO:117;

(16) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:116, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:116, or consists of SEQ ID NO:116; the light chain comprises the amino acid sequence as shown in SEQ ID NO:120, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:120, or consists of SEQ ID NO:120;

(17) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:127, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:127, or consists of SEQ ID NO:127; the light chain comprises the amino acid sequence as shown in SEQ ID NO:128, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:128, or consists of SEQ ID NO:128;

(18) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:137, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:137, or consists of SEQ ID NO:137; the light chain comprises the amino acid sequence as shown in SEQ ID NO:138, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:138, or consists of SEQ ID NO:138;

(19) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:141, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:141, or consists of SEQ ID NO:141; the light chain comprises the amino acid sequence as shown in SEQ ID NO:142, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:142, or consists of SEQ ID NO:142;

(20) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:151, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:151, or consists of SEQ ID NO:151; the light chain comprises the amino acid sequence as shown in SEQ ID NO:152, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:152, or consists of SEQ ID NO:152;

(21) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:160, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:160, or consists of SEQ ID NO:160; the light chain comprises the amino acid sequence as shown in SEQ ID NO:161, or an

amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:161, or consists of SEQ ID NO:161;

(22) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:169, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:169, or consists of SEQ ID NO:169; the light chain comprises the amino acid sequence as shown in SEQ ID NO:170, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:170, or consists of SEQ ID NO:170;

(23) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:174, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:174, or consists of SEQ ID NO:174; the light chain comprises the amino acid sequence as shown in SEQ ID NO:175, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:175, or consists of SEQ ID NO:175;

(24) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:181, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:181, or consists of SEQ ID NO:181; the light chain comprises the amino acid sequence as shown in SEQ ID NO:182, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:182, or consists of SEQ ID NO:182;

(25) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:191, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:191, or consists of SEQ ID NO:191; the light chain comprises the amino acid sequence as shown in SEQ ID NO:192, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:192, or consists of SEQ ID NO:192;

(26) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:200, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:200, or consists of SEQ ID NO:200; the light chain comprises the amino acid sequence as shown in SEQ ID NO:201, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:201, or consists of SEQ ID NO:201;

(27) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:206, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:206, or consists of SEQ ID

NO:206; the light chain comprises the amino acid sequence as shown in SEQ ID NO:207, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:207, or consists of SEQ ID NO:207;

(28) the heavy chain comprises the amino acid sequence as shown in SEQ ID NO:216, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:216, or consists of SEQ ID NO:216; the light chain comprises the amino acid sequence as shown in SEQ ID NO:217, or an amino acid sequence having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% , 99% or more sequence identity to the amino acid sequence of SEQ ID NO:217, or consists of SEQ ID NO:217.

8. The anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-7, wherein the antigen-binding fragment is selected from a Fab, Fab'-SH, Fv, scFv, or $(Fab')_2$ fragment.

9. The anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-8, wherein the antibody or antigen-binding fragment thereof binds MUC17 with an affinity of about 1×10^{-7} M or less.

10. An isolated nucleotide molecule encoding the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9, or a heavy chain variable region and/or a light chain variable region thereof, or a heavy chain and/or a light chain.

11. An expression vector comprising the nucleotide molecule of claim 10.

12. A host cell comprising the nucleotide molecule of claim 10 or the expression vector of claim 11.

13. An anti-MUC17 antibody-drug conjugate of formula (I), an isomer thereof, a pharmaceutical acceptable salt thereof, or a mixture thereof:

Ab-(L-D)m [Formula (I)]

wherein,

L is a linker unit;

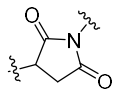
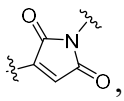
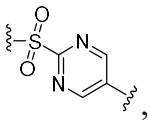
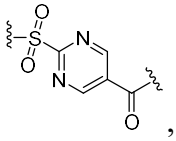
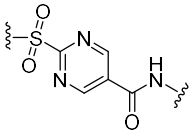
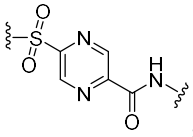
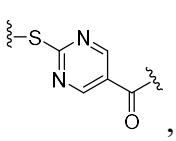
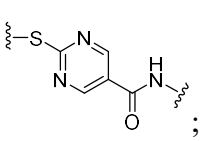
D is a cytotoxic small molecule drug;

m is an average number of L-D units conjugated to Ab, and m is selected from 1 to 10, preferably 2 to 8;

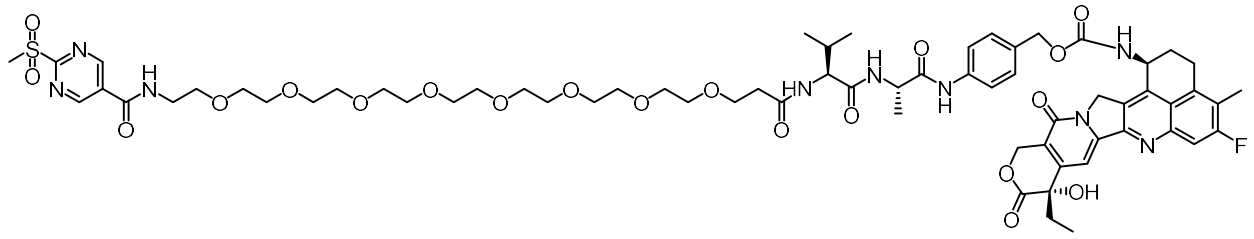
Ab is the anti-MUC17 antibody or the antigen-binding fragment thereof according to any one of claims 1 to 9.

14. The anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof according to claim 13, wherein, D is a monomethyl auristatins, camptothecins or mertansine alkaloids; the monomethyl auristatins may be monomethyl auristatin E (MMAE) or monomethyl auristatin F (MMAF); the camptothecins may be Exatecan, Dxd(1), Dxd(2), SN-38; the mertansine alkaloids may be DM1, DM3 or DM4; the antibody-drug conjugate comprises multiple D components, said multiple D components may be a combination of different therapeutic active substances or pharmaceutical active ingredients, or a combination of same therapeutic active substances or pharmaceutical active ingredients;

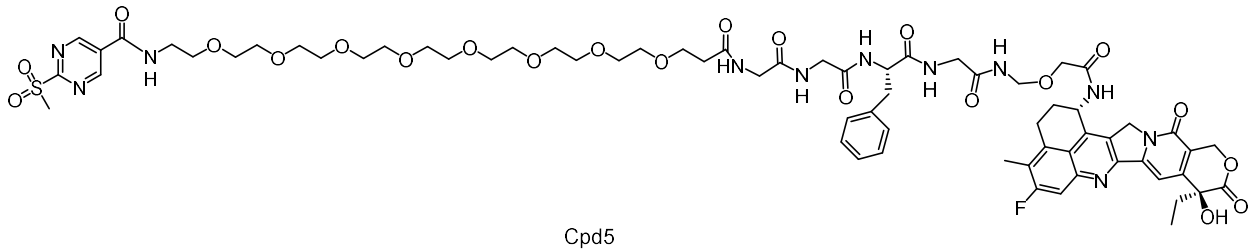
and/or, the L is a combination of one or more L', wherein the L' is selected from carbonyl, amino, amido, aminoacyl, -$(PEG)_n$-, -$(CH_2)_n$-, -$(CH_2)_n$- comprising a hetreoatom, -(C≡C)-, -(CH=CH)-, -O-, -S-, maleimido (mc), maleimide propionyl (MP), methylsulfonyl pyrimidinyl, valine-citrulline (val-cit), valine-alanine (val-ala), N-succinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate (SMCC), alanine-phenylalanine (ala-phe), phenylalanine-lysine (phe-lys), p-aminobenzyloxycarbonyl (PAB), dimethyl ethanediamine (DMED), N-succinimidyl 4-(2-pyridinylthio)pentanoate (SPP), N-succinimidyl 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (SMCC), N-succinimidyl (4-iodo-acetyl)aminobenzoate (SIAB), N-succinimidyl 4-(2-pyridinyldithio)butanoate (SPDB), N-succinimidyl 3-(pyridin-2-yldithio)-propionate (SPDP), glycine-glycine-phenylalanine-glycine (GGFG), acetyl-lysine-valine-citrulline-p-aminobenzyloxycarbonyl (AcLys-vc-PABC); n is independently selected from an integer of 1 to 20;

and/or, said L may be J-L_1-L_2-X-L_3; said J is selected from , , , , , , , ; L_1 is selected from a single bond, -$(PEG)_n$- or -$(CH_2)_n$-, said -$(CH_2)_n$- may optionally comprises 1 to 6 heteroatoms selected from N, O, S; wherein n is independently selected from an integer of 1 to 20; L_2 is selected from a combination of one or more of a single bond, -O-, -S-, -CH_2-, -NH-, -C(O)-; wherein said -CH_2- and -NH- may be optionally substituted 1 to 3 times by $C_{1\sim6}$ alkyl or halogen; X is selected from a single bond or a combination of 1 to 4 X', said X' is independently selected from amino acid; L_3 is selected from a combination of one or more of a single bond, -O-, -S-, -CH_2-, -NH-, -C(O)-, -phenyl-, -cyclopropyl-, -cyclobutyl -, -cyclohexyl-; wherein said -CH_2-, -NH-, -phenyl-, -cyclopropyl-, -cyclobutyl-, -cyclohexyl- may be optionally substituted 1 to 3 times by $C_{1\sim6}$ alkyl, halogen, cyano or hydroxy.

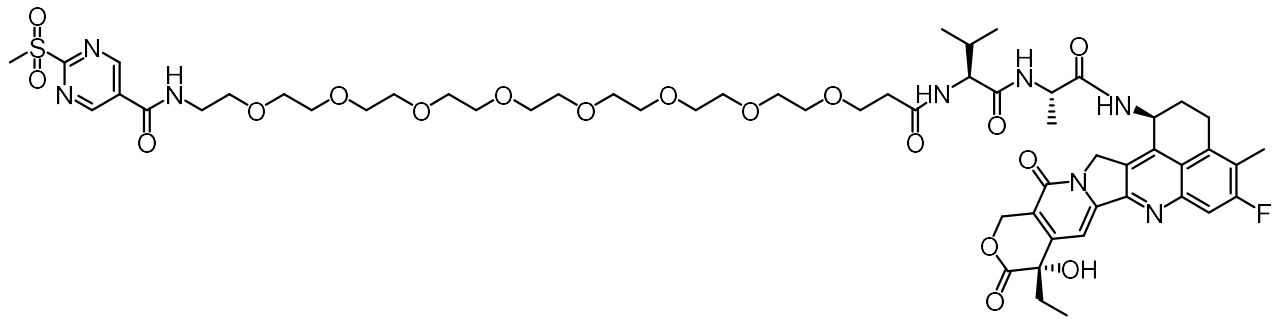
15. The anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof according to claim 13, wherein the (L-D) moiety is derived from a structure as shown in Formula Cpd3, Formula Cpd5 and Formula Cpd6:



Cpd3 ,

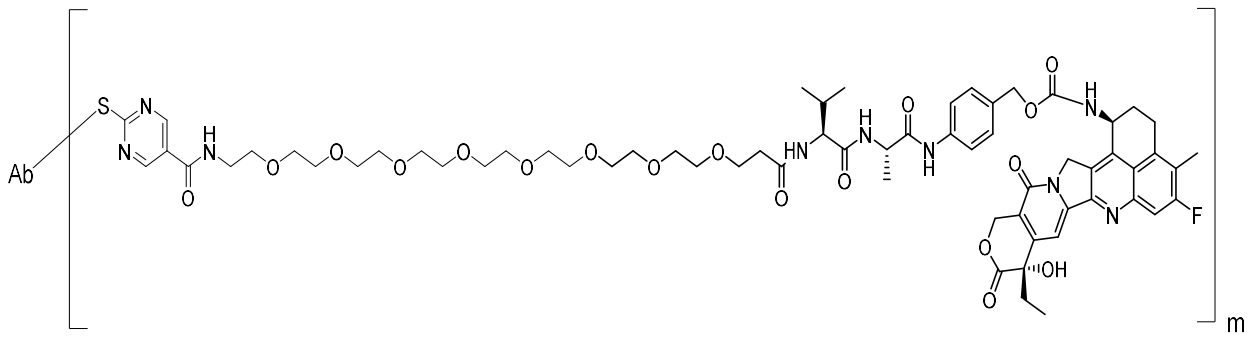


Cpd5 ,

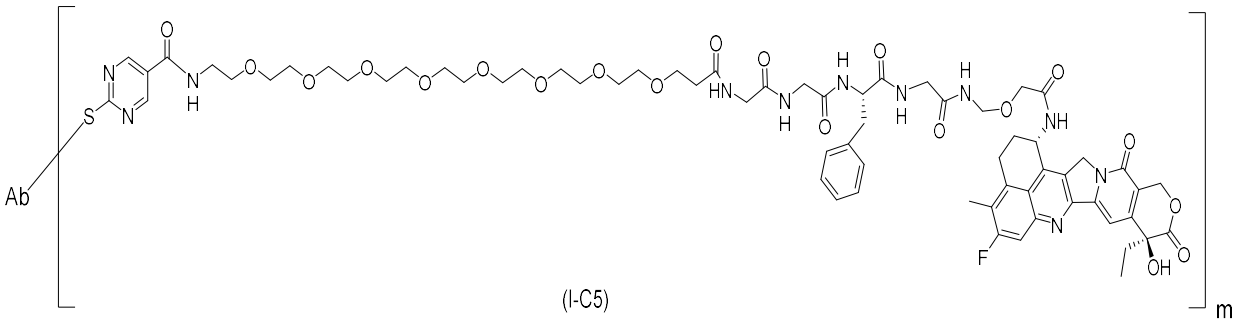


Cpd6 .

16. The anti-MUC17 antibody-drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof according to claim 13 or 15, wherein, the (L-D) moiety is conjugated with the sulfhydryl group on Ab by forming a thiopyrimidine structure, and the antibody-drug conjugate has a structure as shown in Formula (I-C3), Formula (I-C5) and Formula (I-C6):

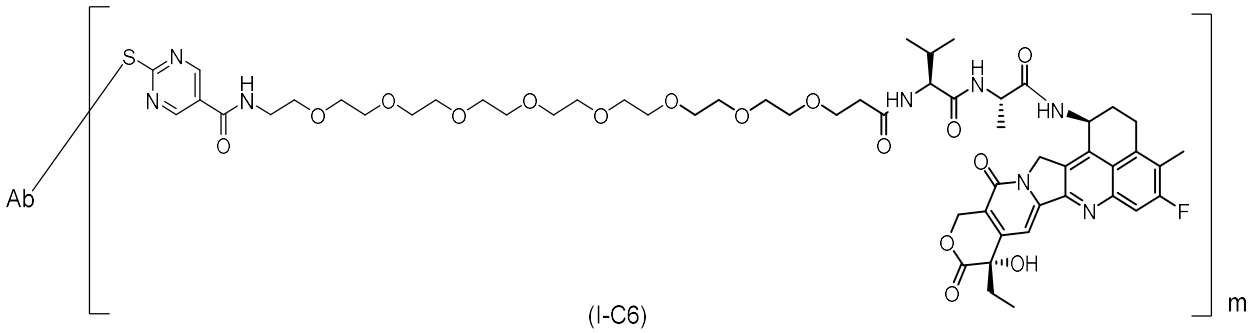


(I-C3) ,



(I-C5)

,

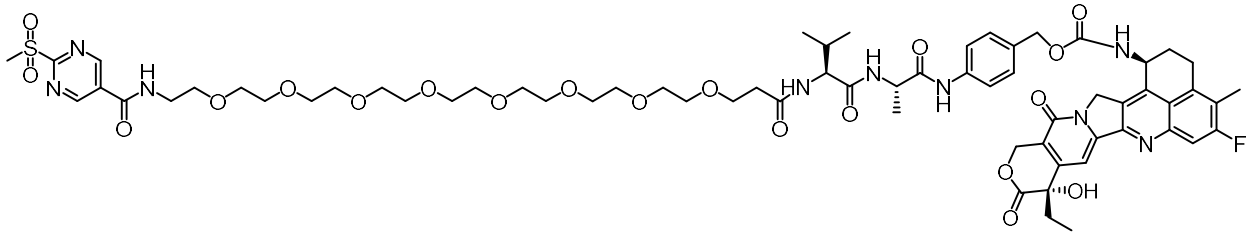


(I-C6)

,

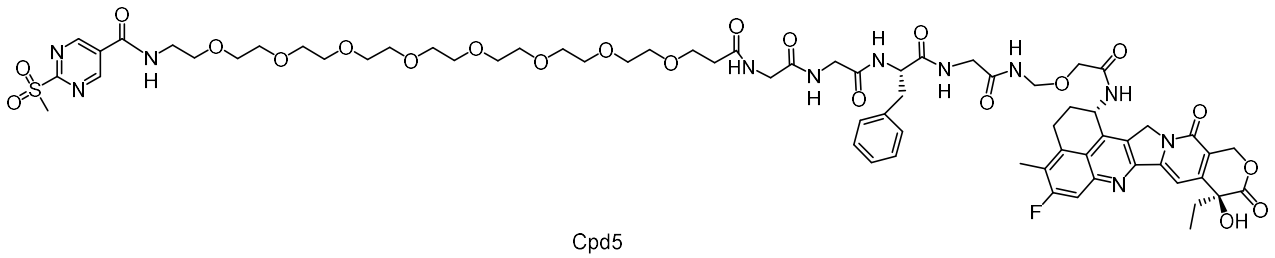
wherein m is an average conjugation number, and m is independently selected from 1 to 10; Ab is the antibody or the antigen-binding fragment thereof according to any one of claims 1 to 9.

17. A linker unit-cytotoxic small molecule drug selected from:



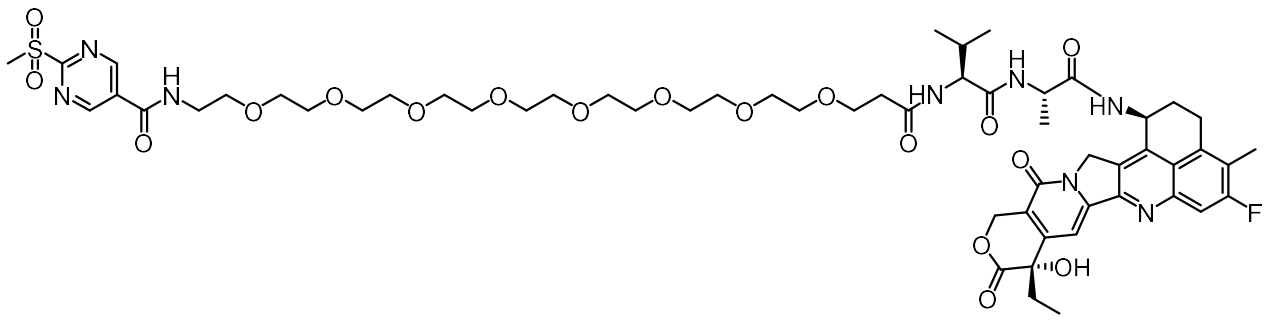
Cpd3

,



Cpd5

,



Cpd6

,

an isomer thereof, a pharmaceutical acceptable salt thereof, or a mixture thereof.

18. A composition comprising the anti-MUC17 antibody drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof according to any one of claims 13 ~ 16, wherein the molar ratio of D to Ab in the composition (DAR value) is a decimal or integer between 1 and 10.

19. A pharmaceutical composition comprising the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9, or the isolated nucleotide molecule of claim 10, or the expression vector of claim 11, or the host cell of claim 12, or the anti-MUC17 antibody drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof of any one of claims 13-16, or the linker unit-cytotoxic small molecule drug of claim 17, or the composition of claim 18, and a pharmaceutically acceptable excipient.

20. Use of the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9, or the isolated nucleotide molecule of claim 10, or the expression vector of claim 11, or the host cell of claim 12, or the anti-MUC17 antibody drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof of any one of claims 13-16, or the linker unit-cytotoxic small molecule drug of claim 17, or the composition of claim 18 or the pharmaceutical composition of claim 19, in the manufacture of a medicament for the treatment and/or prevention of a MUC17-associated disease or disorder.

21. A method of treating and/or preventing a MUC17-associated disease or disorder comprising administering to a subject in need thereof an effective amount of the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9, or the isolated nucleotide molecule of claim 10, or the expression vector of claim 11, or the host cell of claim 12, or the anti-MUC17 antibody drug conjugate, the isomer thereof, the pharmaceutical acceptable salt thereof, or the mixture thereof of any one of claims 13-16, or the linker unit-cytotoxic small molecule drug of claim 17, or the composition of claim 18, or the pharmaceutical composition of claim 19.

22. The use of claim 20 or the method of claim 21, wherein the MUC17-associated disease or disorder is a cancer and/or tumor selected from the group consisting of: gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junction cancer, gastric cardiac cancer, gastric body cancer, gastric antrum cancer, liver cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, renal cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer, and rectal cancer.

23. A detection system comprising the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9.

24. A method of detecting the presence or determining the level of MUC17 in a sample, comprising: (a) contacting the sample with the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9, and (b) detecting the formation of or determining the amount of an immune complex between the anti-MUC17 antibody or antigen-binding fragment thereof and MUC17 in the sample, to detect the presence of MUC17 in the sample or to determine the level of MUC17 in the sample; wherein the sample is a solid tissue sample or a liquid tissue sample.

25. Use of the anti-MUC17 antibody or antigen-binding fragment thereof of any one of claims 1-9 in the detection system of claim 23, or in the detection method of claim 24.

26. Use of the anti-MUC17 antibody and antigen- binding fragment thereof of any one of claims 1-9, the detection system of claim 23 in a method of diagnosing whether a subject suffers from a MUC17-associated disease or disorder,

preferably, the MUC17-associated disease or disorder is a cancer and/or tumour selected from the group consisting of: gastric cancer, esophageal cancer, pancreatic cancer, gastroesophageal adenocarcinoma, gastroesophageal junction cancer, gastric cardiac cancer, gastric body cancer, gastric antrum cancer, liver cancer, bile duct cancer, gallbladder cancer, melanoma, endometrial cancer, renal cancer, prostate cancer, breast cancer, triple negative breast cancer, colon cancer, colorectal cancer, lung cancer, bone cancer, skin cancer, head and neck cancer, uterine cancer, cervical cancer, ovarian cancer, and rectal cancer.

27. A method for detecting and/or quantifying MUC17 expression in a sample, comprising: (a) using the antibody or antigen-binding fragment thereof of any one of claims 1-9, or use of the detection system of claim 23, for determining the expression amount of MUC17 in a sample; and (b) comparing the expression amount of MUC17 determined in step (a) to: (i) a predefined value of MUC17 expression; (ii) an expression amount of MUC17 determined in a control, or (iii) an expression amount of MUC17 determined in a sample obtained from the same source or subject at a previous time point.